
Reviewer A:

Scientific merit:

The scientific merit of the **AOP Report** is high.

3R relevance:

The **AOP Report** addresses

- reduction of animal experiments.
- refinement of animal experiments (reduction of pain, suffering, distress and harm; improvement of animal welfare).
- replacement of animal experiments.

Overall impression:

The AOP Report

- discusses critically and objectively.
- considers the relevant literature.
- provides a vision for future developments.
- is targeted at an expert audience.

Language and structure:

Language and structure of the AOP Report

are excellent.

Figures:

Figures included in the AOP Report

are well designed and explained.

Comments for editor and authors

Please answer the following charge questions on the **AOP** in detail:

1. Scientific quality:

- Does the AOP incorporate all appropriate scientific literature and evidence?
- Does the scientific content of the AOP reflect current scientific knowledge on this specific topic?

2. Weight of evidence (WoE):

- Is the WoE judgement/scoring well described and justified based on the evidence presented? If not, please explain.
- Please consider WoE for each Key Event Relationship (KER) and the for the AOP as a whole.

1a. Yes, this AOP uses more recent studies. Particularly, updating that not just concentration but duration of SHH signal is affecting the AO in question is important to addressing the AO in question.

1b. Yes, it is up to date.

2a. Yes, more attention needs to be paid to the temporal dynamics of SHH signaling.

2b. They are acceptable

Reviewer B:

Scientific merit:

The scientific merit of the **AOP Report** is

high.

3R relevance:

The **AOP Report** addresses

- reduction of animal experiments.
- replacement of animal experiments.

Overall impression:

The AOP Report

- provides a good overview of the state of the art.
- discusses critically and objectively.
- considers the relevant literature.
- provides a vision for future developments.
- is targeted at an expert audience.

Language and structure:

Language and structure of the AOP Report

are mostly good (specific comments below).

Figures:

Figures included in the AOP Report

are well designed and explained.

Comments for editor and authors

Please answer the following charge questions on the **AOP** in detail:

1. Scientific quality:

a) Does the AOP incorporate all appropriate scientific literature and evidence?

b) Does the scientific content of the AOP reflect current scientific knowledge on this specific topic?

2. Weight of evidence (WoE):

- a) Is the WoE judgement/scoring well described and justified based on the evidence presented? If not, please explain.
- b) Please consider WoE for each Key Event Relationship (KER) and the for the AOP as a whole.

The AOP does seem to incorporate relevant scientific literature and evidence, although the subject matter is outside of my field of expertise. The scientific content seems to reflect the current state of the science.

The authors rationale for their weight of evidence calls is well explained and seems reasonable.

Please see attached file for my detailed review and suggestions for improvement.

We appreciate the detailed and constructive review of this work. We have worked to address the comments and have updated both the manuscript and the AOP-Wiki. We have focused on correcting wording of the KEs and KERs to ensure that they use consistent terminology and that all KEs and KERs are modular. We feel that these corrections have strengthened the AOP and the manuscript we have put together for it. We have included additional responses for the questions below.

Review of Altex AOP Report 460

The authors have developed an AOP linking antagonism of the smoothened receptor to orofacial cleft (OFC). Given the prominence of OFC as a birth defect, the AOP is of high relevance, and as the authors suggest, could help establish the relevance of NAMs for identifying pharmaceuticals or contaminants that could cause OFCs as a result of developmental exposures. The authors development conveys a fairly detailed understanding of the mechanistic processes which are organized into a series of key events and relationships to form the AOP. While much is known about the molecular and cellular processes of SHH signaling, the authors may want to consider whether quite as much detail is needed in terms of separate events for GLI translocation versus its subsequent effect on gene expression. However, lumping versus splitting is at the discretion of the authors and should be based on consideration of what type of indicator endpoints are likely to be measured. The graphical representation of the AOP includes a Key Event for “decrease palatal shelf outgrowth” but in the AOP-Wiki this is titled “decrease outgrowth” only. Adding the specificity for palatal shelf outgrowth is important relative to the way the KERs are structured and the way they are used in the AOP. In my opinion “decrease outgrowth” is not specific enough. Given their focus on the AOP and role of SHH signaling, many of the relationship descriptions either break modularity by making reference to other parts of the AOP that aren’t specifically involved in that relationship. That is inconsistent with the AOP framework and the goal of being able to share KEs and KERs among multiple AOPs and building AOP networks. Similarly, the terminology used doesn’t always match the level of resolution at which the events and relationships are described. While biologically, speaking terms like SHH signaling and GLI mediated expression may be more or less synonymous, for readers that are non-experts, using terms different than those in the Event and Relationship

titles may lead to considerable confusion. I would encourage the authors to really focus on aligning their text with the subject of each independent Event and Relationship page. With some additional revision, I believe this can be a strong and impactful contribution to the AOP-Wiki and the peer-reviewed literature. Specific comments are provided below, starting with the manuscript (comments identified by line number), then the AOP-wiki pages (comments identified by page ID and sub-heading).

1. Line 19. Can “GLI” be defined further, for example as glioma-associated oncogene? Perhaps Gli is the most widely used term.

Corrected

2. Line 24. “NAMs” (new approach methodologies) should be defined on first use.

Corrected

3. Line 25. Data are plural. The sentence should read “...data used to support this AOP were generated....”

Corrected

4. Line 30. Consider something like “This AOP report assembles evidence that links antagonism of the Smoothened (SMO) receptor to orofacial clefts (OFCs).”

Corrected

5. Line 33. While “facial prominences” is a correct technical term here, I’m not sure it is the optimal term to use in the plain language summary. Perhaps something like “early embryonic facial features”

Corrected

6. Line 39. Consider using key words that aren’t already in the title to increase findability during search.

Keywords

Sonic Hedgehog, cleft lip/palate, smoothened receptor, Craniofacial morphology , adverse outcome pathway

7. Line 54. Suggest either “...genetics and environment in the etiology...” or “...genetics and environmental factors in the etiology....”

Corrected

8. Line 82. Suggest “clear approach” instead of “clear mechanism”

Corrected

9. Line 83. “AOP wiki” should be “AOP-Wiki” throughout.

Corrected

10. Line 83. (AOPs, 2024) – unclear what this citation is referring to.

Corrected

11. Line 109. The abbreviation EMi is not used frequently in the text. Consider just spelling it out for clarity.

Corrected

12. Line 133. Should “HH” be “SHH” here? If not, it is likely to create confusion to use both HH and SHH as abbreviations in the paper.

Corrected to SHH

13. Line 152. The sentence “The schematic of AOP 460 appears....” can be deleted. Fig. 1 can be cited parenthetically right after “This AOP...” on line 151.

Corrected

14. Line 153. The project number the authors cite will be meaningless to most readers. Either provide more details about what kind of project you’re referring to (an AOP development project under the OECD Advisory Group on Emerging Science for Chemical Assessment (ESCA)), or remove reference to a specific project and just refer to a larger network of SHH-related AOPs.

Corrected

15. Line 157. Should use “KEs” instead of “Kes”

Corrected

16. Line 161. A significant portion of this sentence is redundant with that on lines 154-155.

Corrected paragraphs combined

17. Lines 161-169. This paragraph could be combined with the previous to provide the same information more concisely without redundancy.

Corrected paragraphs combined

18. Line 172. I don’t think it is necessary to list the “Development status” in the AOP ID Box. By definition, all AOPs that have not undergone a peer review according to OECD guidance on the scientific review of AOPs are regarded as “under development”. After the present review is completed, the status will change.

Deleted

19. Line 180. Provide a link or citation for PubMed.

Link added

20. Lines 180-181. Consider something like “details of the search terms employed and dates of each search are provided in Supplementary Table 1.” Alternatively, just delete the sentence “searches are organized by...” and replace it with the last sentence of this paragraph (Lines 184-185).

Corrected

21. Line 190. The sentence “Table 1 below....” Could be replaced with a simple parenthetical citation of Table 1 at the end of the preceding sentence.

Corrected

22. Lines 194-198. Perhaps more of a curiosity question, but are any of these SMO antagonists relevant as environmental contaminants, or would use of pharmaceuticals be the primary route of human exposure?

Good question. Of the chemicals mentioned, PBO is probably the most likely to have human exposure. The 2021 Rivera-Gonzalez paper we cite summarizes the route of exposure and sources of contamination. It is also important to note that Cyclopamine was identified through natural exposure when cyclopia in sheep was found to be linked to cyclopamine in the plant *Veratrum californicum*.

23. Line 201. Define GD as “gestational day” on first use.

Corrected

24. Line 203. Consider separately addressing both the empirical domain of the evidence (i.e., limited to mice), and the plausible domain (likely applicable to an array of mammals, perhaps

even other vertebrates). See “Development tip 6” of the AOP Developer’s Handbook - **Development tip 6 – Domain of applicability:** When defining domain of applicability, it is useful to think about it in two ways **Empirical domain of applicability:** Species, sexes, life stages, for which there is already demonstrable evidence that the measurement can be made (KEs), the relationship applies (KERs) or the AOP in its entirety is relevant (AOPs). **Biologically plausible domain of applicability:** The broad range of species, sexes, life stages for which the measurement (KE), relationship (KER), or AOP is likely to apply based on scientific reasoning (i.e., molecular conservation of targets/pathways; phylogenetic relatedness; similarity in life history; analogy). Authors are encouraged to present both, and to clearly distinguish between the two based on the “evidence calls” made in the structured table and/or the explanatory text provided in the free text field.

Good idea. We have added text to include the biologically plausible domain.

25. Line 227. SANT – undefined abbreviation

Corrected

26. Line 251. “...few studies have measured by outgrowth....” – awkward phrasing – perhaps some words missing?

Phrasing corrected

27. Line 281. Suggest deleting “for” from “...through binding studies for including....”

Corrected

28. Line 283-285. “while the level of support for most KERs is low....” – should that be the level of empirical support is low. Would you consider plausibility high, but empirical support being the type of evidence that is lacking? Plausibility is generally considered the strongest line of evidence. An AOP with strong plausibility and strong non-adjacent empirical support, but weaker empirical support in the adjacent KERS can often still be considered a well supported AOP.

Corrected

29. Line 289. The sentence “A summary of the dose-concordance....” could be replaced with parenthetical citation of Supplementary Table 2 at the end of the preceding sentence.

Corrected

30. Line 290. “Many studies were found to use a single exposure” – by “single exposure” do you mean a single concentration/dose of the test chemical?

Corrected

31. Lines 298-314. Temporal concordance primarily pertains to the empirical evidence supporting various KERs. The argument that is presented here is largely a plausibility-based argument. If there are a lack of studies where the temporal concordance could be assessed empirically, it is fine to state that. Many studies only measure outcomes at a single time point, so these data are often absent. Lines 301-307 are also highly redundant with similar statements already made in prior text.

Corrected- we have added text describing a lack of temporal concordance data and have removed the redundant text.

32. Lines 315-318. Not sure whether this adds much value.

Agreed section removed

33. Lines 319-338. Rather than a bulleted list of all the KERs for which there are data gaps, consider a more narrative discussion of which endpoints are rarely if ever measured, and the types of studies, currently lacking, that would be desired.

34. Line 345. Add year information for Corbit et al.

Corrected

35. Line 358. (53) should use author/year format consistent with the rest of references cited in the paper

Corrected

36. Lines 375-377. The following sentence could be made much more concise “Most of the data found through the literature was obtained from doses at a single dose and was not conducted with dose-response or time-course in mind.

Corrected

37. Lines 387-389. The following sentence could be more clear and concise “There is a need for development of NAMs to increase understanding of the....” – as currently written, I’m not sure it really adds much to the paragraph, and it is difficult to both understand what point the authors are trying to make and how it links to the sentences that follow. Perhaps it could just be deleted.

Corrected- sentence split and additional context added

38. Lines 382-434. This section as a whole seems to lack focus. The final sentence (lines 427-428) was the most direct, and to the point sentence among the whole section. Line 383 “This AOP can help serve as a guide linking *in vitro* chemical testing data to traditional *in vivo* adverse outcomes” – that is basically the entire point of the AOP framework. The authors seem to touch on the AOPs as a way to establish the relevance of NAMs for detecting/characterizing chemicals with potential to cause OFC. However, they also speak multiple times to using the AOPs to guide the development of NAMs and their organization into an IATA or defined approach. Those are all reasonable applications, but as currently structured, I find it hard to follow and the authors seem to dance around their point without directly stating it. Suggest revising this section to make it more clear and concise as a whole. Right now it seems like the authors were struggling to define their intended application(s).

We agree that the initial submission lacked focus. We have updated the section to increase the focus and make the points clear to the reader.

39. Table 1. Support for essentiality of the KEs section. The second two bullets don’t seem to pertain to essentiality per se. In general, evidence is evidence and I don’t think it’s productive to get too hung up on exactly the type of evidence, so I leave it to the authors to decide where these points fit. The key is to really critically assess how well the overall body of evidence supports a causal relationship between the sequence of KEs.

We agree that these points may not be the perfect fit for this table. After review we decided to leave them in as we felt they needed to be included and did not feel there was a more appropriate place.

40. Table 1. Empirical evidence for relationship 2894. **Dose-response:** Multiple studies demonstrate a dose dependent incidence of clefting – dose response concordance is not just a measure of whether the downstream event occurs in a dose-dependent manner. Rather, it considers the relative doses at which the upstream and downstream events occur. At what concentration is smoothed antagonized versus the concentrations that cause OFC. Concentrations that elicit the downstream effect should be equal to or higher than those that cause the effect defined by the upstream event (MIE in this case).

Good point. We have added additional text to make this distinction clear.

41. Supplementary Table 2. Useful. Highlights the approach to AOP development taken by the authors and helps to reinforce the authors points about the lack of studies designed for evaluation of temporal concordance, dose-response concordance, etc. (which is not uncommon).

42. AOP Page 460, Abstract: “This decrease in gene expression which causes a....” – could delete “which”

AOP-Wiki updated

43. AOP Page 460, Context: “The etiology of OFCs is complex with approximately 50% of CPO and 70% of CL/P considered non-syndromic (2011).” – add author information to the reference citation.

AOP-Wiki updated

44. AOP Page 460, Context: As per the Developer’s Handbook, Context is intended to define “Why” this AOP was developed. The information provided here is useful biological context/background, but it does not describe the authors’ motivations and goals. From the Handbook “This subsection describes key elements of *why* the AOP was developed and for whom (e.g., funding sources; stakeholders; etc.).” - <https://aopwiki.org/handbooks/5#section-1-%E2%80%93-aop-description-27>

This AOP was developed as part of a larger network of AOPs linking disruption of SHH signaling with OFCs (OECD Advisory Group on Emerging Science in Chemicals Assessment (ESCA) workplan project 1.101.). This was the first AOP of the network to be developed and was selected due most stressors of the SHH pathway being believed to work at the level of SMO. Development was led by the Johnson lab at Michigan State University and coached by Dr. Judy Choi. This AOP serves as the primary literature for graduate student Jacob Reynolds’ dissertation project. This work was supported by the National Institutes of Health R00-ES028744 and the National Institute of Environmental Health Sciences P42ES004911.

45. AOP Page 460, Strategy: As per the Handbook, the Strategy section is intended to describe “*how* the AOP was developed. Specifically, what was the strategy, focus and workflow for identification and assembly of relevant evidence to meet the objective/envisaged application?” – think of this as sort of the Methods section of an AOP development project. The early part of this section “*This AOP was developed as part of a larger network of AOPs linking disruption of SHH signaling with OFCs (EAGMST workplan project 1.101.). Orofacial clefts (OFCs) are one of the most common human birth defects and occur in approximately 1-2/1,000 live births (Lidral, Moreno et al. 2008). Early orofacial development involves epithelial ectoderm derived SHH ligand driving tissue outgrowth through an induced gradient of SHH dependent transcription in the underlying mesenchyme, which is thought to drive mesenchymal proliferation (Lan and Jiang 2009, Kurosaka 2015). The SHH pathway is sensitive to chemical disruption at multiple molecular targets along the signaling cascade, with exposure during critical windows in development leading to OFCs (Lipinski and Bushman 2010, Heyne, Melberg et al. 2015). The molecular targets of this disruption include SHH ligand modification with cholesterol and palmitoylate, ligand secretion, mesenchymal reception, and signal transduction (Jeong and McMahon 2002, Lauth, Bergström et al. 2007, Petrova, Rios-Esteves et al. 2013).*” Would probably align better with Context. Starting at “This AOP focuses on the disruption to SHH signaling resulting in antagonism of the SMO receptor. To select the key events for the AOP, we used....” The text is relevant to strategy.

Wiki updated- To select the key events for the AOP, we used existing knowledge of the pathway along with reviews of the SHH pathway to assemble a path that was physiologically plausible. Care was taken to select events that would be of direct regulatory relevance (i.e. a method to quantify exists). To identify sources and data for each Key Event Relationship (KER), Pubmed was used. Initially results were screened for relevance off title/abstract and any of suspected relevance were reviewed in full to determine their applicability for the KER. Each KER includes a table of relevant search information (date, search terms, citations, etc). It is the hope of the authors that this AOP is used as a tool for risk assessment for drug and chemical exposures during embryonic development when disruption to SHH through antagonism of SMO occurs.

46. AOP Page, 460. As per the handbook, “Prototypical stressors Prototypical stressors are stressors for which responses at multiple KEs in addition to the MIE have been well documented. Experiments with the prototypical stressor(s) may have provided much of the empirical support for the AOP and/or quantitative understanding of the KERs. Thus, prototypical stressors identified may serve as useful “positive controls” for evaluating responses of other stressors that may act on this pathway and/or provide insights into the types of structures or properties that may be relevant to the stressor domain that is relevant to this AOP. The relative potency of various other stressors, compared to the prototypical stressor(s) may also be informative relative to quantitative understanding of the KERs and associated applications of the AOP.” Please critically evaluate whether all the stressors listed meet the definition. Based on some of the uncertainty around cyclopamine, for example, perhaps that should not be listed. The goal is not to provide a comprehensive list, but rather a small number of stressors that are emblematic of the AOP.

We have reviewed the provided list and have removed cyclopamine and PBO from the prototypic stressors. While we are confident that these compounds antagonize SMO, we agree that they may not have the level of evidence to classify as prototypic stressors for this AOP.

47. AOP Page 460. Domain of applicability – chemical. PBO should be spelled out on first use to make it clear you’re referring to piperonyl butoxide.

Wiki updated

48. AOP Page 460. Domain of applicability – taxonomic. Would it more appropriate to indicate that the empirical domain of the applicability is mouse. Consider remarking on the plausible domain of applicability as well. Seems like it would apply pretty broadly to mammals. Not necessarily to non-mammalian vertebrates though.

Wiki updated- Taxonomic: At present, the empirical taxonomic applicability domain of this AOP is mouse (*mus musculus*). Most of the toxicological data that this AOP is based on has used mice as their model organism. Mice are a good analog of human craniofacial development and undergo similar signaling by SHH. The plausible domain of applicability for this AOP is mammals due to the largely conserved mechanisms of orofacial development and embryonic pathway signaling.

49. AOP Page 460. Relationship 2726. “OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced mesenchymal?” – sentence should end with a period, not a question mark.

Wiki updated

50. AOP Page 460 – Biological plausibility section – “Multiple antagonists of the SMO receptor have been identified through [binding studies for including] cyclopamine, vismodegib, PBO, and the SANT compounds” - missing word(s) and/or punctuation in area indicated by brackets.

Wiki updated- Multiple antagonists of the SMO receptor have been identified through binding studies. Identified SMO antagonists include cyclopamine, vismodegib, PBO, and the SANT

compounds (Lipinski, Dengler et al. 2007, Lipinski, Song et al. 2010, Wang, Lu et al. 2012, Everson, Sun et al. 2019, Rivera-González, Beames et al. 2021).

51. AOP Page 460 – Concordance of dose-response relationships – Concordance is evaluated under empirical evidence. In general, the section would benefit from some reorganization and streamlining. Currently doesn't flow well.

Agreed, Wiki updated- There are a limited number of studies in which multiple key events were assessed in the same study following exposure to known SMO antagonists. These studies form the basis of the dose-response concordance of this AOP. A summary of the dose-concordance can be found in Supplementary Table 2. Many of the studies identified while researching this AOP were performed using a single dose of antagonist making the study not suited for dose response concordance. This AOP would benefit greatly from increased studies designed to explore the dose-response concordance of the proposed relationships. The concentration-dependence of the key event responses regarding concentration of known in vitro and/or in vivo for some of the KEs in this AOP is summarized below.

- Concentration dependent clefting with cyclopamine exposure (Omnell, Sim et al. 1990)
- Dose dependent binding to SMO (Chen, Taipale et al. 2002)
- Concentration dependent decrease in SMO-ciliary accumulation in vitro for vismodegib exposure (Wang, Arvanites et al. 2012)

52. AOP Page 460. Temporal concordance. Much of this section pertains more to plausibility, chemical modulators. Its really only the final statement that has much to do with temporal concordance. Consider removing most of the extraneous text and keep this focused.

Otherwise, the user of the AOP has to constantly sift through redundant background and over-exposition to find the key information they are looking for in each section.

Wiki updated- extraneous text removed last sentence retained

53. AOP Page 460 – assessment of the quantitative understanding of the AOP: “Most of the data found through the literature search was obtained from doses at a single dose and was not conducted with dose-response or time-course in mind.” - Perhaps instead something like “...was obtained from studies that employed a single dose....”

Most of the data found through the literature search was obtained from studies that employed a single dose and were not conducted with dose-response or time-course in mind.

54. AOP Page 460 – considerations for potential applications of the AOP: This section on the AOP page is much better focused than that in the accompanying AOP report.

55. Event 2027 – life stages: “Aberrant activation of HH signalling is known to cause cancer (Dahmane, Lee et al. 1997, Kimura, Stephen et al. 2005).” The relevance of this defining the life stage applicability of this key event is not clear. Suggest deleting.

Wiki updated- we felt that including both the embryonic and cancer angle supports the defined life stages. “Life stages- The Hedgehog pathway is a major pathway in embryonic development. While the pathway is largely inactive following development, aberrant activation of SHH signaling is known to cause cancer (Dahmane, Lee et al. 1997, Kimura, Stephen et al. 2005). For these reasons all stages of life are of relevance.”

56. Event 2027 – taxonomic. If SMO is conserved in both vertebrates and invertebrates, why are the controlled vocabulary terms for taxonomic applicability limited to vertebrates?

Wiki updated- this was a oversight since I was thinking only in the context of AOP 460

57. Event 2027 – How it is measured or detected. QPCR cannot be used to determine antagonism of SMO, therefore, should not be included here.

Wiki updated- removed

58. Event 2044 – Life stage – can a decrease in SMO relocation and activation only be determined in embryos? If not, the KE itself should be applicable to more life stages, even if the rest of the AOP is not.

[Wiki updated- All life stages added](#)

59. Event 2028 – Life stage – does translocation of GLI1/2 only occur during embryonic development? If it occurs later in life as well, the life stage applicability of this KE should be expanded, even if the rest of the AOP does not apply to later life stages. Also, the text contradicts the controlled vocabulary selection – which indicates all life stages are relevant.

[Wiki updated- All life stages added](#)

60. Event 2040 – Sex – “....and differences in gene expression has not been demonstrated....” - “has” should be “have”

[Wiki updated](#)

61. Event 2040. Life stages – only refers to HH pathway. In order for this to make sense to readers, the role of GLI1/2 as part of the HH pathway should be stated as part of this line of argument.

[Wiki updated- Life stages- The Hedgehog pathway with the main transcription factors of GLI1/2 is a major pathway in embryonic development. Aberrant activation of HH signaling is known to cause cancer \(Dahmane, Lee et al. 1997, Kimura, Stephen et al. 2005\). For these reasons all stages of life are of relevance](#)

62. Event 2040. Key Event Description – “...on SMO is relieved. SMO this then able to....” – “this” should be “is”

[Wiki updated](#)

63. Event 1262. I realize the current authors may not have been responsible for this Key Event description, but the following information violates the modularity of KE descriptions that is recommended in the AOP Developer’s Handbook as well as other guidance on AOP development “Several stimuli such as hypoxia, nucleotides deprivation, chemotherapeutical drugs, DNA damage, and mitotic spindle damage induce p53 activation, leading to p21 activation and cell cycle arrest [Pucci et al., 2000]. The SAHA or TSA treatment on neonatal human dermal fibroblasts (NHDFs) for 24 or 72 hrs inhibited proliferation of the NHDF cells [Glaser et al., 2003]. Considering that the acetylation of histone H4 was increased by the treatment of SAHA for 4 hrs, histone deacetylase inhibition may be involved in the inhibition of the cell proliferation [Glaser et al., 2003]. The impaired proliferation was observed in HDAC1-/- ES cells, which was rescued with the reintroduction of HDAC1 [Zupkovitz et al., 2010]. The present AOP focuses on the p21 pathway leading to apoptosis, however, alternative pathways such as NF-kappaB signaling pathways may be involved in the apoptosis of spermatocytes [Wang et al., 2017].”

[We agree that this text of this KE violates the modularity of the KE. We did not create or edit this event and do not feel it is our responsibility to edit this information. This event is shared by so many authors that getting consent from all authors that use this AOP would likely prove problematic and time-consuming. We brought this concern up with our Coach \(Judy Choi\) and she was going to bring this concern up to the OECD advisory group and the other AOP coaches.](#)

64. Event 2043. Ok

65. Event 1821. Ok

66. Event 2041. Event component – since the process terms relate to failure to meet at midline and abnormal shelf fusion, shouldn’t the action term in the event components be increased?

This event focuses on the outgrowth of the palatal shelves, not specifically fusion. We updated the event components to now include the process “palatal shelves fail to meet at midline” with objects of primary and secondary palate and action increased. Upon further review of the KE we decided to remove the components regarding fusion as the event focuses on tissue outgrowth, not on the process of fusion. We feel that while the event components are increased, the KE focuses on the outgrowth of the tissue which in this case is decreased.

67. Event 2042. Title – there should be an action term like “increased”

[Wiki updated- Increase, Orofacial clefing](#)

68. Relationship 2734. Relationship description – the following sentence does not seem relevant to this specific relationship “This relocation then leads to signaling to effectors resulting in the activation of the GLI transcription factors and the subsequent induction of HH target gene expression (Alexandre, Jacinto et al. 1996, Von Ohlen and Hooper 1997).”

[Wiki updated- sentence removed](#)

69. Relationship 2734 – in vitro – presumably um should be μ M (micromolar, not micrometers)

[Wiki updated- u to \$\mu\$](#)

70. Relationship 2734 – in vivo – the first evidence bullet would be better suited for relationship 2894. “The presence of critical periods for disruption of SHH was investigated using C57BL/6J mice. Vismodegib was suspended at 3mg/ml in 0.5% methyl cellulose and 0.2% tween. Pregnant dams were administered 40mg/kg vismodegib at GD7.0, 7.25, 7.5, 7.75, 8.0, 8.25, 8.5, 8.625, 8.75, 8.875, 9.0, 9.25, 9.5, 9.75, and 10.0. Cyclopamine was dosed at 120mg/kg/d via subcutaneous infusion between GD8.25-9.375. Pregnant dams were euthanized at GD17 and fetal specimens were collected and fixed for imaging. The control group consisted of fetuses exposed to 0.5% methyl cellulose and 0.2% tween at GD7.75, 8.875, or 9.5. Acute exposure to vismodegib resulted in a peak incidence of lateral cleft lip and palate at GD8.875 (13%). Exposure at GD9.0 and 10.0 resulted in clefts of the secondary palate only (34%). A higher penetrance (81%) was found for cyclopamine exposure (Heyne, Melberg et al. 2015).”

[We agree that this study is not directly relevant to KER 2734. We have removed it from KER 2734 and have made sure it is included in KER 2894.](#)

71. Relationship 2734 – in vivo – the following line of evidence does not seem to directly pertain to SMO antagonism leading to SMO relocation. “To explore how a conditional loss of primary cilia on neural crest cells Kif3af/f Wnt1-Cre mice were used to explore the molecular basis of aglossia. Aglossia was found to be due to a lack of mesoderm derived muscle precursor migration. RNA-seq was used on E11.5 embryos on the mandibular prominences of wildtype and knock mice. The key SHH readout, GLI1 was downregulated two-fold in mutants (Millington, Elliott et al. 2017).”

[We agree that these data are not directly relevant to the KER in question. It has been removed and the Wiki updated.](#)

72. Relationship 2735. “and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs)” – this statement is specific to the AOP and does not pertain to this specific relationship. Suggest deleting to maintain modularity of the Relationship. Same comment for “Multiple ciliopathies are associated with clefting in humans including Meckel-Gruber syndrome (OMIM 249000) and Ellis-van Creveld syndrome (OMIM 225500)(Brugmann, Cordero et al. 2010).”

[Wiki updated](#)

73. Relationship 2735 – in vivo – the fact that GLI1 was downregulated in mutants that develop aglossia does not seem pertinent to a relationship between decreased relocation of SMO and

activation of GLI1/2. None of the bullets under the in vivo subheading seem to speak directly to the two Events that make up this relationship.

We agree that the data reported here is not specific to the relationship in question. We have removed it and updated the wiki.

74. Relationship 2735 – uncertainties and inconsistencies. It would be helpful if the authors could add a sentence or two regarding why knowing the exact mechanism of SMO ciliary trafficking is critical to understanding whether or not SMO relocation will activate GLI1/2.

Good idea. We have added the following text to the Wiki. “Improving understanding of SMO ciliary trafficking will increase the fields’ understanding of SHH signaling. Understanding the mechanisms at play will help identify when SMO relocation will affect the SHH signaling cascade and subsequent GLI1/2 translocation.”

75. Relationship 2735 – quantitative understanding – it is not clear to me why the role of SUFU in SHH signal transduction is relevant to this particular relationship.

We have updated the section. “The data presented in support of this KER includes in vitro studies. The in vitro work offers data that SMO relocates to the tip of the primary cilium and that this plays a role in the translocation of the GLI transcription factors to the nucleus. The quantitative understanding of this linkage is low as studies including dose-response and time-course were not found.”

76. Relationship 2721 – “The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs). For this reason, this KER is applicable to the embryonic stage with a high level of confidence.” – the domain of applicability for the relationship should be evaluated solely on the taxa, species, and life stages for which the GLI translocation leading to decreased GLI target gene expression is relevant. The fact that the rest of the AOP leads to OFC which is only relevant during development does not affect the domain of applicability for this particular relationship, which can be shared with other AOPs (same comment applies to Relationships 2731,2732, 2724, 2882 as well).

Thank you for catching this. We have reviewed the mentioned events and have removed the problematic text to ensure modularity of the KERs.

2721, 2731,2732, 2724, 2882 - Wiki updated text removed

77. Relationship 2721 – in vivo. The following line of evidence does not appear to have any direct relationship to GLI (at least none is clearly stated). “To study whether SHH signalling regulates the developmental fate of the ecto-mesenchyme via regulation of gene activity in the facial primordia, Wnt1-Cre;Smon/c, (removal of SHH signalling) and Wnt1-Cre;R26SmoM2 (activation of SHH signalling). Positive regulation from SHH activity was found for Foxc2, Foxd1, Foxd2, Foxf1, and Foxf2. The Fox genes were found to be dissimilar in expression pattern with spatial activation even with uniform activation of the SHH pathway. Foxc2 and Foxd1 were found to be expressed ubiquitously in the MNA except at the midline, while Foxf1 is expressed at the lateral ends. Foxd2 and Foxf2 are both expressed along the mediolateral axis with Foxd2 having an increasing gradient from medial to lateral and Foxf2 having an opposing gradient (Jeong, Mao et al. 2004).”

We agree that as originally written the connection to GLI1/2 is not apparent. We have added additional text including: “These data support that disrupting GLI1/2 translocation via disruption of the SHH signaling pathway disrupts transcription of Foxc2, Foxd1, Foxd2, Foxf1, and Foxf2.” The Wiki has been updated.

78. Relationship 2731 – Here and elsewhere it may be confusing for readers if the authors use shh target gene expression and GLI target gene expression more or less interchangeably. The

relationship speaks to GLI – therefore the text should make it clear that what you’re referring to is GLI-mediated expression. This is a significant issue that makes the relationship description and evidence hard to follow. The relationship between the broad term SHH signaling and the role of GLI may be obvious to experts in this biology, but it is critical that users of the AOP, who will not necessarily be experts on this topic, can follow the logic and lines of evidence.

We have reviewed the event and updated the text to be expand on the relationship between SHH and GLI and specify GLI mediated transcription.

79. Relationship 2731 – The following has nothing to do with this specific relationship. Breaks the modularity of the relationship description: “A network of reciprocal growth factor signaling between the epithelium and mesenchyme is required for proper growth and patterning of the early palatal shelves.” Could start with “Activation of the SHH pathway...” – but even that isn’t entirely modular, as the relationship is focused on GLI mediated gene expression, which seems more specific.

We have removed this text from the Wiki.

80. Relationship 2731 – An explicit statement or list of “the following genes are thought to be regulated by GLI as a component of SHH signaling”, or something to that effect, may be useful: e.g., BMP2, BMP4, Fgf10

Wiki updated- Activation of the Sonic Hedgehog (SHH) pathway results in a downstream signaling cascade resulting in the relocation of GLI to the nucleus and subsequent gene transcription (Carballo, Honorato et al. 2018). This gene expression drives secondary messenger signaling for the pathway. The following genes are believed to be regulated by GLI as a component of SHH signaling: FGF10, BMP2, BMP4.

81. Relationship 2732 – “A network of reciprocal growth factor signaling between the epithelium and mesenchyme is required for proper growth and patterning of the early palatal shelves.” – this sentence is outside of the scope of the current relationship. Same applies to “Activation of the SHH pathway results in a downstream signaling cascade resulting in the relocation of GLI to the nucleus and subsequent gene transcription (Carballo, Honorato et al. 2018)”

Wiki updated- text removed

82. Relationship 2732 – Unclear how the current lines of evidence relate to cell proliferation “To determine if SHH can induce Fgf10, SHH overexpressing cells were implanted in the anterior region of the wing bud of chick embryos. By 27 hours, the expression of Fgf10 had significantly increased and expanded from the anterior mesenchyme to the bifurcating wing bud (Ohuchi, Nakagawa et al. 1997). To investigate whether MSX-1 is in the same pathway as Fgf10, MSX-1 expression was examined in Fgf10-/- mice and Fgf10 expression was examined in Msx-1-/- mice. No change in.....”; “Fgf8 activity was found to sustain ccnd 2 expression in the neural groove and that the attenuation of fgf signalling is necessary for the up regulation of ccnd 1. This was conducted using chick embryos and replacing a small piece of the rostral presomitic mesoderm with an Fgf8 soaked bead. To test the necessity of the Fgf pathway, SU5402 treatment was used (Lobjois, Benazeraf et al. 2004). Cyclopamine treatment of stage 9-10 chick embryos in the neural tube and neural groove resulted in a strong down regulation of ccnd 1 transcripts as well as SHH target genes (e.g. Gli1). Toxicity was assessed using sox2 and effects due to non-specific toxicity were not found. Ccnd 2 expression was not affected by cyclopamine treatment. This suggests that the initiation of ccnd 1 in the neural groove is SHH dependent while ccnd 2 is not (Lobjois, Benazeraf et al. 2004).

We have revised the list of evidence with a focus on relating to the specific relationship. The problematic lines noted have been removed.

83. Relationship 2724 – Title “decrease outgrowth” – outgrowth of what? Event title and associated relationship title should convey more clearly what kind of “outgrowth” the event

refers to. Remember, the event and relationship pages are modular and should be able to stand independent of the specific AOP they are linked to. Probably should be “decrease outgrowth of facial prominences” or “outgrowth of palatal shelf”

We have updated this to decrease, facial prominence outgrowth. While KE 2041 was titled correctly, we had the short name simply as decrease, outgrowth. This has been corrected and updated.

84. Relationship 2724 – KER description – without better defining what kind of “outgrowth” is being referred to, the paragraph on the development of the face seems out of context – or at least unclear why this is here.

We have updated the title to include specificity to the facial prominences.

85. Relationship 2726 – More specificity to “decrease outgrowth” is needed for OFC to make sense. Also, because the short title of the Event is used for the KER title, I would recommend spelling out orofacial cleft even in the short title of the OFC event.

Wiki updated- Decrease, facial prominence outgrowth leads to orofacial cleft

86. Relationship 2792 – This statement would make more sense here if outgrowth was specifically defined as outgrowth of facial prominences or palatal shelf “The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs).”

Wiki updated- facial prominences specified

87. Relationship 2792 – The last sentence of the KER description is the only one that seems to make any reference to the role of apoptosis in the outgrowth process. The relationship to apoptosis should be better explained.

Wiki updated- we agree that the original description was lacking. We have added additional text and references to better explain the role that apoptosis is believed to play in cleft formation.

88. Relationship 2792 – this specific relationship has nothing to do with SHH signaling (should be able to exist independent of its relationship to SHH signaling). Therefore, under biological plausibility “The SHH pathway is known to be associated with cell survival and that disruption of SHH signaling can lead to increased apoptosis.” Doesn’t really have anything to do with the current relationship.

Wiki updated- text pertaining to SHH removed.

89. Relationship 2792 – the following lines of evidence have no direct relevance to this relationship, as they make no mention of apoptosis “SHH expressed in thickened palatal epithelium prior to palatal shelf outgrowth (E13.0-14.5) (Rice, Connor et al. 2006) SHH is expressed in oral epithelium and shown as a key signal for palatal shelf outgrowth in explant culture (Lan and Jiang 2009).”

Wiki updated- we have removed the evidence that does not directly relate the events in question.

90. Relationship 2792 – the relationship is between apoptosis and outgrowth, so why is the “uncertainties and inconsistencies” section focused on SHH and cell survival. Again, this may seem obvious to the authors, but will be confusing for readers who are non-experts.

Wiki updated- this was a problem with modularity. We have corrected the wiki to remove mention of SHH and focus only on apoptosis and orofacial development.

91. Relationship 2882 – The current relationship description has nothing to do with the two key events being linked here. The description should be completely revised.

Wiki updated- we agree that the initial description was lacking. We have revised and updated it.

92. Relationship 2882 – the first sentence of “biological plausibility” is not relevant to this relationship. Delete or revise.

[Wiki updated- deleted](#)

93. Relationship 2882 – in vivo – good, these lines of evidence are directly relevant to the two events being linked

94. Relationship 2894. The in vitro data basically establish the types of stressors that one would predict to lead to OFCs if this relationship holds up. Might want to add a sentence explaining that relationship to the in vivo evidence since OFC itself cannot be evaluated in vitro.

[Good idea. We have updated the Wiki to include text to explain this connection.](#)

95. Relationship 2894. The relevance of this line of evidence to relationship 2894 is unclear “To explore how a conditional loss of primary cilia on neural crest cells Kif3af/f Wnt1-Cre mice were used to explore the molecular basis of aglossia. Aglossia was found to be due to a lack of mesoderm derived muscle precursor migration. RNA-seq was used on E11.5 embryos on the mandibular prominences of wildtype and knock mice. The key SHH readout, GLI1 was downregulated two-fold in mutants (Millington, Elliott et al. 2017).”

[Wiki updated- this entry has been removed.](#)

96. Relationship 2894. Uncertainties. Whether or not cyclopamine blocks SMO relocation to primary cilia has no relevance to the pair of KEs linked by this relationship. Suggest removing from this KER. Similarly under time scale, it is unclear why the authors are focused on “relocation” which is not relevant to this particular KER.

[Wiki updated- we have removed the text relating to SMO relocation and have updated both the uncertainties and time scale sections.](#)

1 **Article type:** AOP Report

2 **Title:** AOP 460: Antagonism of Smoothened receptor leading to orofacial clefting

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10 **Summary**

11 Sonic Hedgehog (SHH) is a major intercellular signaling pathway involved in the orchestration of
12 embryogenesis, including orofacial morphogenesis. The SHH pathway is sensitive to disruption, including
13 both genetic predisposition as well as chemical induced disruption at multiple molecular targets
14 including antagonism of the SHH signal transducer Smoothened (SMO). Here we report the Adverse
15 Outcome Pathway (AOP) that describes the linkage between antagonism of the SMO receptor, a key
16 intermediate in the Hedgehog signaling and orofacial clefts (OFCs) (AOP 460 in the Collaborative
17 Adverse Outcome Pathway Wiki). Multiple antagonists of SMO have been identified including natural
18 compounds, synthetic pharmaceuticals, and a common pesticide synergist. Activation of the SHH
19 pathway causes a signaling cascade that culminates with the transcription of genes driven by glioma-
20 associated oncogene (GLI) transcription factors. When SMO is antagonized during normal development,
21 the cascade is disrupted causing myriad phenotypes at different critical windows of exposure ranging
22 from major structural defects and spontaneous abortion early in gestation to reduced outgrowth of the
23 facial prominences and the formation of an OFC later in development. There is high evidence that
24 antagonism of SMO causes OFCs that include a dose response relationship with incidence of clefting.
25 Several emerging new approach methodologies (NAMs) offer the ability to monitor intermediate key
26 events and test for temporal and dose response relationships *in vitro*. While most data used to support
27 this AOP were generated using mouse (*Mus musculus*) models during embryonic development, SHH and
28 the development of the face is largely conserved between mouse and human making this AOP able to
29 be extrapolated to risk assessment for human exposures.

30 **Plain language summary**

31 This AOP report assembles evidence that links antagonism of the Smoothened (SMO) receptor to
32 orofacial clefts (OFCs). The Sonic Hedgehog (SHH) pathway, crucial for orofacial development, can be
33 disrupted by various SMO antagonists. Inhibiting SMO during critical developmental windows disrupts
34 the SHH pathway, leading to reduced growth of early embryonic orofacial features and the formation of
35 OFCs. This AOP was found to have high biological plausibility, but with multiple data gaps in dose
36 response or time course data. This AOP is intended to serve as a tool for risk assessment for drug and
37 environmental exposures during embryonic development. It is hoped that the information presented

38 can help form a basis for the development of new approaches to testing to reduce the animal testing
39 burden.

40 **Keywords**

41 Sonic Hedgehog, cleft lip/palate, smoothened receptor, craniofacial morphology, adverse outcome
42 pathway

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49 **1. Introduction and background**

50 Orofacial clefts (OFCs) are one of the most common structural human birth defects and occur in
51 approximately 1 in 700 live births (Mossey et al., 2009; Dixon et al., 2011a). Elucidating the complex
52 etiologies that underly OFCs is paramount to working towards the goal of reducing OFCs. Many genetic
53 sequencing studies on children with OFCs and their family have been completed, yet approximately 80%
54 of OFCs are found to be of an unknown origin (Yaqoob et al., 2013; Feldkamp et al., 2017), reviewed in
55 (Ye and Ahmed, 2022). Twin studies suggest complex genetics and environmental factors in the etiology
56 where monozygotic twins have a 50% proband concordance and dizygotic twins have a concordance
57 rate of 8% for cleft lip with or without cleft palate (CL/P) indicating a role of both genetics and
58 environmental in the etiology of CL/P (Lin et al., 1999; Grosse et al., 2011).

59 Contributions to OFCs from environmental causes, including chemical exposures to human populations
60 during critical windows of development is highly probable but remains underexplored. Using data from
61 the 2014 US EPA ToxRefDB V1.0 dataset, we identified that 37 of 672, or 5.5% of all chemicals tested for
62 prenatal developmental toxicity in animal models showed an increased incidence of cleft lip and/or
63 palate (2014). In humans, maternal smoking has been shown to have a moderate role in etiology
64 increasing the odds ratio for OFC incidence to 1.42 (reviewed in (Fell et al., 2022)). Variants in GSTT1
65 (glutathione S-transferase theta) or NOS3 (nitric oxide synthase 3) have been found to increase the risk
66 of clefting when combined with maternal smoking indicating that gene-environment interactions also
67 play a role in OFC etiology (reviewed in (Dixon et al., 2011b)).

68 There are tens of thousands of chemicals in commerce that have not undergone developmental and
69 reproductive toxicity (DART) testing and new strategies are required to evaluate and prioritize further
70 testing of these compounds. Both the critical window of orofacial development sensitive to exposure
71 and multifactorial causes of disruption challenge elucidation of the underlying disruptions leading to
72 OFCs, but some established mechanisms are known. Orofacial development requires precise signaling
73 through multiple pathways including Sonic Hedgehog (SHH), transforming growth factor beta (TGF- β),
74 bone morphogenic protein (BMP), epidermal growth factor (EGF), Wingless (WNT), and other pathways
75 (Bush and Jiang, 2012; Jiang et al., 2006; Lan et al., 2015). Environmental disruption of these primary
76 morphogenetic signaling pathways in the embryo can lead to OFCs. The SHH pathway is known to have
77 critical windows when signaling is sensitive to exposure (Heyne et al., 2015). For example, multiple
78 studies in animal models exposed to higher concentrations of the Hedgehog (HH) pathway receptor
79 Smoothened (SMO) antagonists, namely Vismodegib and Cyclopamine have high incidence of OFCs
80 (Heyne et al., 2015; Lipinski et al., 2010a). In order to facilitate regulatory decision making on the testing
81 and registration of new chemical entities, robust assays capable of detecting disruption at multiple
82 places along these embryonic signaling pathways are needed to replace traditional animal testing.
83 Thorough mapping of the pathways and identifying the endpoints of interest is the first step in creating
84 these assays.

85 The Adverse Outcome Pathway (AOP) is an analytical framework that describes the biological pathway
86 between exposure to a stressor (e.g. environmental toxicant) and an adverse outcome (AO) (OECD,
87 2024b). This framework provides a clear approach to continue mapping these pathways and organizes
88 the information needed for assay development in a central repository (AOP-Wiki) (SAAOP, 2024). This
89 AOP focuses on disruption of the SHH pathway through antagonism of the SMO receptor leading to
90 OFCs. This AOP is intended to serve as a tool for risk assessment for drug and chemical exposures during

91 embryonic development, when disruption to SHH through antagonism of SMO occurs. It is hoped that
92 increasing the fields' understanding of what exposures are risks for causing OFCs can lead to targeted
93 prevention strategies and improved patient outcomes.

94 **Development of the orofacial processes** The development of the face occurs early in embryogenesis and
95 involves precise coordination of multiple tissues (reviewed in (Som and Naidich, 2013)). Briefly, the
96 oropharyngeal membrane appears early in the 4th week of human gestation and gives rise to the
97 frontonasal process and the 1st pharyngeal arch. The frontonasal process is derived from the neural crest
98 derived mesenchyme along with neuroectoderm and surface ectoderm. It in turn gives rise to two medial
99 nasal processes and two lateral nasal processes that later fuse and form the intermaxillary process. The
100 pharyngeal arch is derived from mesoderm and the neural crest. It gives rise to two mandibular processes
101 and two maxillary processes (Som and Naidich, 2013). These processes are comprised of mesenchymal
102 cells from neural crest migration and the craniopharyngeal ectoderm and are coated in an epithelium
103 (Ferguson, 1988). The upper lip forms during early embryogenesis and fuses during weeks 5-7 (~E10-11.5
104 in mouse) when the maxillary processes grow towards the midline and fuses with the medial nasal
105 (intermaxillary) processes that form the philtrum and columella (Kim et al., 2004; Warbrick, 1960; Lan and
106 Jiang, 2022). The palate develops between week 6-12 (~E11.5-14.0 in mouse) from an intermaxillary
107 process derived from the nasal process and a pair of lateral palatine processes (Lan and Jiang, 2022). The
108 primary palate is formed from the posterior extension of the medial nasal (intermaxillary) processes. The
109 lateral palatine processes arise as medial mesenchymal processes from both maxillary processes. These
110 processes initially grow inferiorly until the tongue is pulled downwards by the elongation of the maxilla
111 and mandible. Once above the tongue, the lateral processes grow medially until they make contact and
112 fuse at the midline (Som and Naidich, 2014).

113 **SHH in Orofacial Development** . SHH is an important modulator of epithelial-mesenchyme interaction
114 during embryonic development and disruption in animal models has been linked with OFCs (Heyne et
115 al., 2015; Lipinski et al., 2010a). The epithelial derived SHH ligand drives orofacial development via a
116 morphogenic gradient of high proximal and low distal binding in the underlying mesenchyme, relative to
117 the epithelium (Kurosaka, 2015; Lan and Jiang, 2009). This morphogenic gradient induces cellular
118 proliferation in the proximal mesenchyme and drives outgrowth of the facial prominences (Lan and
119 Jiang, 2009). SHH signaling has also been implicated in microvasculature formation and stability through
120 perivascular SHH signaling to the endothelium (Sun et al., 2020). This combination of tissue outgrowth,
121 paired with the formation of the microvasculature, makes SHH signaling critical for proper formation of
122 the lips and palate.

123 Reception and transduction of SHH ligand has been extensively studied, yet some details are still not
124 fully understood. The interaction between the SHH cell surface receptors Patched (PTCH) and SMO
125 continues to be elucidated. The SMO receptor is a Class F, G protein coupled receptor involved in signal
126 transduction of the Sonic Hedgehog (SHH) pathway. It includes distinct functional groups including
127 ligand binding pockets, cysteine rich domain (CRD), transmembrane helix (TM), extracellular loop (ECL),
128 intracellular loop (ICL), and a carboxyl-terminal tail (C-term tail) (Arensdorf et al., 2016). SMO signaling
129 is dependent upon its relocation to a subcellular location. In the absence of SHH ligand, PTCH
130 suppresses the activation of SMO. When SHH ligand binds to PTCH, suppression on SMO is released and
131 SMO can relocate, accumulate, and signal to intracellular effectors (Denef et al., 2000; Rohatgi and
132 Scott, 2007). It has been shown that SMO localization to the tip of the primary cilia (PC) is essential for
133 the SHH signaling cascade in vertebrates and typically occurs within 20 minutes of agonist stimulation
134 (Rohatgi et al., 2009; Rohatgi et al., 2007; Corbit et al., 2005; Arensdorf et al., 2016; Huangfu and

135 Anderson, 2005). This signaling cascade leads to signaling to effectors resulting in the activation of the
136 GLI transcription factors and the subsequent induction of GLI target gene expression (Von Ohlen and
137 Hooper, 1997; Alexandre et al., 1996).

138 The SHH pathway is sensitive to chemical disruption and can be disrupted at multiple molecular
139 initiating events (MIE) along the signaling cascade . The targets of this disruption include ligand
140 production and post-translational modification, ligand secretion, downstream sensing, and transduction
141 (Jeong and McMahon, 2002; Lauth et al., 2007; Petrova et al., 2013b). Disruption of SHH during critical
142 windows of development causing OFCs is believed to work in an epithelial-mesenchyme interaction
143 dependent, but epithelial-mesenchyme transition (Emt) independent manner due to a reduction in
144 epithelial induced proliferation and the subsequent decrease in tissue outgrowth causing the failure of
145 the facial processes to meet and fuse (Heyne et al., 2015; Lipinski et al., 2010a). Chemical modulators of
146 the HH pathway have been identified including the natural alkaloid cyclopamine, both natural and
147 synthetic pharmaceuticals, and a pesticide synergist (Piperonyl Butoxide (PBO)) (Lipinski et al., 2007;
148 Lipinski et al., 2010a; Wang et al., 2012a; Everson et al., 2019; Rivera-González et al., 2021). It should be
149 noted that Indian and Desert Hedgehog (IHH and DHH respectively) are other Hedgehog pathways that
150 are active during development but are not believed to contribute significantly to orofacial development.
151 These pathways signal in a similar manner through PTCH/SMO suggesting that exposures identified in
152 the context of SHH should also be considered in the context of IHH and DHH. Due to the focus of this
153 AOP on disruption to proper orofacial development, SHH will be the focus of discussion.

154 **1. Brief description of AOP**

155 This AOP links antagonism of the SMO receptor, MIE to the adverse outcome, orofacial clefting (**Fig 1**).
156 This AOP is intended to fit within a larger AOP network for SHH disruption leading to OFCs being
157 developed through the OECD Advisory Group on Emerging Science in Chemicals Assessment workplan.
158 The SHH pathway is sensitive to chemical disruption at multiple MIEs along the signaling cascade, albeit
159 only those that occur during critical windows in development can lead to OFCs (Lipinski et al., 2010a;
160 Heyne et al., 2015). Other MIEs include posttranslational SHH ligand modification with cholesterol and
161 palmitoylate, ligand secretion, mesenchymal reception, and signal transduction (Jeong and McMahon,
162 2002; Lauth et al., 2007; Petrova et al., 2013a). This AOP covers one of these events; antagonism of the
163 SMO receptor. Chemical antagonism of SMO is followed by a series of key events (KEs) ultimately
164 leading to the adverse outcome (AO) orofacial clefting. This pathway occurs in the mesenchyme initially
165 at the macromolecular level. The KEs were selected following a thorough review of the SHH pathway
166 and by taking into consideration events that would be of regulatory interest and that would be possible
167 to have a measurement/assay for. To select the key events for the AOP, we used existing knowledge of
168 the pathway along with reviews of the SHH pathway to assemble a path that was physiologically
169 plausible. Care was taken to select events that would be of direct regulatory relevance (i.e. a method to
170 quantify exists).

171
172

Box1: AOP ID Box

- AOP title: Antagonism of Smoothened receptor leads to orofacial clefting
- AOP Authors: Jacob I. Reynolds, Brian P. Johnson
- AOP Contributors: Jacob I. Reynolds
- AOP number: 460
- OECD workplan number: Project 1.101: Disruption of the sonic hedgehog pathway during development leads to orofacial clefting
- List of Key Events
 - MIE 2027 Antagonism, Smoothened receptor
 - KE 2044 Decrease, Smoothened relocation, and activation
 - KE 2028 Decrease, GLI1/2 translocation to nucleus
 - KE 2040 Decrease, GLI1/2 target gene expression
 - KE 1262 Apoptosis
 - KE 2043 Decrease, Second messenger production
 - KE 1821 Decrease, Cell proliferation
 - KE 2041 Decrease, palatal shelf outgrowth
 - AO 2042 Orofacial clefting

173

174

175 **2. Overview of AOP development approach**

176 This AOP was developed using a “bottom up” (MIE-AO) approach. This AOP was developed by the
 177 Johnson Lab at Michigan State University as part of the OECD AOP Development Program Project n°
 178 1.101 (OECD, 2024a). At the time of creation, the AOP-Wiki did not include any events for SHH signaling.
 179 With the exception of KE 1821 Decrease, Proliferation, and KE 1262 Apoptosis, all of the MIE, KE, KERs,
 180 and AO in this AOP were created and developed by the authors (OECD, 2021).

181 [Pubmed](#) was used as the primary database for evidence collection. Search results were initially screened
 182 through review of the title and abstract for potential for data relating a decrease in outgrowth and OFC.
 183 Each selected publication and its' data were then examined to determine if support or lack thereof
 184 existed for the KER in questions. Papers that did not show any data relating to the KER were discarded.
 185 The search terms, date of search, and references identified are organized in **Supplementary table 1**.

186 **3. Summary of scientific evidence assessment**187 **Overall Assessment**

188 This AOP was assessed for its domains of applicability, the essentiality of the events, the empirical
 189 evidence presented, temporal concordance, dose-response concordance, consistency, and biological
 190 plausibility (**Table 1**).

191 **Domain(s) of Applicability**

192 **Chemical:** This AOP applies to antagonists of the SMO receptor. Chemical modulators of the SHH
 193 pathway have been identified, including the natural alkaloid cyclopamine, both natural and synthetic

194 pharmaceuticals (e.g. Vismodegib), and a widely used pesticide synergist (PBO) with established human
195 exposures (Lipinski et al., 2007; Lipinski et al., 2010a; Wang et al., 2012a; Everson et al., 2019; Rivera-
196 González et al., 2021).

197 **Sex:** This AOP is unspecific to sex.

198 **Life Stages:** The relevant life stage for this AOP is embryonic development. More specifically, the
199 development of the craniofacial region which occurs between gestational day (GD) 10.0 and GD 14.0 in
200 the mouse and week 4-12 in human.

201 **Taxonomic:** At present, the assumed taxonomic applicability domain of this AOP is mouse (*Mus*
202 *musculus*). Most of the toxicological data that this AOP is based on has used mice as their model. Mice
203 are a good analog of human craniofacial development and undergo similar signaling by SHH (Jiang et al.,
204 2006). The biological plausible domain of applicability extends to mammals as the mechanisms of
205 orofacial development and early embryonic signaling including SHH are largely conserved.

206 **Essentiality of the Key Events**

207 To date, few studies have addressed the essentiality of the proposed sequence of key events. Evidence
208 linking SHH disruption through a decrease in proliferation exists. The hypothesized sequence of events
209 has a high temporal concordance for canonical SHH signaling pathway and orofacial development.

- 210 • Studies have shown that SHH signaling is required for normal facial development and plays a
211 critical role in the growth of the facial processes that form the upper palate and lip (Bush and
212 Jiang, 2012; Kurosaka, 2015; Kurosaka et al., 2014).
- 213 • The epithelial derived SHH drives orofacial development through an induced gradient in the
214 underlying mesenchyme (Kurosaka, 2015; Lan and Jiang, 2009; Kurosaka et al., 2014). This
215 gradient of SHH induces cellular proliferation and outgrowth of the mesenchyme (Lan and Jiang,
216 2009).
- 217 • OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced
218 proliferation of the mesenchyme and the subsequent decrease in tissue outgrowth and the
219 failure of the facial processes to meet and fuse (Heyne et al., 2015; Lipinski et al., 2010a).

220 **Evidence Assessment**

- 221 • KER ID-Title-[Adjacency], [Evidence], [Quantitative Understanding]
- 222 • Relationship 2734: Antagonism Smoothened (Event 2027) leads to Decrease, SMO relocation
223 (Event 2044)-[Adjacent], [Moderate], [Low]-There is a high biological plausibility of this
224 relationship and SMO localization to the primary cilia is essential for proper SHH signaling in
225 vertebrates (Rohatgi et al., 2009; Rohatgi et al., 2007; Corbit et al., 2005). There is good
226 evidence that the Smoothend Antagonist (SANT) compounds block the localization of SMO to
227 the tip of the primary cilia. Contradictory *In vivo* data was found regarding whether
228 cyclopamine blocks SMO relocation to the primary cilia. Further work is required to determine if
229 SMO antagonism via cyclopamine results in decrease in SMO relocation.
- 230 • Relationship 2735: Decrease, SMO relocation (Event 2044) leads to Decrease, GLI1/2
231 translocation (Event 2028)-[Adjacent], [Moderate], [Low]- Moderate evidence is presented to
232 support that a loss of SMO relocation to the primary cilia leads to a significant decrease in GLI1.
233 GLI1 requires activation prior to nuclear translocation.

- Relationship 2721: Decrease, GLI1/2 translocation (Event 2028) leads to Decrease, GLI1/2 target gene expression (Event 2040)-[Adjacent], [Low], [Low]- There is high biological plausibility of this relationship but to date few studies were found to explore the relationship.
- Relationship 2731: Decrease GLI1/2 target gene expression (Event 2040) leads to Decrease, SHH second messenger production (Event 2043)-[Adjacent], [Low], [Low]-Coordinated signaling is paramount for proper embryonic development and the GLI signaling cascade drives feedback/forward loops with FGF and BMP signaling pathways. Support was found for SHH having a feedforward loop with FGF10 and BMP4, however further investigation into the interaction of these pathways and their crosstalk is required.
- Relationship 2732: Decrease SHH second messenger production (Event 2043) leads to Decrease, cell proliferation. (Event 1821)-[Adjacent], [Low], [Low]- SHH is a known mitogen and drives proliferation through its' secondary messengers. SHH was found to induce proliferation and FGF10 *In vivo*.
- Relationship 2724: Decrease, Cell proliferation (Event 1821) leads to Decrease, outgrowth (Event 2041)-[Adjacent], [Low], [Low]-SHH is a known mitogen that helps to drive the proper development of the face which includes the outgrowth of the facial prominences. To date, few studies have measured outgrowth of the facial prominences and proliferation. Hypoplasia of pharyngeal arch 1 was found in SHH-/ embryos supporting that outgrowth is driven by proliferation and is reduced when proliferation is decreased.
- Relationship 2726: Decrease, outgrowth (Event 2041) leads to OFC (Event 2042)-[Adjacent], [Moderate], [Low]- OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced mesenchymal proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski et al., 2010b; Heyne et al., 2015). Mice with disrupted SHH signaling are found to have palatal shelves that are spaced apart supporting that the cleft results from an epithelial-mesenchyme dependent, but epithelial-mesenchyme transition (Emt) independent manner.
- Relationship 2792: Apoptosis (Event 1262) leads to Decrease, outgrowth (Event 2041)- [Adjacent], [Low], [Low]- SHH signaling is known to be associated with cell survival and there is a high biological plausibility that increasing apoptosis would cause a decrease in outgrowth. Supporting evidence is offered with increases in apoptosis in the mandibular arch seen in SHH signaling disrupted mice that exhibit decreased outgrowth.
- Relationship 2882: Decrease, GLI1/2 target gene expression (Event 2040) leads to Apoptosis (Event 1262) -[Adjacent], [Low], [Low]- To date few studies have examined the relationship of GLI1/2 target gene expression. There is a high biological plausibility that SHH plays a role in cell survival and death through GLI1/2 target gene expression. Decreased GLI1/2 target gene expression is seen in RA exposed dams alongside increased apoptosis on the cranial neural crest cells (CNCC).
- Relationship 2894: Antagonism Smoothened (Event 2027) leads to OFC (Event 2042)-[Non-adjacent], [High], [Moderate]- multiple studies have demonstrated *In vivo* that administration of SMO antagonists during critical windows of exposure leads to birth defects including OFC in a dose-dependent fashion.

275 **Biological Plausibility**

276 Biological plausibility refers to the structural and/or functional relationship that exists between the key
277 events based on our understanding of normal biology. SHH signaling is largely conserved in mammals
278 and is required for normal facial development and plays a critical role in the growth of the facial
279 processes that form the upper palate and lip (Bush and Jiang, 2012; Kurosaka, 2015). Multiple
280 antagonists of the SMO receptor have been identified through binding studies including cyclopamine,
281 vismodegib, PBO, and the SANT compounds (Lipinski et al., 2007; Lipinski et al., 2010a; Wang et al.,
282 2012a; Everson et al., 2019; Rivera-González et al., 2021). While the level of empirical support for most
283 of the KERs is low, there is high empirical support for the non-adjacent relationship linking antagonism
284 of SMO and OFC as well as high plausibility of the AOP.

285 **Concordance of dose-response relationships**

286 There are a limited number of studies in which multiple key events were assessed in the same study
287 following exposure to known SMO antagonists. These studies form the basis of the dose-response
288 concordance of this AOP (**Supplementary Table 2**). Many studies were found to use a single
289 concentration.

290 The concentration-dependence of the key event responses regarding concentration of known *in vitro*
291 and/or *in vivo* for some of the KEs in this AOP.

- 292 • Concentration dependent clefting with cyclopamine exposure (Omnell et al., 1990)
- 293 • Dose dependent binding to SMO (Chen et al., 2002)
- 294 • Concentration dependent decrease in SMO-ciliary accumulation *in vitro* for vismodegib
295 exposure (Wang et al., 2012b)

296 **Temporal concordance**

297 Temporal concordance refers to the degree to which the data supports the hypothesized sequence of
298 Molecular Initiating Event (MIE) leading to the Adverse Outcome (AO) through a series of Key Events
299 (KEs). This work has identified a lack of studies that address the temporal concordance of this AOP.
300 While a lack of data for temporal concordance exists, there remains a high plausibility of the proposed
301 relationship. Canonical SHH signaling through PTCH-SMO-GLI is well understood and our AOP remains
302 consistent with the pathway. SHH signaling is required for normal facial development and plays a critical
303 role in the growth of the facial processes that form the upper palate and lip (Bush and Jiang, 2012;
304 Kurosaka, 2015). The epithelial derived SHH drives orofacial development through an induced gradient
305 in the underlying mesenchyme (Kurosaka, 2015; Lan and Jiang, 2009). This gradient of SHH induces
306 cellular proliferation and outgrowth of the mesenchyme (Lan and Jiang, 2009). The hypothesized
307 sequence of events is supported by the existing data and follow the field's current understanding of the
308 canonical SHH signaling pathway.

309 **Consistency**

310 The AO is not specific to this AOP. Many of the events in this AOP will overlap with AOPs linking
311 disruption of SHH to OFC and some are expected to overlap with AOPs linking other developmental
312 signaling pathways to OFCs.

313 **Uncertainties, inconsistencies, and data gaps**

314 This AOP would be strengthened by studies examining the dose-response and time-course relationships
315 for these KERs. The main data gaps for this AOP exist in the lack of studies that have examined the
316 relationship in the context of dose response or time course. Additional studies using mouse models
317 along with the development of NAMs would help to strengthen this AOP.

318 **Data gaps:**

319

320 • Dose response and time course studies relating a Decrease, SMO relocation leads to Decrease,
321 GLI1/2 translocation.

322 • Dose response and time course studies relating a decrease GLI translocation leads to decrease
323 GLI target gene expression.

324 • Dose response and time course studies relating a Decrease, GLI1/2 target gene expression leads
325 to Decrease, SHH second messenger production.

326 • Dose response and time course studies relating a Decrease, SHH second messenger production
327 leads to Decrease, Cell proliferation.

328 • Dose response and time course studies relating a Decrease, Cell proliferation leads to Decrease,
329 outgrowth.

330 • Dose response and time course studies relating a Decrease, outgrowth leads to OFC.

331 • Dose response and time course studies relating Apoptosis leads to Decrease, Outgrowth

332 • Dose response and time course studies relating a Decrease, GLI1/2 target gene expression leads
333 to Apoptosis.

334 **Inconsistencies:**

335 • While it is well understood that cyclopamine is an antagonist of SMO, contradictory *In vitro* data
336 was found regarding whether cyclopamine blocks SMO relocation to the primary cilia. Rohatgi et
337 al used NIH 3T3s cell and found that cyclopamine did not inhibit the accumulation of SMO in the
338 cilia even when dosed at 5-10um (>10 fold above Kd). The three antagonists (SANT-1, SANT-2,
339 and cyclopamine) tested by Rohatgi et al 2009 inhibited SHH pathway transduction and target
340 gene expression (Rohatgi et al., 2009). In a 2005 study, Corbit et al used a renal epithelial MDCK
341 (Madin-Darby canine kidney) line engineered to express Myc-tagged SMO. Following culture for
342 1hr in SHH conditioned media, SMO presence in the primary cilium is upregulated while cells
343 cultured in the presence of cyclopamine see a downregulation of SMO in the primary cilia
344 (Corbit et al., 2005). Further work is required to determine if SMO antagonism via cyclopamine
345 results in decrease in SMO relocation.

346 **Uncertainties:**

347 • While we know that entry to the cilia is tightly controlled, the exact mechanism of SMO ciliary
348 trafficking is not fully understood. The primary cilia (PC) is separated from the plasma
349 membrane by the ciliary pockets and the transition zone which function together to regulate the
350 movement of lipids and proteins in and out of the organelle (Rohatgi and Snell, 2010; Goetz et
351 al., 2009). The SHH receptor PTCH contains a ciliary localization sequence (CLS) in its' carboxy
352 tail. Localization of PTCH to the PC is essential for inhibition of SMO as deletion of the CLS in
353 PTCH prevents PTCH localization as well as inhibition of SMO (Kim et al., 2015). SMO also

354 contains a CLS, but only accumulates in the PC upon ligand binding (Corbit et al., 2005). The
355 entry of SMO into the PC is thought to occur either laterally through the ciliary pockets or
356 internally via recycling endosomes (Milenkovic et al., 2009). Once inside the PC, SMO can diffuse
357 freely, however it will usually accumulate in specific locations depending upon its' activation
358 state. Inactive SMO will accumulate more at the base of the PC while active SMO will
359 accumulate in the tip of the PC (Milenkovic et al., 2015).

- 360 • The relationships and feedback/feedforward loops that exist between SHH and its' secondary
361 messengers primarily FGF10 and BMP4 are not well understood. More investigation into these
362 relationships is warranted.
- 363 • The exact mechanism through which SHH promotes cell survival is not well understood
364 (Cobourne et al., 2001). Further studies are needed to illuminate the mechanism that links SHH
365 signaling with cell survival.
- 366 • The relationship between GLI1/2 target gene expression and increased apoptosis has a high
367 biological plausibility although there is currently a lack of studies that address this relationship.

368 **Assessment of quantitative understanding of the AOP:**

369 The quantitative understanding for this AOP except for the non-adjacent relationship between
370 Antagonism Smoothened leads to OFC is low. Most of the data found through the literature was
371 obtained from studies that investigated a single compound that performed their investigation using a
372 single concentration. Few studies were found to conduct either dose response or time course studies.
373 For the non-adjacent relationship connecting Antagonism Smoothend to OFC there are several studies
374 with dose response data showing a dose-dependent incidence of clefting were found. This AOP would
375 benefit from the generation of additional data that addresses these relationships in a dose response and
376 time course methodology to allow for an increased quantitative understanding of the linkage.

377 **4. Potential applications**

378 This AOP provides an opportunity from a regulatory standpoint, to facilitate the reduction or
379 replacement animal testing for developmental toxicity testing (e.g., OECD test guideline 414). There are
380 currently no OECD-validated *in vitro* assays to identify chemicals likely to cause a cleft prior to
381 manifestation. Such developmental toxicants are primarily identified when structural abnormalities (e.
382 g., OFC) had already occurred and detected in a developmental toxicity assay such as OECD Test No.
383 414: Prenatal Developmental Toxicity Study (OECD, 2018). AOP 460 provides an understanding of a
384 mechanism leading to OFCs, such that if there were validated *in vitro* methods that could detect the
385 earlier key events before the *in vivo* manifestation of OFCs, this would be highly relevant for the
386 regulatory community.

387

388 Existing or new data from *in silico* and *in vitro* high-throughput screening assays (HTS) can also be
389 applied to this AOP to guide early identification of chemicals for further investigation using more
390 representative models of orofacial development using a tiered testing approach. For example, data has
391 been generated by the National Center for Advancing Translational Sciences (NCATS) Toxicology in the
392 21st Century program (Tox21) for HH agonists and antagonists at the transcriptional level using a GLI3
393 luminescent reporter 3T3 line (Huang et al., 2018; Huang et al., 2016). A HTS assay has also been
394 developed to detect potential inhibitors or activators of the auto processing that the SHH ligand
395 undergoes upstream of SMO (Ciulla et al., 2022). Microphysiological models (MPMs) offer increased
396 physiological relevance over traditional 2D cell culture providing the ability to capture disruption at

397 multiple MIEs. For example, research groups are already engineering models to facilitate the study of
398 both normal and abnormal orofacial development including palatal fusion (Belair et al., 2018; Wolf et al.,
399 2018; Belair et al., 2017; Wolf et al., 2023; Reynolds et al., 2022; Johnson et al., 2021). Leveraging these
400 data and carefully designed *in vitro* models, there is the potential to aid developmental toxicity testing
401 and reduce animal use.

402

403 This AOP can also serve as a reference for method developers to identify and incorporate the relevant
404 and early biological endpoints in developmental and reproductive toxicology (DART), for which new
405 assays (NAMs) could be developed. Our lab engineered one of the MPMs of orofacial development
406 discussed above to study SHH signaling (Reynolds et al., 2022; Johnson et al., 2021). A major motivation
407 for our completing this AOP is to apply a bottom-up approach to identify data gaps and guide
408 experimental direction related to OFCs (Reynolds et al., 2024). Through development of this AOP and
409 the larger AOP network we have identified data gaps of direct regulatory interest. As detailed above,
410 most of the identified gaps involve a lack of studies addressing dose response or time course in an
411 experiment designed to test the KER. The plan is to use the MPM of orofacial development our lab has
412 developed and generate data to help fill these gaps. Understanding the data gaps and any
413 inconsistencies or uncertainties is crucial both for risk assessment as well as for experiment planning.
414 Pairing this increased understanding of the pathway and regulatory needs can guide application of
415 engineered models and HTS assays.

416

417 Finally, the ability to detect disruption of the SHH pathway has broader consequences and impact than
418 just OFCs. The SHH pathway is known to play a role in many aspects of embryonic development
419 including patterning of the limbs, digit development, and development of the clinical phenotype,
420 holoprosencephaly (Roessler et al., 1996; Scherz et al., 2007; Tickle and Towers, 2017; Sasai et al., 2019).
421 The creation of complex *in vitro* NAMs that are sensitive to disruption of SHH has important implications
422 in developmental toxicity testing including identifying chemicals that would be predicted to cause birth
423 defects in these other areas. Mapping and *in vitro* modeling of the key intermediate events that are
424 shared in these processes may broaden the applicability of these models furthering hazard
425 identification. In summary, this AOP and the subsequent work can lead to improved methods or
426 development of NAMs for DART testing and a shift away from traditional animal use.

427

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436 **6. AOP Editors and Reviewers**

437 **7. Disclaimer**

438 **8. Data availability statement**

439 Data, associated metadata, and calculation tools are available from the corresponding author
 440 (bjohnson@msu.edu). All review reports can be accessed at <https://aopwiki.org/aops/460>. The final
 441 snapshot pdf of this AOP can be accessed at <https://aopwiki.org/aops/460/snapshots>. The snapshot pdf
 442 that was used during the review process can be found at <https://aopwiki.org/aops/460/snapshots>.
 443

444 **Figure 1:** Schematic of AOP 460. Adjacent and nonadjacent relationships are depicted as solid and
 445 dashed lines respectively.

446 **Table 1:** Assessment of the relative level of confidence in the overall AOP based on rank ordered weight
 447 of evidence elements.

448

449 **Supplementary table 1:** Organization of search terms and results for all KERs.

450 **Supplementary table 2:** Dose concordance for AOP. Studies were recorded for dose and any indication
 451 of any of the KEs in the AOP were noted.

452

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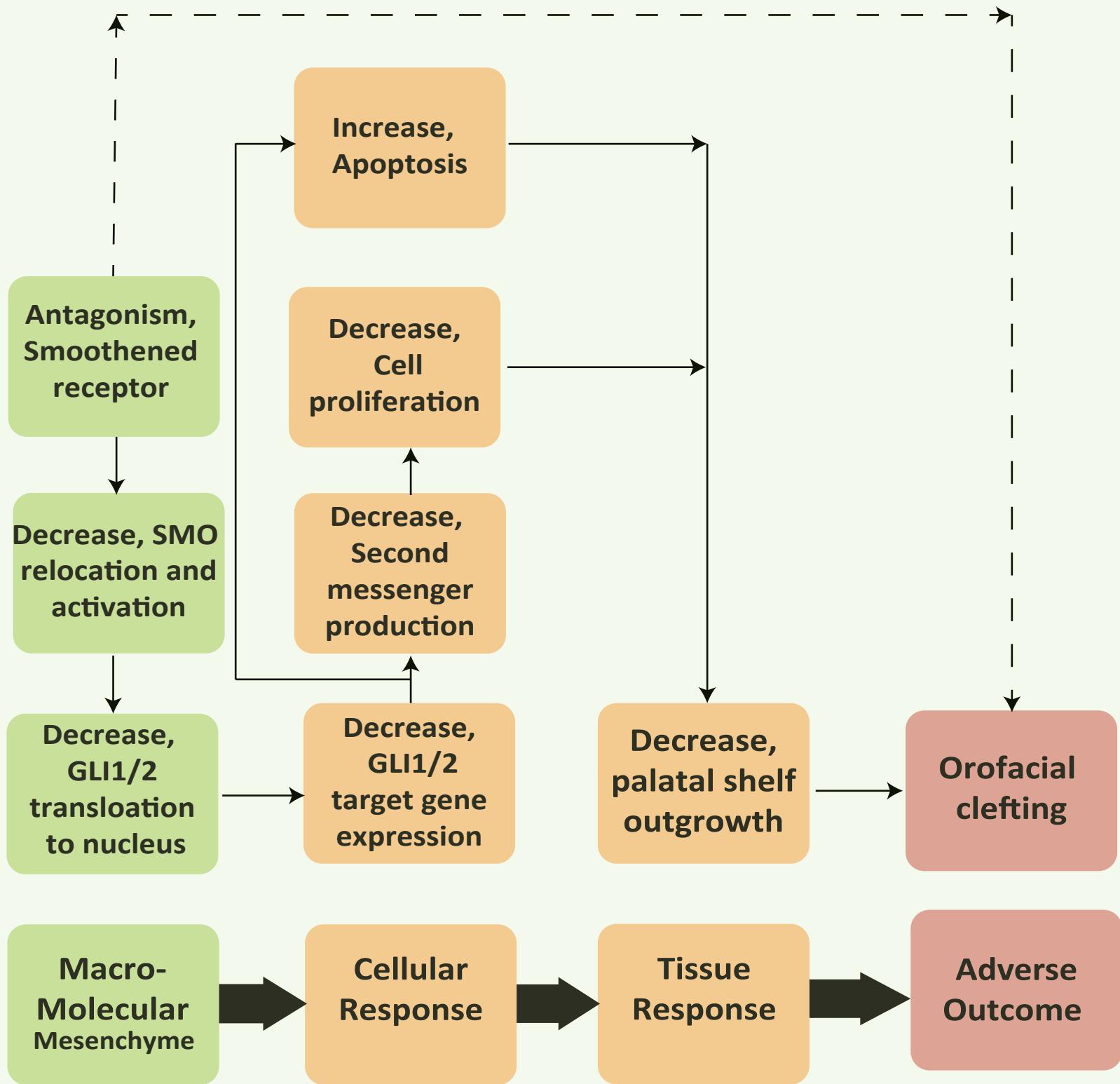


Table 1: Assessment of the relative level of confidence in the overall AOP based on rank ordered weight of evidence elements.

Defining Question	High (Strong)	Moderate	Low (Weak)
1. Support for Biological Plausibility of KERS			
a) Is there a mechanistic relationship between KE _{up} and KE _{down} consistent with established biological knowledge?	Extensive understanding of the KER based on extensive previous documentation and broad acceptance.	KER is plausible based on analogy to accepted biological relationships, but scientific understanding is incomplete	Empirical support for association between KEs, but the structural or functional relationship between them is not understood.
Relationship 2734: Antagonism Smoothened (Event 2027) leads to Decrease, SMO relocation (Event 2044)		STRONG SMO signaling is well understood to be dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). It has been shown that SMO localization to the tip of the primary cilia is essential for the SHH signaling cascade in vertebrates (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Rohatgi, Milenkovic et al. 2009)	
Relationship 2735: Decrease, SMO relocation (Event 2044) leads to Decrease, GLI1/2 translocation (Event 2028)		MODERATE SMO causes the GLI family to become dislodged from their complex with the negative regulator of HH signaling, Suppressor of Fused (Sufu) (Kogerman, Grimm et al. 1999, Pearse, Collier et al. 1999, Stone, Murone et al. 1999, Tukachinsky, Lopez et al. 2010). The GLI-Sufu complex maintains retention of GLI in the cytosol allowing for exposure to phosphorylation via protein kinase A (PKA) which inhibits downstream signal transduction (Tuson, He et al. 2011). When SMO is activated, the GLI2/3-Sufu complex is dismantled allowing for retrograde transport of GLI back into the nucleus (Kim, Kato et al. 2009).	
Relationship 2721: Decrease, GLI1/2 translocation (Event 2028) leads to Decrease, GLI1/2 target gene expression (Event 2040)		STRONG It is well established that activation of the SHH pathway results in a downstream signaling cascade resulting in the relocation of GLI to the nucleus and subsequent gene transcription (Carballo, Honrato et al. 2018).	
Relationship 2731: Decrease GLI1/2 target gene expression (Event 2040) leads to Decrease, SHH second messenger production (Event 2043)		WEAK While it is understood that there is extensive crosstalk between SHH and other pathways during development there is an incomplete understanding of these interactions and their feedback and feed forward loops.	
Relationship 2732: Decrease SHH second messenger production (Event 2043) leads to Decrease, cell proliferation (Event 1821)		STRONG SHH is a known mitogen and known to regulate cellular proliferation.	
Relationship 2724: Decrease, Cell proliferation (Event 1821) leads to Decrease, outgrowth (Event 2041)		MODERATE The SHH pathway is well known to be associated with cellular proliferation and growth of the facial prominences.	
Relationship 2726: Decrease, outgrowth (Event 2041) leads to OFC (Event 2042)		STRONG OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015).	
Relationship 2792: Apoptosis (Event 1262) leads to Decrease, outgrowth (Event 2041)		WEAK The SHH pathway is known to be associated with cell survival and that disruption of SHH signaling can lead to increased apoptosis. The understanding of this relationship is weak and further work is warranted to increase understanding.	
Relationship 2882: Decrease, GLI1/2 target gene expression (Event 2040) leads to Apoptosis (Event 1262)		WEAK The SHH pathway is well known to be associated with cellular proliferation and cell survival. Further investigation into how GLI1/2 gene expression regulates cellular survival is needed	

Relationship 2894: Antagonism Smoothened (Event 2027) leads to OFC (Event 2042)		STRONG The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs)	
Defining Question	High (Strong)	Moderate	Low (Weak)
2. Support for Essentiality of KEs			
Are downstream KEs and/or the AO prevented if an upstream KE is blocked?	Direct evidence from specifically designed experimental studies illustrating essentiality for at least one of the important KEs	Indirect evidence that sufficient modification of an expected modulating factor attenuates or augments a KE	No or contradictory experimental evidence of the essentiality of any of the KEs.
Essentiality of the KEs was assessed for the AOP as a whole – rationale for the individual KE calls is provided.			
<p>To date, few studies have addressed the essentiality of the proposed sequence of key events. Evidence linking SHH disruption through a decrease in proliferation exists. The hypothesized sequence of events has a high temporal concordance for canonical SHH signaling pathway and orofacial development.</p> <ul style="list-style-type: none"> Studies have shown that SHH signaling is required for normal facial development and plays a critical role in the growth of the facial processes that form the upper palate and lip (Bush and Jiang 2012, Kurosaka 2015). The epithelial derived SHH drives orofacial development through a high proximal low distal gradient of GLI activity in the underlying mesenchyme (Lan and Jiang 2009, Kurosaka 2015). This gradient of GLI induced transcription induces cellular proliferation and outgrowth of the mesenchyme (Lan and Jiang 2009). OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015). 			
Defining Question	High (Strong)	Moderate	Low (Weak)
3. Empirical Support for KERs			
Are downstream KEs and/or the AO prevented if an upstream KE is blocked?	Direct evidence from specifically designed experimental studies illustrating essentiality for at least one of the important KEs	Indirect evidence that sufficient modification of an expected modulating factor attenuates or augments a KE	No or contradictory experimental evidence of the essentiality of any of the KEs.
Relationship 2734: Antagonism Smoothened (Event 2027) leads to Decrease, SMO relocation (Event 2044)	<p>MODERATE</p> <p>There is good evidence that the SANT compounds block the localization of SMO to the tip of the primary cilia. Contradictory in vivo data was found regarding whether cyclopamine blocks SMO relocation to the primary cilia. Further work is required to determine if SMO antagonism via cyclopamine results in decrease in SMO relocation.</p> <p>Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER.</p> <p>Temporality: There are currently no time-course studies addressing these events.</p> <p>Uncertainties: Contradictory data was found for whether or not cyclopamine causes a change in SMO relocation. Further investigation is needed to increase understanding of this discrepancy.</p>		
Relationship 2735: Decrease, SMO relocation (Event 2044) leads to Decrease, GLI1/2 translocation (Event 2028)	<p>MODERATE</p> <p>Moderate evidence is presented to support that a loss of the primary cilia leads to a significant decrease in GLI1. GLI1 requires activation prior to nuclear translocation.</p> <p>Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER.</p> <p>Temporality: There are currently no time-course studies addressing these events.</p> <p>Uncertainties: While we know that entry to the cilia is tightly controlled, the exact mechanism of SMO ciliary trafficking is not fully understood.</p>		
Relationship 2721: Decrease, GLI1/2 translocation (Event 2028) leads to Decrease, GLI1/2 target gene expression (Event 2040)	<p>LOW</p> <p>There is high biological plausibility of this relationship but to date few studies were found to explore the relationship.</p> <p>Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER.</p> <p>Temporality: There are currently no time-course studies addressing these events.</p>		

Relationship 2731: Decrease GLI1/2 target gene expression (Event 2040) leads to Decrease, SHH second messenger production (Event 2043)	LOW Coordinated signaling is paramount for proper embryonic development and the GLI signaling cascade drives feedback/forward loops with FGF and BMP signaling pathways. Support was found for SHH having a feedforward loop with FGF10 and BMP4 however further investigation into the interaction of these pathways and their crosstalk is required. Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER. Temporality: There are currently no time-course studies addressing these events.
Relationship 2732: Decrease SHH second messenger production (Event 2043) leads to Decrease, cell proliferation (Event 1821)	LOW SHH was found to induce proliferation and FGF10 in vivo. In FGF10 deficient models SHH was found to be reduced. Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER. Temporality: There are currently no time-course studies addressing these events.
Relationship 2724: Decrease, Cell proliferation (Event 1821) leads to Decrease, outgrowth (Event 2041)	LOW SHH is a known mitogen that helps to drive the proper development of the face which includes the outgrowth of the facial prominences. To date, few studies have measured by outgrowth of the facial prominences and proliferation. Hypoplasia of pharyngeal arch 1 was found in SHH-/- embryos supporting that outgrowth is driven by proliferation and is reduced when proliferation is decreased. Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER. Temporality: There are currently no time-course studies addressing these events.
Relationship 2726: Decrease, outgrowth (Event 2041) leads to OFC (Event 2042)	MODERATE OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015). Mice with disrupted SHH signaling are found to have palatal shelves that are spaced apart supporting that the cleft results from an EMT dependent, but epithelial-mesenchyme transition (EMT) independent manner. Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER. Temporality: There are currently no time-course studies addressing these events. However, critical periods of exposure for clefting have been identified.
Relationship 2792: Apoptosis (Event 1262) leads to Decrease, outgrowth (Event 2041)	LOW SHH signaling is known to be associated with cell survival and there is a high biological plausibility that increasing apoptosis would cause a decrease in outgrowth. Supporting evidence is offered with increases in apoptosis in the mandibular arch seen in SHH signaling disrupted mice that exhibit decreased outgrowth. Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER. Temporality: There are currently no time-course studies addressing these events.
Relationship 2882: Decrease, GLI1/2 target gene expression (Event 2040) leads to Apoptosis (Event 1262)	LOW To date few studies have examined the relationship of GLI1/2 target gene expression. There is a high biological plausibility that SHH plays a role in cell survival and death through GLI1/2 target gene expression. Decreased GLI1/2 target gene expression is seen in RA exposed dams alongside increased apoptosis on the CNCC. Dose-response: Data compiled thus far are insufficient to evaluate dose-response concordance for this KER. Temporality: There are currently no time-course studies addressing these events.
Relationship 2894: Antagonism Smoothened (Event 2027) leads to OFC (Event 2042)	HIGH Multiple studies have demonstrated <i>in vivo</i> that administration of SMO antagonists during critical windows of exposure leads to birth defects including OFC in a dose-dependent fashion.

Dose-response: Multiple studies demonstrate a dose dependent incidence of clefting. It should be noted that a lack of studies investigating the dose concordance of this relationship were identified.

Temporality: Critical exposure windows for OFC formation have been identified.

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Supplementary table 1: Organization of search terms and results for all KERs.

KER	Search date	Search terms	Number of search results	Title/abstract review	Citations meeting title/abstract review	Number of citations in scope	Citations
2721	1/25/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("down regulation"[MeSH Terms] OR "down regulation"[All Fields] OR ("down"[All Fields] AND "regulation"[All Fields]) OR "down regulation"[All Fields]) AND "orofacial"[All Fields]	1	1	Everson et al 2017	1	Everson et al 2017
2721	1/25/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("trans activators"[MeSH Terms] OR "trans activators"[All Fields] OR ("trans"[All Fields] AND "activators"[All Fields]) OR "trans activators"[All Fields]) AND ("neural crest"[MeSH Terms] OR ("neural"[All Fields] AND "crest"[All Fields]) OR "neural crest"[All Fields]) AND ("face"[MeSH Terms] OR "face"[All Fields])	10	1	Jeong et al 2004	1	Jeong et al 2004
2721	1/27/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("gene	13	1	Lauth et al 2007	1	Lauth et al 2007

Supplementary table 1: Organization of search terms and results for all KERs.

		expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("zinc finger protein gli1"[MeSH Terms] OR ("zinc"[All Fields] AND "finger"[All Fields] AND "protein"[All Fields] AND "gli1"[All Fields]) OR "zinc finger protein gli1"[All Fields]) AND ("transcription, genetic"[MeSH Terms] OR ("transcription"[All Fields] AND "genetic"[All Fields]) OR "genetic transcription"[All Fields] OR ("transcription"[All Fields] AND "genetic"[All Fields]) OR "transcription genetic"[All Fields]) AND ("drug effects"[MeSH Subheading] OR ("drug"[All Fields] AND "effects"[All Fields]) OR "drug effects"[All Fields]) AND ("dna"[MeSH Terms] OR "dna"[All Fields])					
2721	1/27/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("cell survival"[MeSH Terms] OR ("cell"[All Fields] AND "survival"[All Fields]) OR "cell survival"[All Fields]) AND ("gene expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("phenotype"[MeSH	27	4	Miyake et al 2005, Li et al 2017, Katoh et al 2009, Billmyre et al 2015	1	Katoh et al 2009

Supplementary table 1: Organization of search terms and results for all KERs.

		Terms] OR "phenotype"[All Fields] OR "phenotypes"[All Fields] OR "phenotyped"[All Fields] OR "phenotypic"[All Fields] OR "phenotypical"[All Fields] OR "phenotypically"[All Fields] OR "phenotyping"[All Fields] OR "phenotypings"[All Fields])					
2721	1/27/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("mutate"[All Fields] OR "mutated"[All Fields] OR "mutates"[All Fields] OR "mutating"[All Fields] OR "mutation"[MeSH Terms] OR "mutation"[All Fields] OR "mutations"[All Fields] OR "mutation s"[All Fields] OR "mutational"[All Fields] OR "mutator"[All Fields] OR "mutators"[All Fields]) AND ("palatalization"[All Fields] OR "palatalized"[All Fields] OR "palatally"[All Fields] OR "palatals"[All Fields] OR "palate"[MeSH Terms] OR "palate"[All Fields] OR "palatal"[All Fields] OR "palates"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])	15	4	Zhang et al 2002, thomason et al 2008, Lan et al 2009, Li et al 2018	1	Lan et al 2009
2724	1/27/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("mutate"[All Fields]	15	4	Zhang et al 2002, thomason et al 2008, Lan et al	1	Lan et al 2009

Supplementary table 1: Organization of search terms and results for all KERs.

		OR "mutated"[All Fields] OR "mutates"[All Fields] OR "mutating"[All Fields] OR "mutation"[MeSH Terms] OR "mutation"[All Fields] OR "mutations"[All Fields] OR "mutation s"[All Fields] OR "mutational"[All Fields] OR "mutator"[All Fields] OR "mutators"[All Fields]) AND ("palatalization"[All Fields] OR "palatalized"[All Fields] OR "palatally"[All Fields] OR "palatals"[All Fields] OR "palate"[MeSH Terms] OR "palate"[All Fields] OR "palatal"[All Fields] OR "palates"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])			2009, Li et al 2018		
2724	2/6/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("fibroblast growth factors"[MeSH Terms] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factors"[All Fields]) OR "fibroblast growth factors"[All Fields] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields]) OR "fibroblast growth factor"[All Fields]) AND ("cleft palate"[MeSH Terms] OR ("cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])	15	1	Rice et al 2004,	1	Rice et al 2004
2724	3/10/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("embryology"[MeSH Subheading] OR	21	1	Yamagishi et al 2006,	1	Yamagishi et al 2006,

Supplementary table 1: Organization of search terms and results for all KERs.

		"embryology"[All Fields] OR ("embryonic"[All Fields] AND "development"[All Fields]) OR "embryonic development"[All Fields] OR "embryonic development"[MeSH Terms] OR ("embryonic"[All Fields] AND "development"[All Fields])) AND ("branchial region"[MeSH Terms] OR ("branchial"[All Fields] AND "region"[All Fields]) OR "branchial region"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields])) OR "signal transduction"[All Fields])					
2724	3/10/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("mesoderm"[MeSH Terms] OR "mesoderm"[All Fields] OR "mesodermal"[All Fields] OR "mesodermalization"[All Fields] OR "mesodermalized"[All Fields] OR "mesodermalizing"[All Fields] OR "mesodermally"[All Fields] OR "mesodermic"[All Fields] OR "mesoderms"[All Fields]) AND ("neural crest"[MeSH Terms] OR ("neural"[All Fields] AND "crest"[All Fields]) OR "neural crest"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields])) OR "signal transduction"[All Fields]) AND ("membrane proteins"[MeSH Terms] OR ("membrane"[All Fields] AND "proteins"[All Fields]) OR "membrane proteins"[All Fields])	6		Jeong et al 2004, Hammond et al 2018	1	Jeong et al 2004
2726	1/27/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields])	15	4	Zhang et al 2002,	1	Lan et al 2009

Supplementary table 1: Organization of search terms and results for all KERs.

		OR "hedgehog proteins"[All Fields] AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("mutate"[All Fields] OR "mutated"[All Fields] OR "mutates"[All Fields] OR "mutating"[All Fields] OR "mutation"[MeSH Terms] OR "mutation"[All Fields] OR "mutations"[All Fields] OR "mutation s"[All Fields] OR "mutational"[All Fields] OR "mutator"[All Fields] OR "mutators"[All Fields]) AND ("palatalization"[All Fields] OR "palatalized"[All Fields] OR "palatally"[All Fields] OR "palatals"[All Fields] OR "palate"[MeSH Terms] OR "palate"[All Fields] OR "palatal"[All Fields] OR "palates"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])			thomason et al 2008, Lan et al 2009, Li et al 2018		
2726	2/6/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("fibroblast growth factors"[MeSH Terms] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factors"[All Fields]) OR "fibroblast growth factors"[All Fields] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields]) OR "fibroblast growth factor"[All Fields]) AND ("cleft palate"[MeSH Terms] OR ("cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])	15	1	Rice et al 2004,	1	Rice et al 2004

Supplementary table 1: Organization of search terms and results for all KERs.

2731	2/2/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("cell survival"[MeSH Terms] OR ("cell"[All Fields] AND "survival"[All Fields]) OR "cell survival"[All Fields]) AND ("gene expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("phenotype"[MeSH Terms] OR "phenotype"[All Fields] OR "phenotypes"[All Fields] OR "phenotyped"[All Fields] OR "phenotypic"[All Fields] OR "phenotypical"[All Fields] OR "phenotypically"[All Fields] OR "phenotyping"[All Fields] OR "phenotypings"[All Fields])	27	4	Miyake et al 2005, Li et al 2017, Katoh et al 2009, Billmyre et al 2015	1	Katoh et al 2009
2731	2/6/2023	("cleft palate"[MeSH Terms] OR ("cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields]) AND (("molecular"[All Fields] OR "moleculars"[All Fields]) AND ("aetiologie"[All Fields] OR "aetiologies"[All Fields] OR "aetiology"[All Fields] OR "etiologies"[All Fields] OR "etiology"[MeSH Subheading] OR "etiology"[All Fields] OR "causality"[MeSH Terms] OR "causality"[All Fields])) AND ("fibroblast growth factor 10"[MeSH Terms] OR "fibroblast growth	1	1	Alappat et al 2005	1	Alappat et al 2005

Supplementary table 1: Organization of search terms and results for all KERs.							
		factor 10"[All Fields]) AND ("transforming growth factor beta"[MeSH Terms] OR ("transforming"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields] AND "beta"[All Fields]) OR "transforming growth factor beta"[All Fields])					
2731	2/6/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("mutate"[All Fields] OR "mutated"[All Fields] OR "mutates"[All Fields] OR "mutating"[All Fields] OR "mutation"[MeSH Terms] OR "mutation"[All Fields] OR "mutations"[All Fields] OR "mutation s"[All Fields] OR "mutational"[All Fields] OR "mutator"[All Fields] OR "mutators"[All Fields]) AND ("palatalization"[All Fields] OR "palatalized"[All Fields] OR "palatally"[All Fields] OR "palatals"[All Fields] OR "palate"[MeSH Terms] OR "palate"[All Fields] OR "palatal"[All Fields] OR "palates"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])	15	4	Zhang et al 2002, thomason et al 2008, Lan et al 2009, Li et al 2018	1	Lan et al 2009
2731	2/6/2023	("gene expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("fibroblast growth factor 10"[MeSH Terms] OR "fibroblast growth factor 10"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields]	8	2	Ohuchi et al 1997, Rice et al 2001	1	Ohuchi et al 1997

Supplementary table 1: Organization of search terms and results for all KERs.

		AND "proteins"[All Fields] OR "hedgehog proteins"[All Fields] AND ("fibroblast growth factor 8"[MeSH Terms] OR "fibroblast growth factor 8"[All Fields])					
2731	2/6/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields] AND ("fibroblast growth factors"[MeSH Terms] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factors"[All Fields]) OR "fibroblast growth factors"[All Fields] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields]) OR "fibroblast growth factor"[All Fields]) AND ("cleft palate"[MeSH Terms] OR ("cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])	15	1	Rice et al 2004,	1	Rice et al 2004
2732	1/27/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields] AND ("cell proliferation"[MeSH Terms] OR ("cell"[All Fields] AND "proliferation"[All Fields]) OR "cell proliferation"[All Fields]) AND ("mutate"[All Fields] OR "mutated"[All Fields] OR "mutates"[All Fields] OR "mutating"[All Fields] OR "mutation"[MeSH Terms] OR "mutation"[All Fields] OR "mutations"[All Fields] OR "mutation s"[All Fields] OR "mutational"[All Fields] OR "mutator"[All Fields] OR "mutators"[All Fields]) AND ("palatalization"[All Fields] OR "palatalized"[All Fields] OR "palatally"[All Fields])	15	4	Zhang et al 2002, thomason et al 2008, Lan et al 2009, Li et al 2018	2	Lan et al 2009, Zhang et al 2002

Supplementary table 1: Organization of search terms and results for all KERs.

		Fields] OR "palatals"[All Fields] OR "palate"[MeSH Terms] OR "palate"[All Fields] OR "palatal"[All Fields] OR "palates"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])					
2732	2/6/2023	("gene expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("fibroblast growth factor 10"[MeSH Terms] OR "fibroblast growth factor 10"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("fibroblast growth factor 8"[MeSH Terms] OR "fibroblast growth factor 8"[All Fields])	8	2	Ohuchi et al 1997, Rice et al 2001	1	Ohuchi et al 1997
2732	2/6/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("fibroblast growth factors"[MeSH Terms] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factors"[All Fields]) OR "fibroblast growth factors"[All Fields] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields]) OR "fibroblast growth factor"[All Fields]) AND ("cleft palate"[MeSH Terms] OR ("cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])	15	1	Rice et al 2004,	1	Rice et al 2004

Supplementary table 1: Organization of search terms and results for all KERs.

2732	2/6/2023	("cleft palate"[MeSH Terms] OR ("cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields]) AND ((("molecular"[All Fields] OR "moleculars"[All Fields]) AND ("aetiologie"[All Fields] OR "aetiologies"[All Fields] OR "aetiology"[All Fields] OR "etiologies"[All Fields] OR "etiology"[MeSH Subheading] OR "etiology"[All Fields] OR "causality"[MeSH Terms] OR "causality"[All Fields])) AND ("fibroblast growth factor 10"[MeSH Terms] OR "fibroblast growth factor 10"[All Fields]) AND ("transforming growth factor beta"[MeSH Terms] OR ("transforming"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields] AND "beta"[All Fields]) OR "transforming growth factor beta"[All Fields]))	1	1	Alappat et al 2005	1	Alappat et al 2005
2732	2/10/2023	("cyclin d1"[MeSH Terms] OR ("cyclin"[All Fields] AND "d1"[All Fields]) OR "cyclin d1"[All Fields]) AND ("cyclin d2"[MeSH Terms] OR ("cyclin"[All Fields] AND "d2"[All Fields]) OR "cyclin d2"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("mitogene"[All Fields] OR "mitogenes"[All Fields] OR "mitogenic"[All Fields] OR "mitogenically"[All Fields] OR "mitogenicity"[All Fields] OR "mitogens"[Pharmacological Action] OR "mitogens"[MeSH Terms] OR "mitogens"[All Fields] OR "mitogen"[All Fields]))	2	1	Kenney et al 2000	1	Kenney et al 2000
2732	2/10/2023	("cyclin d1"[MeSH Terms] OR ("cyclin"[All Fields] AND "d1"[All Fields]) OR "cyclin d1"[All Fields]) AND ("cycline"[All Fields] OR "cyclines"[All Fields] OR	4	2	Lan et al 2009,	2	Lan et al 2009,

Supplementary table 1: Organization of search terms and results for all KERs.

		"cyclins"[MeSH Terms] OR "cyclins"[All Fields] OR "cyclin"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("fibroblast growth factors"[MeSH Terms] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factors"[All Fields]) OR "fibroblast growth factors"[All Fields] OR ("fibroblast"[All Fields] AND "growth"[All Fields] AND "factor"[All Fields]) OR "fibroblast growth factor"[All Fields])			Lobjois et al 2004		Lobjois et al 2004
2734	1/18/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("receptor"[All Fields] OR "receptor s"[All Fields] OR "receptors"[All Fields]) AND "g-protein-coupled"[All Fields] AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("binding sites"[MeSH Terms] OR ("binding"[All Fields] AND "sites"[All Fields]) OR "binding sites"[All Fields]) AND ("trans activators"[MeSH Terms] OR "trans activators"[All Fields] OR ("trans"[All Fields] AND "activators"[All Fields]) OR "trans activators"[All Fields])	8	3	Frank-Kamenetsky et al 2002, Chen et al 2002a, Chen et al 2002b	2	Chen et al 2002a, Chen et al 2002b
2734	1/23/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields] OR ("hedgehog"[All Fields] AND "protein"[All Fields]) OR "hedgehog protein"[All Fields]) AND ("smoothened receptor"[MeSH Terms] OR	10	2	Frank-Kamenetsky et al 2002, Taipale et al 2000,	1	Taipale et al 2000

Supplementary table 1: Organization of search terms and results for all KERs.

		("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("receptors, g protein coupled"[MeSH Terms] OR ("receptors"[All Fields] AND "g protein coupled"[All Fields]) OR "g-protein-coupled receptors"[All Fields] OR "receptors g protein coupled"[All Fields]) AND "patch*"[All Fields] AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("trans activators"[MeSH Terms] OR "trans activators"[All Fields] OR ("trans"[All Fields] AND "activators"[All Fields]) OR "trans activators"[All Fields]) AND ("drug effects"[MeSH Subheading] OR ("drug"[All Fields] AND "effects"[All Fields]) OR "drug effects"[All Fields]) AND ((("cytoplasm"[MeSH Terms] OR "cytoplasm"[All Fields] OR "intracellular"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields] OR "signaling"[All Fields] OR "signal"[All Fields] OR "signal s"[All Fields] OR "signaled"[All Fields] OR "signaler"[All Fields] OR "signaler s"[All Fields] OR "signalers"[All Fields] OR "signalings"[All Fields] OR "signalization"[All Fields] OR "signalled"[All Fields] OR "signaller"[All Fields] OR "signaller s"[All Fields] OR "signallers"[All Fields] OR "signalling"[All Fields] OR "signallings"[All Fields] OR "signals"[All Fields]))					
2734	1/23/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("human	2	2	Taipale et al 2000,	2	Taipale et al 2000,

Supplementary table 1: Organization of search terms and results for all KERS.

	s"[All Fields] OR "humans"[MeSH Terms] OR "humans"[All Fields] OR "human"[All Fields]) AND "neoplasms/metabolism"[MeSH Terms] AND ("therapeutics"[MeSH Terms] OR "therapeutics"[All Fields] OR "therapies"[All Fields] OR "therapy"[MeSH Subheading] OR "therapy"[All Fields] OR "therapy s"[All Fields] OR "therapys"[All Fields]) AND ("patched receptors"[MeSH Terms] OR ("patched"[All Fields] AND "Receptors"[All Fields]) OR "patched receptors"[All Fields]) AND ("proto oncogene mas"[MeSH Terms] OR ("proto oncogene"[All Fields] AND "mas"[All Fields]) OR "proto oncogene mas"[All Fields] OR ("proto"[All Fields] AND "oncogene"[All Fields] AND "mas"[All Fields]) OR "proto oncogene mas"[All Fields]) AND "receptors, cell surface/metabolism"[MeSH Terms] AND ("receptors, g protein coupled"[MeSH Terms] OR ("Receptors"[All Fields] AND "g protein coupled"[All Fields]) OR "g-protein-coupled receptors"[All Fields] OR "receptors g protein coupled"[All Fields]) AND ("metabolic"[All Fields] OR "metabolical"[All Fields] OR "metabolically"[All Fields] OR "metabolics"[All Fields] OR "metabolism"[MeSH Terms] OR "metabolism"[All Fields] OR "metabolisms"[All Fields] OR "metabolism"[MeSH Subheading] OR "metabolities"[All Fields] OR "metabolization"[All Fields] OR "metabolize"[All Fields] OR "metabolized"[All Fields] OR "metabolizer"[All Fields] OR "metabolizers"[All Fields] OR "metabolizes"[All Fields] OR "metabolizing"[All Fields])			Rohatgi et al 2007	Rohatgi et al 2007
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Supplementary table 1: Organization of search terms and results for all KERs.

		Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields])					
2734	1/23/2023	"cleft lip/chemically induced"[MeSH Terms] AND ("metabolic"[All Fields] OR "metabolical"[All Fields] OR "metabolically"[All Fields] OR "metabolics"[All Fields] OR "metabolism"[MeSH Terms] OR "metabolism"[All Fields] OR "metabolisms"[All Fields] OR "metabolism"[MeSH Subheading] OR "metabolities"[All Fields] OR "metabolization"[All Fields] OR "metabolize"[All Fields] OR "metabolized"[All Fields] OR "metabolizer"[All Fields] OR "metabolizers"[All Fields] OR "metabolizes"[All Fields] OR "metabolizing"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields] OR "hedgehog proteins"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("cleft palate"[MeSH Terms] OR ("Cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields])	2	2	Heyne et al 2015, Lipinski et al 2008	1	Heyne et al 2015
2734	1/23/2023	("cholesterol"[MeSH Terms] OR "cholesterol"[All Fields] OR "cholesterol s"[All Fields] OR "cholesterole"[All Fields] OR "cholesterols"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields] OR "hedgehog proteins"[All Fields]) AND	8	1	Incardona et al 1998	1	Incardona et al 1998

Supplementary table 1: Organization of search terms and results for all KERs.

		("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("trans activators"[MeSH Terms] OR "trans activators"[All Fields] OR ("trans"[All Fields] AND "activator"[All Fields]) OR "trans activator"[All Fields]) AND ("alkaloidal"[All Fields] OR "alkaloide"[All Fields] OR "alkaloidic"[All Fields] OR "alkaloids"[MeSH Terms] OR "alkaloids"[All Fields] OR "alkaloid"[All Fields])					
2734	1/23/2023	("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("cilia"[MeSH Terms] OR "cilia"[All Fields] OR "eyelashes"[MeSH Terms] OR "eyelashes"[All Fields] OR "cilia" OR "eyelashes" OR "cilia" OR "eyelashes" AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("sonic"[All Fields] OR "sonically"[All Fields] OR "sonicate"[All Fields] OR "sonicated"[All Fields] OR "sonicates"[All Fields] OR "sonicating"[All Fields] OR "sonication"[MeSH Terms] OR "sonication"[All Fields] OR "sonications"[All Fields] OR "sonicator"[All Fields] OR "sonicators"[All Fields] OR "sonics"[All Fields]) AND ("craniofacial"[All Fields] OR "craniofacies"[All Fields])	13	2	Niida et al 2021, Millington et al 2017	1	Millington et al 2017
2734	1/23/2023	"cilia/drug effects"[MeSH Terms] AND ("metabolic"[All Fields] OR "metabolical"[All Fields] OR "metabolically"[All Fields] OR "metabolics"[All Fields] OR "metabolism"[MeSH Terms] OR "metabolism"[All Fields] OR "metabolisms"[All Fields] OR "metabolism"[MeSH Subheading] OR	7	3	Peluso et al 2014, Maurya et al 2017, Wang et al 2012	2	Maurya et al 2017, Wang et al 2012

Supplementary table 1: Organization of search terms and results for all KERs.

		"metabolities"[All Fields] OR "metabolization"[All Fields] OR "metabolize"[All Fields] OR "metabolized"[All Fields] OR "metabolizer"[All Fields] OR "metabolizers"[All Fields] OR "metabolizes"[All Fields] OR "metabolizing"[All Fields]) AND "hedgehog proteins/metabolism"[MeSH Terms] AND ("Cilia"[MeSH Terms] OR "Cilia"[All Fields] OR "eyelashes"[MeSH Terms] OR "eyelashes"[All Fields] OR "cilia"[All Fields]) AND ("drug effects"[MeSH Subheading] OR ("drug"[All Fields] AND "effects"[All Fields]) OR "drug effects"[All Fields]) AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields])					
2735	1/12/2023	((("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields] OR ("hedgehog"[All Fields] AND "protein"[All Fields]) OR "hedgehog protein"[All Fields]) AND ("cilia"[MeSH Terms] OR "cilia"[All Fields] OR "eyelashes"[MeSH Terms] OR "eyelashes"[All Fields] OR "cilia"[All Fields]) AND ("zinc fingers"[MeSH Terms] OR ("zinc"[All Fields] AND "fingers"[All Fields]) OR "zinc fingers"[All Fields] OR	17	4	Kim et al 2009, quin et al 2011, tukachinsky et al 2010, may et al 2005	1	Kim et al 2009

Supplementary table 1: Organization of search terms and results for all KERs.							
		("zinc"[All Fields] AND "finger"[All Fields]) OR "zinc finger"[All Fields] AND ("protein transport"[MeSH Terms] OR ("protein"[All Fields] AND "transport"[All Fields]) OR "protein transport"[All Fields])) NOT (neuro*)					
2735	1/12/2023	("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("patched receptors"[MeSH Terms] OR ("patched"[All Fields] AND "receptors"[All Fields]) OR "patched receptors"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("gene expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("receptors, cell surface"[MeSH Terms] OR ("receptors"[All Fields] AND "cell"[All Fields] AND "surface"[All Fields]) OR "cell surface receptors"[All Fields] OR ("receptors"[All Fields] AND "cell"[All Fields] AND "surface"[All Fields]) OR "receptors cell surface"[All Fields]) AND ("canonic"[All Fields] OR "canonical"[All Fields] OR "canonically"[All Fields] OR "canonicals"[All Fields])	5	2	Doheny et al 2020, Blotta et al 2012	1	Blotta et al 2012
2735	1/12/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND	6	2	rhogati et al 2007,	1	Huang et al 2016

Supplementary table 1: Organization of search terms and results for all KERs.

		("cholesterol"[MeSH Terms] OR "cholesterol"[All Fields] OR "cholesterol s"[All Fields] OR "cholesterole"[All Fields] OR "cholesterols"[All Fields]) AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("protein binding"[MeSH Terms] OR ("protein"[All Fields] AND "binding"[All Fields]) OR "protein binding"[All Fields]) AND ("oxysterols"[MeSH Terms] OR "oxysterols"[All Fields] OR "oxysterol"[All Fields])			Huang et al 2016		
2735	1/13/2023	("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("cilia"[MeSH Terms] OR "cilia"[All Fields] OR "eyelashes"[MeSH Terms] OR "eyelashes"[All Fields] OR "cilias"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("sonic"[All Fields] OR "sonically"[All Fields] OR "sonicate"[All Fields] OR "sonicated"[All Fields] OR "sonicates"[All Fields] OR "sonicating"[All Fields] OR "sonication"[MeSH Terms] OR "sonication"[All Fields] OR "sonications"[All Fields] OR "sonicator"[All Fields] OR "sonicators"[All Fields] OR "sonics"[All Fields]) AND ("craniofacial"[All Fields] OR "craniofacies"[All Fields])	13	2	Niida et al 2021, Millington et al 2017	1	Millington et al 2017
2735	1/13/2023	("gene expression regulation"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields] AND "regulation"[All Fields]) OR "gene expression regulation"[All Fields]) AND ("transcription	11	2	Zhang et al 2013, Kogerman et al 1999	1	Kogerman et al 1999

Supplementary table 1: Organization of search terms and results for all KERs.

		factors"[MeSH Terms] OR ("transcription"[All Fields] AND "factors"[All Fields]) OR "transcription factors"[All Fields] AND "gli1"[All Fields] AND (("zinc fingers"[MeSH Terms] OR ("zinc"[All Fields] AND "fingers"[All Fields]) OR "zinc fingers"[All Fields] OR ("zinc"[All Fields] AND "finger"[All Fields]) OR "zinc finger"[All Fields]) AND ("protein s"[All Fields] OR "proteinous"[All Fields] OR "proteins"[MeSH Terms] OR "proteins"[All Fields] OR "protein"[All Fields])) AND ("embryo s"[All Fields] OR "embryoes"[All Fields] OR "embryonic structures"[MeSH Terms] OR ("embryonic"[All Fields] AND "structures"[All Fields]) OR "embryonic structures"[All Fields] OR "embryo"[All Fields] OR "embryos"[All Fields]) AND (("suppressor"[All Fields] OR "suppressors"[All Fields]) AND ("fused"[All Fields] OR "fuses"[All Fields] OR "fusing"[All Fields]))					
2882	4/10/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("cell death"[MeSH Terms] OR ("cell"[All Fields] AND "death"[All Fields]) OR "cell death"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("gene expression"[MeSH Terms] OR ("gene"[All Fields] AND "expression"[All Fields]) OR "gene	17	1	Ahlgren et al 2002	1	Ahlgren et 2002

Supplementary table 1: Organization of search terms and results for all KERs.

		expression"[All Fields] AND ("patched receptors"[MeSH Terms] OR ("patched"[All Fields] AND "receptors"[All Fields]) OR "patched receptors"[All Fields])					
2882	5/1/2023	("apoptosis"[MeSH Terms] OR "apoptosis"[All Fields]) AND ("embryology"[MeSH Subheading] OR "embryology"[All Fields] OR ("embryonic"[All Fields] AND "development"[All Fields]) OR "embryonic development"[All Fields] OR "embryonic development"[MeSH Terms] OR ("embryonic"[All Fields] AND "development"[All Fields])) AND (("hedgehogs"[MeSH Terms] OR "hedgehogs"[All Fields] OR "hedgehog"[All Fields]) AND "protiens"[All Fields] AND ("embryonic development"[MeSH Terms] OR ("embryonic"[All Fields] AND "development"[All Fields])) OR "embryonic development"[All Fields] OR "embryogenesis"[All Fields] AND ("cleft"[All Fields] OR "clefted"[All Fields] OR "clefing"[All Fields] OR "clefts"[All Fields]) AND ("n n bis 2 chloroethyl nitrosocarbamoyl cystamine"[Supplementary Concept] OR "n n bis 2 chloroethyl nitrosocarbamoyl cystamine"[All Fields] OR "cncc"[All Fields]))	1	1	Kurosaka et al 2019	1	Kurosaka et al 2019
2894	1/23/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields] OR ("hedgehog"[All Fields] AND "protein"[All Fields]) OR "hedgehog protein"[All Fields]) AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All	10	2	Frank-Kamenetsky et al 2002, Taipale et al 2000,	1	Taipale et al 2000

Supplementary table 1: Organization of search terms and results for all KERs.

		Fields]) OR "smoothened receptor"[All Fields]) AND ("receptors, g protein coupled"[MeSH Terms] OR ("receptors"[All Fields] AND "g protein coupled"[All Fields]) OR "g-protein-coupled receptors"[All Fields] OR "receptors g protein coupled"[All Fields]) AND "patch*"[All Fields] AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("trans activators"[MeSH Terms] OR "trans activators"[All Fields] OR ("trans"[All Fields] AND "activators"[All Fields]) OR "trans activators"[All Fields]) AND ("drug effects"[MeSH Subheading] OR ("drug"[All Fields] AND "effects"[All Fields]) OR "drug effects"[All Fields]) AND (("cytoplasm"[MeSH Terms] OR "cytoplasm"[All Fields] OR "intracellular"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields] OR "signaling"[All Fields] OR "signal"[All Fields] OR "signal s"[All Fields] OR "signaled"[All Fields] OR "signaler"[All Fields] OR "signaler s"[All Fields] OR "signaler s"[All Fields] OR "signaling s"[All Fields] OR "signaling s"[All Fields] OR "signaling s"[All Fields] OR "signalled"[All Fields] OR "signaller"[All Fields] OR "signaller s"[All Fields] OR "signallers"[All Fields] OR "signalling"[All Fields] OR "signallings"[All Fields] OR "signallings"[All Fields] OR "signals"[All Fields]))					
2894	1/18/2023	("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("receptor"[All Fields] OR "receptor s"[All Fields] OR	8	3	Frank-Kamenetsky et al 2002, Chen et al	1	Chen et al 2002

Supplementary table 1: Organization of search terms and results for all KERs.

		"receptors"[All Fields] AND "g-protein-coupled"[All Fields] AND ("smoothened receptor"[MeSH Terms] OR ("smoothened"[All Fields] AND "receptor"[All Fields]) OR "smoothened receptor"[All Fields]) AND ("binding sites"[MeSH Terms] OR ("binding"[All Fields] AND "sites"[All Fields]) OR "binding sites"[All Fields]) AND ("trans activators"[MeSH Terms] OR "trans activators"[All Fields] OR ("trans"[All Fields] AND "activators"[All Fields]) OR "trans activators"[All Fields])			2002a, Chen et al 2002b		
2894	1/23/2023	"cleft lip/chemically induced"[MeSH Terms] AND ("metabolic"[All Fields] OR "metabolical"[All Fields] OR "metabolically"[All Fields] OR "metabolics"[All Fields] OR "metabolism"[MeSH Terms] OR "metabolism"[All Fields] OR "metabolisms"[All Fields] OR "metabolism"[MeSH Subheading] OR "metabolities"[All Fields] OR "metabolization"[All Fields] OR "metabolize"[All Fields] OR "metabolized"[All Fields] OR "metabolizer"[All Fields] OR "metabolizers"[All Fields] OR "metabolizes"[All Fields] OR "metabolizing"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal transduction"[All Fields]) AND ("cleft palate"[MeSH Terms] OR ("Cleft"[All Fields] AND "palate"[All Fields]) OR "cleft palate"[All Fields])	2	2	Heyne et al 2015, Lipinski et al 2008	1	Heyne et al 2015
2894	1/23/2023	("signal transduction"[MeSH Terms] OR ("signal"[All Fields] AND "transduction"[All Fields]) OR "signal	13	2	Niida et al 2021,	1	Millington et al 2017

Supplementary table 1: Organization of search terms and results for all KERs.

		transduction"[All Fields]) AND ("cilia"[MeSH Terms] OR "cilia"[All Fields] OR "eyelashes"[MeSH Terms] OR "eyelashes"[All Fields] OR "cilias"[All Fields]) AND ("hedgehog proteins"[MeSH Terms] OR ("hedgehog"[All Fields] AND "proteins"[All Fields]) OR "hedgehog proteins"[All Fields]) AND ("sonic"[All Fields] OR "sonically"[All Fields] OR "sonicate"[All Fields] OR "sonicated"[All Fields] OR "sonicates"[All Fields] OR "sonicating"[All Fields] OR "sonication"[MeSH Terms] OR "sonication"[All Fields] OR "sonications"[All Fields] OR "sonicator"[All Fields] OR "sonicators"[All Fields] OR "sonics"[All Fields]) AND ("craniofacial"[All Fields] OR "craniofacies"[All Fields])			Millington et al 2017		
2894	5/2/2023	("cyclopamine"[Supplementary Concept] OR "cyclopamine"[All Fields]) AND ("cleft"[All Fields] OR "clefted"[All Fields] OR "clefing"[All Fields] OR "clefts"[All Fields])	14	2	Lipinski et al 2010, Lipinski et al 2014	2	Lipinski et al 2010, Lipinski et al 2014

Supplementary table 2: Dose concordance for AOP. Studies were recorded for dose and any indication of any of the KEs in the AOP were noted.

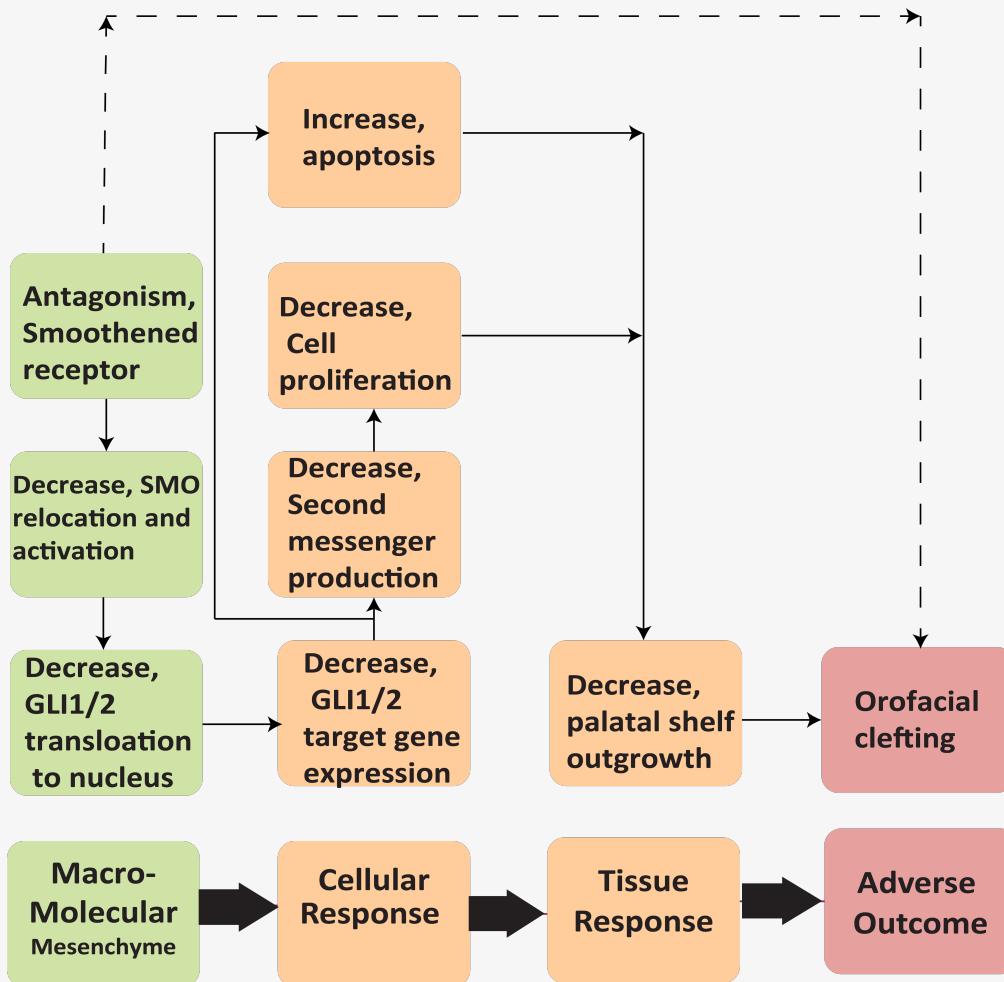
Reference	Taxonomic Applicability	Life stage/ exposure period	Type	Conc entra tion	Additional exposure details	MIE 2027	KE 2044	KE 2028	KE 2040	KE 1262	KE 2043	KE 1821	KE 2041	AO 2042	Notes
Heyne et al 2015	mouse- C57BL/6J	embryonic GD 7.0-10.0	vismod egib (GDC-0449)	40mg /kg	oral gavage									X	
Heyne et al 2015	mouse- C57BL/6J	embryonic GD 8.25-9.9375	cyclopamine	120mg g/kg/d	subcutaneous									X	
Lipinski, Song et al 2010	mouse- C57BL/6J	embryonic GD 8.25	cyclopamine	120mg g/kg/d	subcutaneous micro osmotic pump									X	25/45 pups had cleft
Millington et al 2017	mouse- Kif3af/f; Wnt1-Cre	embryonic						X						X	GLI1 downregulation evidenced via RNA-seq
Maurya et al 2017	mouse- C57BL/6J	postnatal day 12-14	vismod egib (GDC-0449)	40mg /kg	5 doses 12h apart subcutaneous		X								Evidenced using decreased ciliary immunofluorescence for M71/M72
Maurya et al 2018	mouse- Smofl/fi; CRE	E18.5					X								Evidenced via BrdU that exogenous SHH induced proliferation in palatal mesenchyme explants
Incardona et al 1998	white leghorn chick- neural plate explant	stage 9-10	cyclopamine	120nm		X									disruption of SHH signaling evidenced via immunostaining for pax7
Kogerman, Grimm et al 1999	mouse	GD 8.5-15.5						X							disruption of SHH signaling evidenced via immunostaining for pax7
Eversen, Fink et al 2017	mouse- C57BL/6J	GD 8.25-9.375	cyclopamine	120mg g/kg/d	subcutaneous micro osmotic pump				X			X		X	Evidenced via RT-PCR showing down regulation of GLI1 and PTCH1 as well as nine Fox members: Foxa2, Foxb2, Foxc1, Foxc2, Foxd1, Foxe1, Foxf1, Foxf2, Foxl1 Evidenced via ki-67 staining showing decrease proliferation in for GD 10.25 embryos in medial portion of the MNP
Lan and Jiang 2009	mouse- Osr2-IresCre;Smoc/c (SMO inactive)	embryonic							X		X	X	X	X	Evidenced by down regulation of PTCH1 and GLI1 in the palatal shelves Evidenced via in situ hybridization showing decrease in FGF10 correlated with down regulation of PTCH1 Evidenced by reduced cnd1 and cnd2 mRNA expression in palatal mesenchyme of mutants Evidenced by mutant E 14.5 palatal shelves having retarded growth and not making contact
Jeong, Mao et al 2005	mouse- Wnt1-Cre;Smoc/c (SMO inactive)	embryonic -GD 9.5, 10.5, 12.5						X		X	X		X		Evidenced via in situ hybridization of facial primordia showing down regulation of PTCH1, FOXC2, FOXD1, FOXD2, FOXF1, FOXF2 Evidenced for CNCCs in MNAs at E9.5, 10.5 via staining using rabbit anti-cleaved- caspase 3 antibody Evidenced in MNAs at E11.5 via staining using anti-phospho-histone H3 antibody Evidenced via decrease in mandibular arch in both PD and DV axes
Ohuchi et al 1997	chick	embryonic									X				Evidenced through observation of rudimentary palatal shelves that are spaced apart without contact
Rice, Spencer-Dene et al 2004	mouse- K14Cre;Shhc/n (shh null epithelium)												X	X	Evidenced through observation of rudimentary palatal shelves that are spaced apart without contact
Rice, Spencer-Dene et al 2005	mouse- K14Cre;Smoc/n (SMO inactive epithelium)														clefting not observed suggesting SHH exerts its' effect on adjacent mesenchyme

Supplementary table 2: Dose concordance for AOP. Studies were recorded for dose and any indication of any of the KEs in the AOP were noted.

Reference	Taxonomic Applicability	Life stage/ exposure period	Type	Conc entra tion	Additional exposure details	MIE 2027	KE 2044	KE 2028	KE 2040	KE 1262	KE 2043	KE 1821	KE 2041	AO 2042	Notes
Rice, Spencer-Dene et al 2006	mouse- Fgf10-/-										X				Evidenced via BrdU that exogenous SHH induced proliferation in palatal mesenchyme explants. Exogenous FGF10 also induced proliferation. Evidenced via <i>in situ</i> hybridization showing decrease in SHH in palatal epithelium
Rice, Spencer-Dene et al 2007	mouse- Fgfr2b-/-										X	X			Evidenced via <i>in situ</i> hybridization showing decrease in SHH in palatal epithelium Evidenced via BrdU that exogenous SHH induced proliferation in palatal mesenchyme explants
Zhang, Song et al 2002	Mouse- CD-1	Embryonic- E13.5										X			Evidenced through SHH beads inducing proliferation in palatal shelves as measured through BrdU
Zhang, Song et al 2002	Mouse- MSX1-/-	Embryonic- E13.5										X			Evidenced through SHH beads inducing proliferation in palatal shelves as measured through BrdU
Yamagishi, Yamagishi et al 2006	mouse-SHH-/-	embryonic									X		X		Evidenced via TUNNEL assay at E9.0 and E9.5 Evidenced via hypoplasia in PA1 at E9.5
Keeler et al 1975	Rat-sprague Dawley	embryonic GD 6-9	cyclopamine	240m g/kg/ day	oral gavage									X	
Keeler et al 1975	golden hamster	embryonic GD 6-9	cyclopamine	170m g/kg/ day	oral gavage									X	
Omnell, Sim et al 1990	mouse- C57BL/6J	embryonic GD 8	jervine	70, 150, 300m g/kg	single dose gavage									X	dose response pattern for CLP
Omnell, Sim et al 1990	mouse- A/J	embryonic GD 8	jervine	70, 150, 300m g/kg	single dose gavage									X	dose response pattern for CLP

AOP ID and Title:

AOP 460: Antagonism of Smoothened receptor leading to orofacial clefting
Short Title: Antagonism SMO leads to OFC

Graphical Representation**Authors**

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Status

Author status	OECD status	OECD project	SAAOP status
Under development: Not open for comment. Do not cite	Under Development	1.101	Included in OECD Work Plan

Abstract

The Sonic Hedgehog (SHH) is a major signaling pathway of intercellular signaling during embryonic development. Disruption of SHH during critical periods of development can lead to orofacial clefts (OFCs). In canonical SHH signaling, the SHH ligand binds to the Patched1 (PTCH1) receptor and relieves its' suppression of Smoothened (SMO) receptor. Antagonism of SMO results in disruption of the downstream SHH signaling cascade. Disruption to the signaling cascade causes a decrease in the translocation of the GLI1/2 transcription factors to the nucleus resulting in a decrease in expression of the GLI1/2 target genes. This decrease in gene expression causes a reduction in production of SHH secondary messengers, namely Fgf10 and members of the BMP family. This reduction in secondary messengers leads to a decrease in cellular proliferation in the palatal shelves. This reduction in cellular proliferation leads to a decrease in palatal shelf outgrowth which ultimately results in a cleft. This AOP is intended to serve as a tool

for risk assessment for drug and chemical exposures during embryonic development when disruption to SHH through antagonism of SMO occurs.

Background

This AOP was developed as part of a larger network of AOPs linking disruption of SHH signaling with OFCs (OECD Advisory Group on Emerging Science in Chemicals Assessment (ESCA) workplan project 1.101.). This was the first AOP of the network to be developed and was selected due most stressors of the SHH pathway being believed to work at the level of SMO. Development was led by the Johnson lab at Michigan State University and coached by Dr. Judy Choi. This AOP serves as the primary literature for graduate student Jacob Reynolds' dissertation project. This work was supported by the National Institutes of Health R00-ES028744 and the National Institute of Environmental Health Sciences P42ES004911.

Summary of the AOP

Events

Molecular Initiating Events (MIE), Key Events (KE), Adverse Outcomes (AO)

Sequence	Type	Event ID	Title	Short name
1	MIE	2027	Antagonism, Smoothened receptor	Antagonism Smoothened
	KE	2044	Decrease, Smoothend relocation and activation	Decrease, SMO relocation
2	KE	2028	Decrease, GLI1/2 translocation to nucleus	Decrease, GLI1/2 translocation
	KE	2040	Decrease, GLI1/2 target gene expression	Decrease, GLI1/2 target gene expression
	KE	1262	Apoptosis	Apoptosis
	KE	2043	Decrease, Sonic Hedgehog second messenger production	Decrease, SHH second messenger production
	KE	1821	Decrease, Cell proliferation	Decrease, Cell proliferation
	KE	2041	Decrease, facial prominence outgrowth	Decrease, facial prominence outgrowth
	AO	2042	Increase, Orofacial clefting	orofacial cleft

Key Event Relationships

Upstream Event	Relationship Type	Downstream Event	Evidence	Quantitative Understanding
Antagonism, Smoothened receptor	adjacent	Decrease, Smoothend relocation and activation	Moderate	Low
Decrease, Smoothend relocation and activation	adjacent	Decrease, GLI1/2 translocation to nucleus	Moderate	Low
Decrease, GLI1/2 translocation to nucleus	adjacent	Decrease, GLI1/2 target gene expression	Low	Low
Decrease, GLI1/2 target gene expression	adjacent	Decrease, Sonic Hedgehog second messenger production	Low	Low
Decrease, Sonic Hedgehog second messenger production	adjacent	Decrease, Cell proliferation	Low	Low
Decrease, Cell proliferation	adjacent	Decrease, facial prominence outgrowth	Low	Low
Decrease, facial prominence outgrowth	adjacent	Increase, Orofacial clefting	Moderate	Low
Apoptosis	adjacent	Decrease, facial prominence outgrowth	Low	Low
Decrease, GLI1/2 target gene expression	adjacent	Apoptosis	Low	Low

Upstream Event	Relationship Type	Downstream Event	Evidence	Quantitative Understanding												
Antagonism, Smoothened receptor	non-adjacent	Increase, Orofacial clefting	High	Moderate												
Stressors																
<table> <thead> <tr> <th>Name</th><th>Evidence</th></tr> </thead> <tbody> <tr> <td>Vismodegib</td><td>High</td></tr> <tr> <td>SANT-1</td><td></td></tr> <tr> <td>SANT-2</td><td></td></tr> <tr> <td>SANT-3</td><td></td></tr> <tr> <td>SANT-4</td><td></td></tr> </tbody> </table>					Name	Evidence	Vismodegib	High	SANT-1		SANT-2		SANT-3		SANT-4	
Name	Evidence															
Vismodegib	High															
SANT-1																
SANT-2																
SANT-3																
SANT-4																
Vismodegib																
<p>Vismodegib (GDC-0449) is small molecule modulator of the sonic hedgehog (shh) pathway. It functions as an antagonist by binding to Smoothened (SMO) blockings its' activation and subsequent downstream signalling cascade. Vismodegib became the first agent approved to target the shh pathway in Jan. 2012 by the US FDA. It was approved by the European Medicines Agency (EMA) in July 2012 (Meiss, Andrlová et al. 2018). It has been used to identify critical periods of development for the shh pathway. Pregnant C57BL/6J mice dosed with 40mg/kg of Vismodegib between E7 and E10.0 had a peak incidence of CPO (34.38%) at E9.5(Heyne, Melberg et al. 2015). Pregnant C57BL/6J mice treated with 100mg/kg vismodegib via oral gavage at E10.5 and E12.5 displayed a 100% penetrance of complete cleft palate (Zhang, Wang et al. 2017). In a HWJSC/HPEKp spheroid fusion model 10µm vismodegib did not affect HPEKp viability or migration, did not affect <i>in vitro</i> fusion (Belair, Wolf et al. 2018).</p>																
Overall Assessment of the AOP																
<p>Annex 1 Table, Assessment of the relative level of confidence in the overall AOP based on rank ordered weight of evidence elements is attached in PDF format.</p>																
Annex 1																
Domain of Applicability																
<p>Life Stage Applicability</p> <p>Life Stage Evidence</p> <table> <tbody> <tr> <td>Embryo</td><td>High</td></tr> </tbody> </table> <p>Taxonomic Applicability</p> <p>Term Scientific Term Evidence Links</p> <table> <tbody> <tr> <td>mouse</td><td>Mus musculus</td><td>NCBI</td></tr> </tbody> </table> <p>Sex Applicability</p> <p>Sex Evidence</p> <table> <tbody> <tr> <td>Unspecific</td><td>High</td></tr> </tbody> </table>					Embryo	High	mouse	Mus musculus	NCBI	Unspecific	High					
Embryo	High															
mouse	Mus musculus	NCBI														
Unspecific	High															
<p>Chemical: This AOP applies to antagonists of the SMO receptor. Chemical modulators of the SHH pathway have been identified including the natural alkaloid cyclopamine, both natural and synthetic pharmaceuticals (e.g. Vismodegib), the widely used pesticide synergist piperonyl butoxide (PBO) with established human exposures (Lipinski, Dengler et al. 2007, Lipinski, Song et al. 2010, Wang, Lu et al. 2012, Everson, Sun et al. 2019, Rivera-González, Beames et al. 2021).</p> <p>Sex: This AOP is unspecific to sex.</p> <p>Life Stages: The relevant life stage for this AOP is embryonic development. More specifically, the development of the craniofacial region which occurs between GD 10.0 and GD 14.0 in the mouse and week 4-12 in human.</p> <p>Taxonomic: At present, the empirical taxonomic applicability domain of this AOP is mouse (mus musculus). Most of the toxicological data that this AOP is based on has used mice as their model organism. Mice are a good analog of human craniofacial development and undergo similar signaling by SHH. The plausible domain of applicability for this AOP is mammals due to the largely conserved mechanisms of orofacial development and embryonic pathway</p>																

signaling.

Essentiality of the Key Events

To date, few studies have addressed the essentiality of the proposed sequence of key events. Evidence linking SHH disruption through a decrease in proliferation exists. The hypothesized sequence of events has a high temporal concordance for canonical SHH signaling pathway and orofacial development.

- Studies have shown that SHH signaling is required for normal facial development and plays a critical role in the growth of the facial processes that form the upper palate and lip (Bush and Jiang 2012, Kurosaka 2015).
- The epithelial derived SHH drives orofacial development through an induced gradient in the underlying mesenchyme (Lan and Jiang 2009, Kurosaka 2015). This gradient of SHH induces cellular proliferation and outgrowth of the mesenchyme (Lan and Jiang 2009).
- OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015).

Weight of Evidence Summary

Evidence Assessment

- **KER ID**-Title-[Adjacency], [Evidence], [Quantitative Understanding]

• **Relationship 2734:** Antagonism Smoothened (Event 2027) leads to Decrease, SMO relocation (Event 2044)-[Adjacent], [Moderate], [Low]-There is a high biological plausibility of this relationship and SMO localization to the primary cilia is essential for proper SHH signaling in vertebrates (Corbit, Aanstad et al. 2005, Rohatgi, Milenovic et al. 2007, Rohatgi, Milenovic et al. 2009). There is good evidence that the SANT compounds block the localization of SMO to the tip of the primary cilia. Contradictory *in vivo* data was found regarding whether cyclopamine blocks SMO relocation to the primary cilia. Further work is required to determine if SMO antagonism via cyclopamine results in decrease in SMO relocation.

• **Relationship 2735:** Decrease, SMO relocation (Event 2044) leads to Decrease, GLI1/2 translocation (Event 2028)-[Adjacent], [Moderate], [Low]- Moderate evidence is presented to support that a loss of SMO relocation to the primary cilia leads to a significant decrease in GLI1. GLI1 requires activation prior to nuclear translocation.

• **Relationship 2721:** Decrease, GLI1/2 translocation (Event 2028) leads to Decrease, GLI1/2 target gene expression (Event 2040)-[Adjacent], [Low], [Low]- There is high biological plausibility of this relationship but to date few studies were found to explore the relationship.

• **Relationship 2731:** Decrease GLI1/2 target gene expression (Event 2040) leads to Decrease, SHH second messenger production (Event 2043)-[Adjacent], [Low], [Low]-Coordinated signaling is paramount for proper embryonic development and the GLI signaling cascade drives feedback/forward loops with FGF and BMP signaling pathways. Support was found for SHH having a feedforward loop with FGF10 and BMP4 however further investigation into the interaction of these pathways and their crosstalk is required.

• **Relationship 2732:** Decrease SHH second messenger production (Event 2043) leads to Decrease, cell proliferation (Event 1821)-[Adjacent], [Low], [Low]- SHH is a known mitogen and drives proliferation through its' secondary messengers. SHH was found to induce proliferation and FGF10 *in vivo*.

• **Relationship 2724:** Decrease, Cell proliferation (Event 1821) leads to Decrease, outgrowth (Event 2041)-[Adjacent], [Low], [Low]-SHH is a known mitogen that helps to drive the proper development of the face which includes the outgrowth of the facial prominences. To date, few studies have measured by outgrowth of the facial prominences and proliferation. Hypoplasia of pharyngeal arch 1 was found in SHH-/- embryos supporting that outgrowth is driven by proliferation and is reduced when proliferation is decreased.

• **Relationship 2726:** Decrease, outgrowth (Event 2041) leads to OFC (Event 2042)-[Adjacent], [Moderate], [Low]- OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced mesenchymal proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015). Mice with disrupted SHH signaling are found to have palatal shelves that are spaced apart supporting that the cleft results from an EMT dependent, but epithelial-mesenchyme transition (EMT) independent manner.

• **Relationship 2792:** Apoptosis (Event 1262) leads to Decrease, outgrowth (Event 2041)-[Adjacent], [Low], [Low]-

SHH signaling is known to be associated with cell survival and there is a high biological plausibility that increasing apoptosis would cause a decrease in outgrowth. Supporting evidence is offered with increases in apoptosis in the mandibular arch seen in SHH signaling disrupted mice that exhibit decreased outgrowth.

- **Relationship 2882:** Decrease, GLI1/2 target gene expression (Event 2040) leads to Apoptosis (Event 1262) - [Adjacent], [Low], [Low]- To date few studies have examined the relationship of GLI1/2 target gene expression. There is a high biological plausibility that SHH plays a role in cell survival and death through GLI1/2 target gene expression. Decreased GLI1/2 target gene expression is seen in RA exposed dams alongside increased apoptosis on the cranial neural crest cells (CNCC).

- **Relationship 2894:** Antagonism Smoothened (Event 2027) leads to OFC (Event 2042)-[Non-adjacent], [High], [Moderate]- multiple studies have demonstrated *in vivo* that administration of SMO antagonists during critical windows of exposure leads to birth defects including OFC in a dose-dependent fashion.

Biological Plausibility

Biological plausibility refers to the structural and/or functional relationship that exists between the key events based on our understanding of normal biology. SHH signaling is largely conserved in mammals and is required for normal facial development and plays a critical role in the growth of the facial processes that form the upper palate and lip (Bush and Jiang 2012, Kurosaka 2015). Multiple antagonists of the SMO receptor have been identified through binding studies. Identified SMO antagonists include cyclopamine, vismodegib, PBO, and the SANT compounds (Lipinski, Dengler et al. 2007, Lipinski, Song et al. 2010, Wang, Lu et al. 2012, Everson, Sun et al. 2019, Rivera-González, Beames et al. 2021). While the level of support for most of the KERs is low, there is high support for the non-adjacent relationship linking antagonism of SMO and OFC.

Concordance of dose-response relationships

Agreed, Wiki updated- There are a limited number of studies in which multiple key events were assessed in the same study following exposure to known SMO antagonists. These studies form the basis of the dose-response concordance of this AOP. A summary of the dose-concordance can be found in Supplementary Table 2. Many of the studies identified while researching this AOP were performed using a single dose of antagonist making the study not suited for dose response concordance. This AOP would benefit greatly from increased studies designed to explore the dose-response concordance of the proposed relationships. The concentration-dependence of the key event responses regarding concentration of known *in vitro* and/or *in vivo* for some of the KEs in this AOP is summarized below.

- Concentration dependent clefting with cyclopamine exposure (Omnell, Sim et al. 1990)
- Dose dependent binding to SMO (Chen, Taipale et al. 2002)
- Concentration dependent decrease in SMO-ciliary accumulation *in vitro* for vismodegib exposure (Wang, Arvanites et al. 2012)

Temporal concordance

The hypothesized sequence of events is supported by the existing data and follow the field's current understanding of the canonical SHH signaling pathway.

Consistency

The AO is not specific to this AOP. Many of the events in this AOP will overlap with AOPs linking disruption of SHH to OFC and some are expected to overlap with AOPs linking other developmental signaling pathways to OFCs.

Uncertainties, inconsistencies, and data gaps

This AOP would be strengthened by studies examining the dose-response and time-course relationships for these KERs. The main data gaps for this AOP exist in the lack of studies that have examined the relationship in the context of dose response or time course. Additional studies using the mice would help to strengthen this AOP.

Data gaps:

- Dose response and time course studies relating a Decrease, SMO relocation leads to Decrease, GLI1/2 translocation
- Dose response and time course studies relating a decrease GLI translocation leads to decrease GLI target gene expression
- Dose response and time course studies relating a Decrease, GLI1/2 target gene expression leads to Decrease, SHH second messenger production
- Dose response and time course studies relating a Decrease, SHH second messenger production leads to Decrease, Cell proliferation
- Dose response and time course studies relating a Decrease, Cell proliferation leads to Decrease, outgrowth
- Dose response and time course studies relating a Decrease, outgrowth leads to OFC
- Dose response and time course studies relating a Apoptosis leads to Decrease, Outgrowth
- Dose response and time course studies relating a Decrease, GLI1/2 target gene expression leads to Apoptosis

Inconsistencies:

- While it is well understood that cyclopamine is an antagonist of SMO, contradictory *in vivo* data was found regarding whether cyclopamine blocks SMO relocation to the primary cilia. Rohatgi et al used NIH 3T3s cell and found

that cyclopamine did not inhibit the accumulation of SMO in the cilia even when dosed at 5-10 μ m (>10 fold above K_d). All three antagonists inhibited SHH pathway transduction and target gene expression (Rohatgi, Milenovic et al. 2009). Corbit et al used a renal epithelial MDCK (Madin-Darby canine kidney) line was engineered to express Myc-tagged SMO. Following culture for 1hr in SHH conditioned media SMO presence in the primary cilium is upregulated while cells cultured in the presence of cyclopamine see a downregulation of SMO in the primary cilia (Corbit, Aanstad et al. 2005). Further work is required to determine if SMO antagonism via cyclopamine results in decrease in SMO relocation.

Uncertainties:

- While we know that entry to the cilia is tightly controlled, the exact mechanism of SMO ciliary trafficking is not fully understood. The primary cilia (PC) is separated from the plasma membrane by the ciliary pockets and the transition zone which function together to regulate the movement of lipids and proteins in and out of the organelle (Goetz, Ocbina et al. 2009, Rohatgi and Snell 2010). The SHH receptor PTCH contains a ciliary localization sequence in its' carboxy tail. Localization of PTCH to the PC is essential for inhibition of SMO as deletion of the CLS in PTCH prevents PTCH localization as well as inhibition of SMO (Kim, Hsia et al. 2015) (53). SMO also contains a CLS, but only accumulates in the PC upon ligand binding (Corbit, Aanstad et al. 2005). The entry of SMO into the PC is thought to occur either laterally through the ciliary pockets or internally via recycling endosomes (Milenovic, Scott et al. 2009). Once inside the PC, SMO can diffuse freely, however it will usually accumulate in specific locations depending upon its' activation state. Inactive SMO will accumulate more at the base of the PC while active SMO will accumulate in the tip of the PC (Milenovic, Weiss et al. 2015).
- The relationships and feedback/feedforward loops that exist between SHH and its' secondary messengers primarily FGF10 and BMP4 are not well understood. More investigation into these relationships is warranted.
- The exact mechanism through which SHH promotes cell survival is not well understood. Further studies are needed to illuminate the mechanism that links SHH signaling with cell survival.
- The relationship between GLI1/2 target gene expression and increased apoptosis has a high biological plausibility although there is currently lack of studies that address this relationship.

Quantitative Consideration

Assessment of quantitative understanding of the AOP:

The quantitative understanding for this AOP with the exception of the non-adjacent relationship between Antagonism Smoothened leads to OFC is low. Most of the data found through the literature search was obtained from studies that employed a single dose and were not conducted with dose-response or time-course in mind. For Antagonism Smoothend leads to OFC several studies with dose response data showing a dose-dependent incidence of clefting were found. This AOP would benefit from the generation of additional data that addresses these relationships in a dose response and time course methodology to allow for an increased quantitative understanding of the linkage.

Considerations for Potential Applications of the AOP (optional)

Considerations for potential applications of the AOP

The intended use of this AOP from a regulatory standpoint is to improve predictive potential of developmental hazards as they relate to the SHH pathway and OFCs. It is hoped that this AOP can be applied to data from *in silico* and *in vitro* high-throughput screening assays (HTS) to guide selection of agents for further investigation in more representative models of orofacial development. Disruption of the Sonic Hedgehog pathway has broader outcomes than just OFCs and SHH is known to play a role in many aspects of embryonic development including patterning of many systems and limb and digit development. This AOP can be used as part of an integrated assessment of toxicity and can help to guide risk assessment for potential exposures during development.

There is a need for development of New Approach Methodologies (NAMs) to increase understanding of the relationships that exist within this AOP to provide facilitate screenings abilities. Humans are exposed to upwards of 80,000 industrial chemicals and natural products, the majority of which have not undergone any type of toxicity testing either alone or in mixtures. Even highly regulated drugs are typically not tested for safety in pregnant women for obvious reasons despite the medical need in this population (Wise 2022). To help address this, we have engineered an *in vitro* microphysiological model (MPM) model of orofacial development to facilitate the study of both normal and abnormal orofacial development including disruption of SHH (Johnson, Vitek et al. 2021, Reynolds, Vitek et al. 2022). Traditional high throughput screening (HTS) assays are optimized for one pathway: one readout. This oversimplifies toxicant metabolism, intercellular pathway interactions, and ultimately makes the assay not representative of real-life exposures. Problems with HTS in drug discovery have been identified including missing intercellular interactions, co-exposures, and off target safety (Macarron, Banks et al. 2011). We can learn from these identified problems and engineer *in vitro* systems to more accurately recapitulate the biology to give a more thorough assessment of chemical and drug exposure.

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Appendix 1

List of MIEs in this AOP

Event: 2027: Antagonism, Smoothened receptor

Short Name: Antagonism Smoothened

Key Event Component

Process	Object	Action
regulation of receptor activity	smoothened	decreased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	MolecularInitiatingEvent

Biological Context

Level of Biological Organization

Molecular

Cell term

Cell term

mesenchymal cell

Domain of Applicability

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
Vertebrates	Vertebrates		NCBI
Invertebrates	Invertebrates		NCBI

Life Stage Applicability

Life Stage Evidence

Embryo	High
All life stages	High

Sex Applicability**Sex Evidence**

Unspecific

- Sex- SMO is present in both male and females and differences in activation or antagonism between sex have not been demonstrated.
- Life stages- The Hedgehog pathway is a major pathway in embryonic development. While the pathway is largely inactive following development, aberrant activation of SHH signaling is known to cause cancer (Dahmane, Lee et al. 1997, Kimura, Stephen et al. 2005). For these reasons all stages of life are of relevance.
- Taxonomic- SMO is conserved in both vertebrates and invertebrates. SMO signaling is dependent upon its relocation to a subcellular location. This occurs in the plasma membrane for flies (Denef, Neubüser et al. 2000) and the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005).

Key Event Description

The Smoothened (SMO) receptor is Class F G protein coupled receptor involved in signal transduction of the Sonic Hedgehog (SHH) pathway. It includes distinct functional groups including ligand binding pockets, cysteine rich domain (CRD), transmembrane helix (TM), extracellular loop (ECL), intracellular loop (ICL), and a carboxyl-terminal tail (C-term tail) (Arensdorf, Marada et al. 2016). SMO signaling is dependent upon its relocation to a subcellular location. This occurs in the plasma membrane for flies (Denef, Neubüser et al. 2000) and the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005).

In the absence of Hedgehog (HH) ligand, the Patched (PTCH) receptor suppresses the activation of SMO. When HH ligand binds to PTCH, suppression on SMO is released and SMO is able to relocate, accumulate, and signal to intracellular effectors (Denef, Neubüser et al. 2000). This signaling to effectors results in the activation of the GLI transcription factors and the subsequent induction of HH target gene expression (Alexandre, Jacinto et al. 1996, Von Ohlen and Hooper 1997). The exact mechanism through which PTCH and SMO interact is not known.

An endogenous ligand for SMO has not been discovered although evidence for one exists and that PTCH controls SMO by controlling its' availability or accessibility. To support this, it has been shown that PTCH and SMO do not physically interact (Chen and Struhal 1998). PTCH acts catalytically with SMO with one PTCH receptor capable of controlling many (~50) SMO receptors (Taipale, Cooper et al. 2002). Since PTCH includes a sterol sensing domain and shares characteristics of ancient bacterial transporters, a model of PTCH functioning by pumping a sterol-like MSO regulator has been proposed (Mukhopadhyay and Rohatgi 2014). SMO is constitutively active in the absence of PTCH suggesting that the elusive molecule is an agonist (Rohatgi and Scott 2007). Conversely, the discovery that oxysterols bind to the CRD binding domain acting as positive modulators suggest that the molecule could be an agonist with PTCH functioning to sequester away or limit cellular concentration (Corcoran and Scott 2006, Nachtergael, Mydock et al. 2012)

The activity of SMO is controlled by ligand binding (Kobilka 2007). Two separate binding pockets, one in the groove of the extracellular CRD and the other in the helices of the TMD have been identified (Nachtergael, Mydock et al. 2012, Rana, Carroll et al. 2013, Wang, Wu et al. 2013, Byrne, Sircar et al. 2016, Huang, Zheng et al. 2018). These two binding pockets have been shown to interact in an allosteric manner (Nachtergael, Mydock et al. 2012). The binding pocket in the helices of the TMD binds several SMO agonists including SAG as well as antagonists Vismodegib and Sonidegib. The CRD binding pocket binds cholesterol and its' oxidized derivates (Byrne, Luchetti et al. 2018). The antagonist cyclopamine binds to the TMD binding pocket and inhibits SHH signal transduction. However, in mSMO carrying the mutations D477G/E552K that disable the TMD binding pocket, cyclopamine binds to the CRD pocket and activates the pathway (Huang, Nedelcu et al. 2016). To date several oxysterols including 20(S)-hydroxycholesterol, 22(S)-hydroxycholesterol, 7-keto-25-hydroxycholesterol and 7-keto-27-hydroxycholesterol have been identified as activators of SMO (Dwyer, Sever et al. 2007, Nachtergael, Mydock et al. 2012, Myers, Sever et al. 2013). A binding site for 24(S),25-epoxycholesterol has been identified in the TMD pocket using cryo-EM of SMO in complex with 24(S),25-epoxycholesterol (Qi, Liu et al. 2019).

How it is Measured or Detected

Verification of binding and affinity for SMO can be measured using fluorescence binding assays and photoaffinity labeling respectively (Chen, Taipale et al. 2002).

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List of Key Events in the AOP

[Event: 2044: Decrease, Smoothend relocation and activation](#)

Short Name: Decrease, SMO relocation

Key Event Component

Process	Object	Action
protein localization to cilium	smoothened	decreased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	KeyEvent

Biological Context

Level of Biological Organization

Cellular

Cell term

Cell term

cell

Domain of Applicability

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
Vertebrates	Vertebrates		NCBI

Life Stage Applicability

Life Stage	Evidence

Life Stage	Evidence
All life stages	
Embryo	
Sex Applicability	
Sex	Evidence
Unspecific	
	<ul style="list-style-type: none"> Sex- SMO and cilia are present in both male and females and differences in gene expression has not been demonstrated. Life stages- The Hedgehog pathway is a major pathway in embryonic development. Taxonomic-SMO relocation to the tip of primary cilia occurs in vertebrates Huangfu and Anderson 2005)
Key Event Description	
	<p>The Smoothened (SMO) receptor is Class F G protein coupled receptor involved in signal transduction of the Sonic Hedgehog (SHH) pathway. It includes distinct functional groups including ligand binding pockets, cysteine rich domain (CRD), transmembrane helix (TM), extracellular loop (ECL), intracellular loop (ICL), and a carboxyl-terminal tail (C-term tail) (Arensdorf, Marada et al. 2016). SMO signaling is dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation (Arensdorf, Marada et al. 2016).</p> <p>In the absence of SHH ligand, the Patched (PTCH) receptor suppresses the activation of SMO. When HH ligand binds to PTCH, suppression on SMO is released and SMO can relocate, accumulate, and signal to intracellular effectors (Denef, Neubüser et al. 2000, Rohatgi and Scott 2007). It has been shown that SMO localization to the tip of the primary cilia is essential for the SHH signaling cascade in vertebrates (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Rohatgi, Milenkovic et al. 2009). This relocation then leads to signaling to effectors resulting in the activation of the GLI transcription factors and the subsequent induction of HH target gene expression (Alexandre, Jacinto et al. 1996, Von Ohlen and Hooper 1997). The exact mechanism through which PTCH and SMO interact is not known.</p> <p>While we know that entry to the cilia is tightly controlled, the exact mechanism of SMO ciliary trafficking is not fully understood. The PC is separated from the plasma membrane by the ciliary pockets and the transition zone which function together to regulate the movement of lipids and proteins in and out of the organelle (Goetz, Ocbina et al. 2009, Rohatgi and Snell 2010). The SHH receptor PTCH contains a ciliary localization sequence in its' carboxy tail. Localization of PTCH to the PC is essential for inhibition of SMO as deletion of the CLS in PTCH prevents PTCH localization as well as inhibition of SMO (Kim, Hsia et al. 2015) (53). SMO also contains a CLS, but only accumulates in the PC upon ligand binding (Corbit, Aanstad et al. 2005). The entry of SMO into the PC is thought to occur either laterally through the ciliary pockets or internally via recycling endosomes (Milenkovic, Scott et al. 2009). Once inside the PC, SMO can diffuse freely, however it will usually accumulate in specific locations depending upon its' activation state. Inactive SMO will accumulate more at the base of the PC while active SMO will accumulate in the tip of the PC (Milenkovic, Weiss et al. 2015).</p>
How it is Measured or Detected	
	<ul style="list-style-type: none"> Fluorescent proteins can be used tag SMO, cilia and the plasma membrane to determine if SMO has relocated to the cilia (Filipova, Diaz Garcia et al. 2020). Fluorescent binding assay can be used to verify if a compound binds to SMO (Chen, Taipale et al. 2002). Cell lines can be engineered to express Myc-tagged SMO. This gives a user friendly readout of SMO activation. (Corbit, Aanstad et al. 2005).
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[Event: 2028: Decrease, GLI1/2 translocation to nucleus](#)

Short Name: Decrease, GLI1/2 translocation

Key Event Component

Process	Object	Action
protein import into nucleus, translocation	zinc finger protein GLI1	decreased
protein import into nucleus, translocation	zinc finger protein GLI2	decreased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	KeyEvent
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	KeyEvent

Biological Context

Level of Biological Organization

Molecular

Cell term

Cell term

cell

Domain of Applicability

Life Stage Applicability**Life Stage Evidence**

Embryo High

All life stages High

Sex Applicability**Sex Evidence**

Unspecific

- Sex- The Gli family of transcription factors is present in both male and females and differences in activation or antagonism between sex have not been demonstrated.
- Life stages- The Hedgehog pathway is a major pathway in embryonic development. Aberrant activation of HH signalling is known to cause cancer (Dahmane, Lee et al. 1997, Kimura, Stephen et al. 2005). For these reasons all stages of life are of relevance.
- Taxonomic-HH signalling including the Gli transcription factors is present in vertebrates and some invertebrates including flies (Denef, Neubüser et al. 2000, Huangfu and Anderson 2005)

Key Event Description

The Glioma-associated oncogene (Gli) family of zinc finger transcription factors (Gli1, Gli2, Gli3) are the primarily downstream effectors of the Hedgehog (HH) signaling cascade. When HH ligand binds to Patched (PTCH), its' inhibition on SMO is relieved. SMO is then able to accumulate to the tip of primary cilium in its' active form (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Kim, Kato et al. 2009). SMO causes the GLI family to become dislodged from their complex with the negative regulator of HH signaling, Suppressor of Fused (Sufu) (Kogerman, Grimm et al. 1999, Pearse, Collier et al. 1999, Stone, Murone et al. 1999, Tukachinsky, Lopez et al. 2010). The GLI-Sufu complex maintains retention of Gli in the cytosol allowing for exposure to phosphorylation via protein kinase A (PKA) which inhibits downstream signal transduction (Tuson, He et al. 2011). When SMO is activated the GLI2/3-Sufu complex is dismantled allowing for retrograde transport of GLI back into the nucleus (Kim, Kato et al. 2009).

The GLI family is found in both a long activator form (GliA) or a proteolytically cleaved repressor form (GliR). Current understanding is that Gli3 functions primarily as a repressor while Gli1 and Gli2 function mainly as activators of the pathway and that recruitment of SMO to the cilium leads to an increase in the ratio of GliA:GliR (Hui and Angers 2011, Liu 2016).

How it is Measured or Detected

- A nuclear translocation assay (NTA) can be applied to determine the amount of protein that translocate into the nucleus (Dixon and Lim 2010).
- Nuclear protein extracts can be analysed to determine if the protein of interest (GLI1/2) translocated to the nucleus (Kim, Kato et al. 2009).
- Immunofluorescence and microscopy can be used to determine how much of a protein has translocated to the nucleus. Primary antibodies can be used to tag GLI in combination with a secondary stain for the nucleus (Blotta, Jakubikova et al. 2012).

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AOP460

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[Event: 2040: Decrease, GLI1/2 target gene expression](#)

Short Name: Decrease, GLI1/2 target gene expression

Key Event Component

Process	Object	Action
gene expression	zinc finger protein GLI1	decreased
gene expression	zinc finger protein GLI2	decreased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	KeyEvent
Aop:491 - Decrease, GLI1/2 target gene expression leads to orofacial clefting	MolecularInitiatingEvent
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	KeyEvent

Biological Context

Level of Biological Organization

Cellular

Cell term

Cell term

cell

Domain of Applicability

Life Stage Applicability

Life Stage Evidence

Life Stage Evidence	
All life stages	
Sex Applicability	
Sex Evidence	
Unspecific	
<ul style="list-style-type: none"> Sex- The GLI family of transcription factors is present in both male and females and differences in gene expression have not been demonstrated. Life stages- The Hedgehog pathway with the main transcription factors of GLI1/2 can be active during all stages of life. It is a major pathway in embryonic development. Aberrant activation of HH signaling is known to cause cancer (Dahmane, Lee et al. 1997, Kimura, Stephen et al. 2005). For these reasons all stages of life are of relevance. Taxonomic-HH signaling including the GLI transcription factors is present in vertebrates and some invertebrates including flies (Denef, Neubüser et al. 2000, Huangfu and Anderson 2005) 	
<h3>Key Event Description</h3> <p>The Glioma-associated oncogene (GLI) family of zinc finger transcription factors (Gli1, Gli2, Gli3) are the primarily downstream effectors of the Hedgehog (HH) signaling cascade. When HH ligand binds to Patched (PTCH), its' inhibition on SMO is relieved. SMO is then able to accumulate to the tip of primary cilium in its' active form (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Kim, Kato et al. 2009). SMO causes the GLI family to become dislodged from their complex with the negative regulator of HH signaling, Suppressor of Fused (Sufu) (Kogerman, Grimm et al. 1999, Pearse, Collier et al. 1999, Stone, Murone et al. 1999, Tukachinsky, Lopez et al. 2010). The GLI-Sufu complex maintains retention of Gli in the cytosol allowing for exposure to phosphorylation via protein kinase A (PKA) which inhibits downstream signal transduction (Tuson, He et al. 2011). When SMO is activated the GLI2/3-Sufu complex is dismantled allowing for retrograde transport of GLI back into the nucleus (Kim, Kato et al. 2009). Following translocation into the nucleus, the GLI family of transcription factors initiates transcription of a variety of genes. The genes transcribed by activation of the SHH pathway are cell type dependent but commonly include GLI1 and PTCH1 (Stamatakis, Ulloa et al. 2005, Cohen, Kicheva et al. 2015, Tickle and Towers 2017). During development of the neural tube SHH is associated with NKX6.1, OLIG2, NKX2.2 and the FOXA2 genes (Vokes, Ji et al. 2007, Kutejova, Sasai et al. 2016). Other genes have known targets of GLI transcription include PTCH2, HHIP1, MYCN, CCND1, CCND2, BCL2, CFLA, FOXF1, FOXFL1, PRDM1, JAG2, GREM1, FOXB2, FOXA2, FOXB2, FOXC1, FOXC2, FOXD1, FOXE1, FOXF1, FOXF2, FOXL1 and follistatin (Katoh and Katoh 2009, Everson, Fink et al. 2017).</p>	
<h3>How it is Measured or Detected</h3> <ul style="list-style-type: none"> Changes in gene expression can be measured using serial analysis of gene expression (SAGE), rapid analysis of gene expression (RAGE), RT-PCR, Northern/Southern blotting, differential display, and DNA microarray assay (Kirby, Heath et al. 2007). 	
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Key Event Component																						
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AOP ID and Name	Event Type
Aop:491 - Decrease, GLI1/2 target gene expression leads to orofacial clefting	KeyEvent
Aop:500 - Activation of MEK-ERK1/2 leads to deficits in learning and cognition via ROS and apoptosis	KeyEvent
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	KeyEvent
Aop:441 - Ionizing radiation-induced DNA damage leads to microcephaly via apoptosis and premature cell differentiation	KeyEvent
Aop:535 - Binding and activation of GPER leading to learning and memory impairments	KeyEvent
Aop:540 - Oxidative Stress in the Fish Ovary Leads to Reproductive Impairment via Reduced Vitellogenin Production	KeyEvent
Aop:563 - Aryl hydrocarbon Receptor (AHR) activation causes Premature Ovarian Insufficiency via Bax mediated apoptosis	KeyEvent

Biological Context

Level of Biological Organization

Cellular

Cell term

Cell term

cell

Organ term

Organ term

organ

Domain of Applicability

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
Homo sapiens	Homo sapiens	High	NCBI
Mus musculus	Mus musculus	High	NCBI
Rattus norvegicus	Rattus norvegicus	High	NCBI
Caenorhabditis elegans	Caenorhabditis elegans	High	NCBI

Life Stage Applicability

Life Stage Evidence

Not Otherwise Specified	High
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Sex Applicability

Sex Evidence

Unspecific	High
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Apoptosis is induced in human prostate cancer cell lines (*Homo sapiens*) [Parajuli et al., 2014].

Apoptosis occurs in B6C3F1 mouse (*Mus musculus*) [Elmore, 2007].

Apoptosis occurs in Sprague-Dawley rat (*Rattus norvegicus*) [Elmore, 2007].

Apoptosis occurs in the nematode (*Caenorhabditis elegans*) [Elmore, 2007].

- Apoptosis occurs in breast cancer cells, human and mouse (Parton)

Key Event Description

Apoptosis, the process of programmed cell death, is characterized by distinct morphology with DNA fragmentation and energy dependency [Elmore, 2007]. Apoptosis, also called “physiological cell death”, is involved in cell turnover, physiological involution, and atrophy of various tissues and organs [Kerr et al., 1972]. The formation of apoptotic bodies involves marked condensation of both nucleus and cytoplasm, nuclear fragmentation, and separation of protuberances [Kerr et al., 1972]. Apoptosis is characterized by DNA ladder and chromatin condensation. Several stimuli such as hypoxia, nucleotides deprivation, chemotherapeutical drugs, DNA damage, and mitotic spindle damage induce p53 activation, leading to p21 activation and cell cycle arrest [Pucci et al., 2000]. The SAHA or TSA treatment on neonatal human dermal fibroblasts (NHDFs) for 24 or 72 hrs inhibited proliferation of the NHDF cells [Glaser et al., 2003]. Considering that the acetylation of histone H4 was increased by the treatment of SAHA for 4 hrs, histone deacetylase inhibition may be involved in the inhibition of the cell proliferation [Glaser et al., 2003]. The impaired proliferation was observed in HDAC1^{-/-} ES cells, which was rescued with the reintroduction of HDAC1 [Zupkovitz et al., 2010]. An AOP focuses exists on p21 pathway leading to apoptosis, however, alternative pathways such as NF-kappaB signaling pathways may be involved in the apoptosis of spermatocytes [Wang et al., 2017].

Apoptosis is defined as a programmed cell death. A decrease in apoptosis or a resistance to cell death is noted is described as a hallmark of cancer by Hanahan et al. It is widely admitted as an essential step in tumor proliferation (Adams, Lowe). Apoptosis occurs after activation of a number of intrinsic and extrinsic signals which activate the protease caspase system which in turn activates the destruction of the cell.

The Bcl-2 is a protein family suppressing apoptosis by binding and inhibiting two proapoptotic proteins (Bax and Bak) and transferring them to the mitochondrial outer membrane. In the absence of inhibition by Bcl2, Bax and Bak destroy the mitochondrial membrane and releases proapoptotic signaling proteins, such as cytochrome *c* which activated the caspase system. An increased expression of these antiapoptotic proteins (Bcl-2, Bcl-x_L) occurs in cancer (Hanahan, Adams, Lowe). Several others pathways such as the loss of TP53 tumor suppressor function, or the increase of survival signals (Igf1/2), or decrease of proapoptotic factors (Bax, Bim, Puma) can also increase tumor growth (Hanahan, Juntilla).

In breast cancer a decrease in apoptosis and a resistance to cell death has been described thoroughly, especially using a dysregulation of the Bcl2 system or TP53 (Parton, Williams, Shahbandi).

How it is Measured or Detected

Apoptosis is characterized by many morphological and biochemical changes such as homogenous condensation of chromatin to one side or the periphery of the nuclei, membrane blebbing and formation of apoptotic bodies with fragmented nuclei, DNA fragmentation, enzymatic activation of pro-caspases, or phosphatidylserine translocation that can be measured using electron and cytochemical optical microscopy, proteomic and genomic methods, and spectroscopic techniques [Archana et al., 2013; Martinez et al., 2010; Taatjes et al., 2008; Yasuhara et al., 2003].

□ DNA fragmentation can be quantified with comet assay using electrophoresis, where the tail length, head size, tail intensity, and head intensity of the comet are measured [Yasuhara et al., 2003].

□ The apoptosis is detected with the expression alteration of procaspases 7 and 3 by Western blotting using antibodies [Parajuli et al., 2014].

□ The apoptosis is measured with down-regulation of anti-apoptotic gene baculoviral inhibitor of apoptosis protein repeat containing 2 (BIRC2, or cIAP1) [Parajuli et al., 2014].

□ Apoptotic nucleosomes are detected using Cell Death Detection ELISA kit, which was calculated as absorbance subtraction at 405 nm and 490 nm [Parajuli et al., 2014].

□ Cleavage of PARP is detected with Western blotting [Parajuli et al., 2014].

□ Caspase-3 and caspase-9 activity is measured with the enzyme-catalyzed release of p-nitroanilide (pNA) and quantified at 405 nm [Wu et al., 2016].

□ Apoptosis is measured with Annexin V-FITC probes, and the relative percentage of Annexin V-FITC-positive/PI-negative cells is analyzed by flow cytometry [Wu et al., 2016].

□ Apoptosis is detected with the Terminal dUTP Nick End-Labeling (TUNEL) method to assay the endonuclease cleavage products by enzymatically end-labeling the DNA strand breaks [Kressel and Groscurth, 1994].

□ For the detection of apoptosis, the testes are fixed in neutral buffered formalin and embedded in paraffin. Germ cell death is visualized in testis sections by Terminal dUTP Nick End-Labeling (TUNEL) staining method [Wade et al., 2008]. The incidence of TUNEL-positive cells is expressed as the number of positive cells per tubule examined for one entire testis section per animal [Wade et al., 2008].

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Event: 2043: Decrease, Sonic Hedgehog second messenger production

Short Name: Decrease, SHH second messenger production

Key Event Component

Process	Object	Action
second-messenger-mediated signaling	sonic hedgehog protein	decreased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	KeyEvent
Aop:491 - Decrease, GLI1/2 target gene expression leads to orofacial clefting	KeyEvent
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	KeyEvent

Biological Context

Level of Biological Organization

Cellular

Cell term

Cell term

cell

Domain of Applicability

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
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Vertebrates Vertebrates [NCBI](#)

Life Stage Applicability

Life Stage Evidence

Embryo

Sex Applicability

Sex Evidence

Unspecific

- Sex- Secondary messenger production of the SHH pathway is present in both male and females and differences in gene expression has not been demonstrated.
- Life stages- The Hedgehog pathway is a major pathway in embryonic development.

- Taxonomic-HH signalling, and its' secondary messenger production is present in vertebrates and some invertebrates including flies (Denef, Neubüser et al. 2000, Huangfu and Anderson 2005)

Key Event Description

During normal Sonic Hedgehog (SHH) signaling, GLI target gene expression regulates several other signaling pathways. Expression of FOXF1 and FOXL1 upregulate BMP4, BMP 2, and FGF10 in the mesenchyme (Katoh and Katoh 2009, Lan and Jiang 2009). Induction of FGF10 in the mesenchyme is able to induce SHH in the adjacent epithelium via a positive feedback loop with FGFR2 (Cobourne and Green 2012). SHH signaling also upregulates BCL2 and CFLAR to promote cell survival (Katoh and Katoh 2009).

How it is Measured or Detected

- Changes in gene expression can be measured using serial analysis of gene expression (SAGE), rapid analysis of gene expression (RAGE), RT-PCR, Northern/Southern blotting, differential display, and DNA microarray assay (Kirby, Heath et al. 2007).
- RNA in situ hybridization can be used to determine sites of gene expression (Nouri-Aria 2008, Abler, Mansour et al. 2009)
- Antibody staining of tissue sections can be used to determine location and amounts of BMP4, BMP2, FGF10

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[Event: 1821: Decrease, Cell proliferation](#)

Short Name: Decrease, Cell proliferation

Key Event Component

Process	Object	Action
cell proliferation	cell	decreased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:263 - Uncoupling of oxidative phosphorylation leading to growth inhibition via decreased cell proliferation	KeyEvent
Aop:290 - Mitochondrial ATP synthase antagonism leading to growth inhibition (1)	KeyEvent
Aop:286 - Mitochondrial complex III antagonism leading to growth inhibition (1)	KeyEvent

AOP ID and Name	Event Type
Aop:399 - Inhibition of Fyna leading to increased mortality via decreased eye size (Microphthalmos)	KeyEvent
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	KeyEvent
Aop:267 - Uncoupling of oxidative phosphorylation leading to growth inhibition via glucose depletion	KeyEvent
Aop:491 - Decrease, GLI1/2 target gene expression leads to orofacial clefting	KeyEvent
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	KeyEvent
Aop:331 - Excessive reactive oxygen species leading to growth inhibition via oxidative DNA damage and reduced cell proliferation	KeyEvent
Aop:332 - Excessive reactive oxygen species leading to growth inhibition via lipid peroxidation and reduced cell proliferation	KeyEvent
Aop:333 - Excessive reactive oxygen species leading to growth inhibition via uncoupling of oxidative phosphorylation	KeyEvent

Stressors

Name

2,4-Dinitrophenol
 Carbonyl cyanide-p-trifluoromethoxyphenylhydrazone
 Carbonyl cyanide m-chlorophenyl hydrazone
 Pentachlorophenol
 Triclosan
 Emodin
 Malonoben

Biological Context

Level of Biological Organization

Cellular

Cell term

Cell term

cell

Domain of Applicability

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
zebrafish	Danio rerio	High	NCBI
human	Homo sapiens	High	NCBI
rat	Rattus norvegicus	High	NCBI
mouse	Mus musculus	High	NCBI

Life Stage Applicability

Life Stage Evidence

Embryo High

Juvenile High

Sex Applicability

Sex Evidence

Sex Evidence

Unspecific High

Taxonomic applicability domain

This key event is in general applicable to all eukaryotes, as most organisms are known to use cell proliferation to achieve growth.

Life stage applicability domain

This key event is in general applicable to all life stages. As cell proliferation not only occurs in developing organisms, but also in adults.

Sex applicability domain

This key event is sex-unspecific, as both genders use the same cell proliferation mechanisms.

Key Event Description

Decreased cell proliferation describes the outcome of reduced cell division and cell growth. Cell proliferation is considered the main mechanism of tissue and organismal growth (Conlon 1999). Decreased cell proliferation has been associated with abnormal growth-factor signaling and cellular energy depletion (DeBerardinis 2008).

How it is Measured or Detected

Multiple types of *in vitro* bioassays can be used to measure this key event:

- ToxCast high-throughput screening bioassays such as “BSK_3C_Proliferation”, “BSK_CASM3C_Proliferation” and “BSK_SAg_Proliferation” can be used to measure cell proliferation status.
- Commercially available methods such as the well-established 5-bromo-2'-deoxyuridine (BrdU) (Raza 1985; Muir 1990) or 5-ethynyl-2'-deoxyuridine (EdU) assay. Both assays measure DNA synthesis in dividing cells to indicate proliferation status.

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Event: 2041: Decrease, facial prominence outgrowth**Short Name: Decrease, facial prominence outgrowth****Key Event Component**

Process	Object	Action
palatal shelves fail to meet at midline	primary palate	increased
palatal shelves fail to meet at midline	secondary palate	increased

AOPs Including This Key Event

AOP ID and Name	Event Type

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	KeyEvent
Aop:491 - Decrease, GLI1/2 target gene expression leads to orofacial clefting	KeyEvent
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	KeyEvent

Biological Context

Level of Biological Organization

Tissue

Domain of Applicability

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
Vertebrates	Vertebrates	High	NCBI

Life Stage Applicability

Life Stage Evidence

Embryo	High
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Sex Applicability

Sex Evidence

Unspecific

- Sex- There are no known differences in palatal outgrowth in terms of sex.
- Life stages- The palate develops early in embryonic development. This begins between the 6th and 12th week of pregnancy in humans and between day 10.0 and 15 in mice (Okuhara and Iseki 2012).
- Taxonomic- Palatal outgrowth is required for proper palate formation in all vertebrates.

Key Event Description

For humans and other mammals, the palate serves as a barrier between the mouth and nasal cavity allowing for simultaneous breathing and eating. The palate consists of an anterior bony hard palate and a posterior muscular soft palate that closes the nasal airways for swallowing and directs airflow to help in generation of speech (Li, Lan et al. 2017). The palate is divided into primary and secondary portions. The primary palate contains the philtrum and the upper incisor region anterior to the incisive foramen while the secondary palate encompasses the remainder of the hard and soft palate (Bush and Jiang 2012). The secondary palate arises during embryonic development as bilateral outgrowths from the maxillary processes. In mammals, these shelves grow first vertically down the tongue before elevating to a position above the dorsum of the tongue where the two shelves meet and fuse to form an intact palate (Ferguson 1988).

How it is Measured or Detected

- Palatal shelf outgrowth can be quantified using imaging techniques such as 3D CT scans during development. Insufficient palatal outgrowth will result in cleft palate. The distance between palatal shelves corelating with outgrowth can be measured and quantified for these individuals.
- Embryos can be dissected and the facial prominences measured (Rice, Connor et al. 2006).

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List of Adverse Outcomes in this AOP

Event: 2042: Increase, Orofacial clefting**Short Name: orofacial cleft****Key Event Component**

Process	Object	Action
Cleft palate		increased
cleft upper lip		increased

AOPs Including This Key Event

AOP ID and Name	Event Type
Aop:460 - Antagonism of Smoothened receptor leading to orofacial clefting	AdverseOutcome
Aop:491 - Decrease, GLI1/2 target gene expression leads to orofacial clefting	AdverseOutcome
Aop:502 - Decrease, cholesterol synthesis leads to orofacial clefting	AdverseOutcome

Biological Context**Level of Biological Organization**

Individual

Domain of Applicability**Taxonomic Applicability**

Term	Scientific Term	Evidence	Links
Vertebrates	Vertebrates		NCBI

Life Stage Applicability**Life Stage Evidence**

Embryo High

Sex Applicability**Sex Evidence**

Unspecific

- Sex- OFC can occur for all sexes. Differences in incidence between males and females have been found however a clear understanding of what causes this difference is not understood. Cleft lip with or without cleft palate is more common in males while cleft palate only is more common for females (Barbosa Martelli, Machado et al. 2012).
- Life stages- Orofacial development and any disruption leading to clefting occurs early in embryonic development. This begins between the 6th and 12th week of pregnancy in humans and between day 10.0 and 15 in mice (Okuhara and Iseki 2012).
- Taxonomic- Orofacial development occurs in all vertebrates.

Key Event Description

Orofacial clefts (OFC) are one of the most common birth defects. Orofacial clefts are commonly divided on the anatomy they affect by clefts of the lip and/or palate (CL/P) and those of the palate only (CPO) (Murray 2002). Clefts can also be classified as either syndromic when they occur with other physical or developmental anomalies or nonsyndromic in the absence of other symptoms (Stanier and Moore 2004). Like most births, the etiology of OFCs are complex and include a combination of genetic and chemical factors (Lipinski and Bushman 2010, Heyne, Melberg et al. 2015). Orofacial development is tightly regulated by multiple signaling pathways and genes including: fibroblast growth factors (Fgfs), Sonic Hedgehog (shh), bone morphogenic protein (Bmp), transforming growth factor beta (Tgf- β) and transcription factors including Dlx, Pitx, Hox, Gli and T-box (Stanier and Moore 2004). Orofacial development requires precise cell migration, growth, differentiation and apoptosis to create the needed orofacial structures from the oropharyngeal membrane (Jugessur and Murray 2005). During the sixth week of human embryogenesis the medial nasal prominences merge to form the primary palate and the upper lip. The mandibular prominences merge across the midline to produce the lower jaw and lip. Development of the secondary palate begins in the

sixth week where the palatal shelves extend internally to the maxillary processes. The shelves then elevate above the tongue and grow towards each other until contact occurs. During weeks 7-8 the medial edges of the palatal shelves fuse through a series of epithelial-mesenchyme transition (EMT) and apoptosis (Jugessur and Murray 2005, Zhang, Tian et al. 2016). Disruption to the complex processes required for proper orofacial development can occur both through genetic factors and environmental (i.e. chemical) exposure by causing disruption to one or multiple steps of orofacial development resulting in OFC.

How it is Measured or Detected

- OFC can be visually observed both in humans and in animals. It can be classified by which tissues (e.g. cleft lip and palate) are affected and its' severity (complete/incomplete, unilateral/bilateral). Techniques such as the revised Smith-modified Kernahan 'Y' classification can be used to describe the type, location, and extent of OFC deformities (Khan, Ullah et al. 2013).

Regulatory Significance of the AO

OFC is one of the most common birth defects occurring in approximately 1 in 700 live births. The etiology of OFC is poorly understood and is believed to be a combination of genetic and environmental factors. Understanding the genetic and environmental factors that can lead to OFC is the first step in preventing this birth defect.

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Appendix 2

List of Key Event Relationships in the AOP

List of Adjacent Key Event Relationships

[Relationship: 2734: Antagonism Smoothened leads to Decrease, SMO relocation](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Moderate	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
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human	Homo sapiens	Low	NCBI
mouse	Mus musculus	High	NCBI

Life Stage Applicability
Life Stage Evidence

Embryo	High
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Sex Applicability
Sex Evidence

Unspecific	Not Specified
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The relationship between antagonism of SMO and a decrease in SMO relocation and activation has been shown repeatedly in mice models as detailed in the empirical evidence section. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question. The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs). For this reason, this KER is applicable to the embryonic stage with a high level of confidence.

Key Event Relationship Description

The Smoothened (SMO) receptor is Class F G protein coupled receptor involved in signal transduction of the Sonic Hedgehog (SHH) pathway. It includes distinct functional groups including ligand binding pockets, cysteine rich domain (CRD), transmembrane helix (TM), extracellular loop (ECL), intracellular loop (ICL), and a carboxyl-terminal tail (C-term tail) (Arensdorf, Marada et al. 2016). SMO signaling is dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation (Arensdorf, Marada et al. 2016).

In the absence of SHH ligand, the Patched (PTCH) receptor suppresses the activation of SMO. When HH ligand binds to PTCH, suppression on SMO is released and SMO can relocate, accumulate, and signal to intracellular effectors (Denef, Neubüser et al. 2000, Rohatgi and Scott 2007). It has been shown that SMO localization to the tip of the primary cilia is essential for the SHH signaling cascade in vertebrates (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Rohatgi, Milenkovic et al. 2009). The exact mechanism through which PTCH and SMO interact is not known.

Evidence Supporting this KER
Biological Plausibility

SMO signaling is dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). It has been shown that SMO localization to the tip of the primary cilia is essential for the SHH signaling cascade in vertebrates (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Rohatgi, Milenkovic et al. 2009)

Empirical Evidence

- In vitro
 - NIH 3t3 (murine fibroblast) were used to study the effects of three SHH pathway antagonists, SANT 1, SANT2, and cyclopamine on SMO localization using fluorescent microscopy. Cells were treated with increasing concentrations of the antagonists in the presence of SHH ligand. SANT1 and SANT2 both blocked SMO localization in the cilia with IC50 values of 5 and 13nM respectively. Cyclopamine did not inhibit the accumulation of SMO in the cilia even when dosed at 5-10 μ m (>10 fold above kd). All three antagonists inhibited SHH pathway transduction and target gene expression (Rohatgi, Milenkovic et al. 2009).
 - A small molecule screen of 10,000 compounds identified six inhibitors of SHH signaling, four of which bind directly to SMO (SANT1-4). Screening was conducted using NIH 3T3 SHH Light2 cells cultured in media conditioned from HEK 293 transfected to stably express Shh-N. Cells were dosed with the compound library at 0.714ug/ml and SHH activity was quantified at 30h using Renilla luciferase activity. A fluorescent binding assay using BODIPY-cyclopamine was used to verify binding to SMO for the SANT compounds. Dose response reported as IC50 for the inhibition of SHH signaling was conducted in NIH 3T3 SHH light2, NIH 3T3 SmoA1-Light2, P2 Ptch1-/- (mouse embryonic fibroblasts) (Chen, Taipale et al. 2002).

Compound/Cell	SHH-Light2 (nM)	SmoA1-Light2 (nM)	Ptch1-/- (nM)
SANT-1	20	30	20
SANT-2	30	70	50
SANT-3	100	80	80
SANT-4	200	300	300

- Direct binding of cyclopamine to SMO was verified using a photoaffinity form of cyclopamine (PA-cyclopamine). PA-cyclopamine had previously been shown to inhibit SHH signaling in NIH 3T3 Shh-LightII cells with similar IC50 values to cyclopamine (300nm and 150nm respectively) (Taipale, Chen et al. 2000). Binding to SMO was verified using a COS-1 (fibroblast, monkey) line transfected to over express SMO. The location of cyclopamine binding was further investigated using BODIPY- cyclopamine and COS-1 cells modified to lack either a N-terminal, extracellular cysteine-rich domain, or the cytoplasmic C terminal of SMO. The findings support that cyclopamine does not require these domains and instead binds directly to the heptahelical domain (Chen, Taipale et al. 2002).
- To investigate whether SMO localization is regulated by SHH, a renal epithelial MDCK (Madin-Darby canine kidney) line was engineered to express Myc-tagged SMO. Following culture for 1hr in SHH conditioned media SMO presence in the primary cilium is upregulated while cells cultured in the presence of cyclopamine see a downregulation of SMO in the primary cilia (Corbit, Aanstad et al. 2005)
- To determine whether PTCH1 regulates localization of SMO MEFs from PTCH1^{-/-} mice were used. These showed SHH activity and SMO localization in the primary cilium in the absence of SHH ligand or SAG. Reintroduction of PTCH1 via a retrovirus suppressed SHH activity and prevented SMO accumulation in primary cilia (Rohatgi and Scott 2007)
- A high content assay to detect compounds that block SMO accumulation to the primary cilia in the presence of SHH was used to screen a library of ~5600 compounds. This screen identified 26 hits with DY131 and its analog GSK4716 further investigated as potent hits. These compounds inhibited SHH induced accumulation of SMO::EGFP with IC50s of 0.8um and 2um respectively. DY131 and GSK4716 both inhibited the activation of a Glireporter with IC50s of 2um and 10um respectively (Wang, Arvanites et al. 2012).
- In vivo
 - Two-week-old mice were dosed with 40mg/kg vismodegib (GDC-0449) via ip injection twice a day for 3 consecutive days. Quantification of immunofluorescence and ciliary length showed that like SMO^{fl/fl} mice, ciliary M71/M72 OR was reduced while cilia lengths were not changed. To determine if SMO regulates ciliary localization an OMP-CRE mouse line was used. It was found that immunofluorescence of M71/M72 was reduced in both SMO^{fl/fl}, SMO^{fl/fl}, as compared to SMO^{+/+} control (Maurya, Bohm et al. 2017).
 - Cyclopamine was found to inhibit SHH signaling in White leghorn neural plate explants. Explants were dissected from stage 9-10 embryo chicks and cultured in collagen gels. Tissues were cultured in Shh-N media from COS-1 cells. Cyclopamine was dissolved in ethanol and added to test tissues. Tissues were fixed at 24-29hr and processed for immunofluorescence. 120nm cyclopamine was found to repress SHH induction as determined by Pax7 repression and the blockage of floor plate and motor neuron induction (Incardona, Gaffield et al. 1998).
 - Multiple ciliopathies associated with clefting in humans including Meckel-Gruber syndrome (OMIM 249000) and Ellis-van Creveld syndrome (OMIM 225500)(Brugmann, Cordero et al. 2010)

Uncertainties and Inconsistencies

While we know that entry to the cilia is tightly controlled, the exact mechanism of SMO ciliary trafficking is not fully understood. The PC is separated from the plasma membrane by the ciliary pockets and the transition zone which function together to regulate the movement of lipids and proteins in and out of the organelle (Goetz, Ocbina et al. 2009, Rohatgi and Snell 2010). The SHH receptor PTCH contains a ciliary localization sequence in its' carboxy tail. Localization of PTCH to the PC is essential for inhibition of SMO as deletion of the CLS in PTCH prevents PTCH localization as well as inhibition of SMO (Kim, Hsia et al. 2015) (53). SMO also contains a CLS, but only accumulates in the PC upon ligand binding (Corbit, Aanstad et al. 2005). The entry of SMO into the PC is thought to occur either laterally through the ciliary pockets or internally via recycling endosomes (Milenkovic, Scott et al. 2009). Once inside the PC, SMO can diffuse freely, however it will usually accumulate in specific locations depending upon its' activation state. Inactive SMO will accumulate more at the base of the PC while active SMO will accumulate in the tip of the PC (Milenkovic, Weiss et al. 2015).

An endogenous ligand for SMO has not been discovered although evidence for one exists and that PTCH controls SMO by controlling its' availability or accessibility. To support this, it has been shown that PTCH and SMO do not physically interact (Chen and Struhl 1998). PTCH acts catalytically with SMO with one PTCH receptor capable of controlling many (~50) SMO receptors (Taipale, Cooper et al. 2002). Since PTCH includes a sterol sensing domain and shares characteristics of ancient bacterial transporters, a model of PTCH functioning by pumping a sterol-like MSO regulator has been proposed (Mukhopadhyay and Rohatgi 2014). SMO is constitutively active in the absence of PTCH suggesting that the elusive molecule is an agonist (Rohatgi and Scott 2007). Conversely, the discovery that oxysterols bind to the CRD binding domain acting as positive modulators suggest that the molecule could be an agonist with PTCH functioning to sequester away or limit cellular concentration (Corcoran and Scott 2006, Nachtergael, Mydock et al. 2012)

The activity of SMO is controlled by ligand binding(Kobilka 2007). Two separate binding pockets, one in the groove of the extracellular CRD and the other in the helices of the TMD have been identified (Nachtergael, Mydock et al. 2012, Rana, Carroll et al. 2013, Wang, Wu et al. 2013, Byrne, Sircar et al. 2016, Huang, Zheng et al. 2018). These two binding pockets have been shown to interact in an allosteric manner (Nachtergael, Mydock et al. 2012). The binding pocket in the helices of the TMD binds several SMO agonists including SAG as well as antagonists Vismodegib and Sonidegib. The CRD binding pocket binds cholesterol and its' oxidized derivates (Byrne, Luchetti et al. 2018). The antagonist cyclopamine binds to the TMD binding pocket and inhibits SHH signal transduction. However, in mSMO carrying the mutations D477G/E552K that disable the TMD binding pocket, cyclopamine binds to the CRD pocket and

activates the pathway (Huang, Nedelcu et al. 2016). To date several oxysterols including 20(S)-hydroxycholesterol, 22(S)-hydroxycholesterol, 7-keto-25-hydroxycholesterol and 7-keto-27-hydroxycholesterol have been identified as activators of SMO (Dwyer, Sever et al. 2007, Nachtergael, Mydock et al. 2012, Myers, Sever et al. 2013) A binding site for 24(S),25-epoxycholesterol has been identified in the TMD pocket using cryo-EM of SMO in complex with 24(S),25-epoxycholesterol (Qi, Liu et al. 2019).

While it is well understood that cyclopamine is an antagonist of SMO, contradictory in vivo data was found regarding whether cyclopamine blocks SMO relocation to the primary cilia. Rohatgi et al used NIH 3T3s cell and found that cyclopamine did not inhibit the accumulation of SMO in the cilia even when dosed at 5-10um (>10 fold above kd). All three antagonists inhibited SHH pathway transduction and target gene expression (Rohatgi, Milenovic et al. 2009). Corbit et al used a renal epithelial MDCK (Madin-Darby canine kidney) line was engineered to express Myc-tagged SMO. Following culture for 1hr in SHH conditioned media SMO presence in the primary cilium is upregulated while cells cultured in the presence of cyclopamine see a downregulation of SMO in the primary cilia (Corbit, Aanstad et al. 2005). Further work is required to determine if SMO antagonism via cyclopamine results in decrease in SMO relocation.

Quantitative Understanding of the Linkage

The data presented in support of this KER includes both in vitro and in vivo studies. The in vivo work identifies multiple antagonists of SMO and validates that they directly bind to SMO. These studies also offer data to show that antagonism of SMO causes a down regulation in SMO relocation the primary cilia. Dose dependent SMO localization is seen in the studies performed by Rohtagi et al 2009 and Chen et al 2002. The response time of SMO antagonism and subsequent time for a decrease in SMO relocation and activation has not been reported. No dose dependent in vivo data for antagonism of SMO and relocation to the cilia was found and all in vivo evidence is conducted under steady state exposure. Dose response data for disruption of SHH using the antagonists exists and is well characterized however quantification of ciliary relocation is lacking. Further studies are needed to expand our quantitative understanding of this linkage.

Response-response relationship

No studies identified

Time-scale

Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation (Arensdorf, Marada et al. 2016). No data was found on how fast antagonism of SMO will stop its' relocation to the primary cilia.

Known Feedforward/Feedback loops influencing this KER

None identified

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[Relationship: 2735: Decrease, SMO relocation leads to Decrease, GLI1/2 translocation](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Moderate	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mice	Mus sp.	High	NCBI
human	Homo sapiens	Low	NCBI

Life Stage Applicability

Life Stage	Evidence
Embryo	High

Sex Applicability

Sex	Evidence
Unspecific	

The relationship between a decrease in translocation of SMO and a decrease in GLI1/2 translocation to the nucleus has been shown repeatedly in mice models as detailed in the empirical evidence section. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question. The SHH pathway is well understood to be fundamental to proper embryonic development. For this reason, this KER is applicable to the embryonic stage with a high level of confidence.

Key Event Relationship Description

The Smoothened (SMO) receptor is Class F G protein coupled receptor involved in signal transduction of the Sonic Hedgehog (SHH) pathway. It includes distinct functional groups including ligand binding pockets, cysteine rich domain (CRD), transmembrane helix (TM), extracellular loop (ECL), intracellular loop (ICL), and a carboxyl-terminal tail (C-term tail) (Arensdorf, Marada et al. 2016). SMO signaling is dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation (Arensdorf, Marada et al. 2016).

The Glioma-associated oncogene (Gli) family of zinc finger transcription factors (Gli1, Gli2, Gli3) are the primarily downstream effectors of the Hedgehog (HH) signaling cascade. When HH ligand binds to Patched (PTCH), its' inhibition on SMO is relieved. SMO is then able to accumulate to the tip of primary cilium in its' active form (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Kim, Kato et al. 2009). SMO causes the GLI family to become dislodged from their complex with the negative regulator of HH signaling, Suppressor of Fused (Sufu) (Kogerman, Grimm et al. 1999,

Pearse, Collier et al. 1999, Stone, Murone et al. 1999, Tukachinsky, Lopez et al. 2010). The GLI-Sufu complex maintains retention of Gli in the cytosol allowing for exposure to phosphorylation via protein kinase A (PKA) which inhibits downstream signal transduction (Tuson, He et al. 2011). When SMO is activated, the GLI2/3-Sufu complex is dismantled allowing for retrograde transport of GLI back into the nucleus (Kim, Kato et al. 2009).).

The GLI family is found in both a long activator form (GliA) or a proteolytically cleaved repressor form (GliR). Current understanding is that Gli3 functions primarily as a repressor while Gli1 and Gli2 function mainly as activators of the pathway and that recruitment of SMO to the cilium leads to an increase in the ratio of GliA:GliR (Hui and Angers 2011, Liu 2016). Downstream transcription is primarily activated by Gli2 and repressed by Gli3(Wang, Fallon et al. 2000, Bai, Auerbach et al. 2002, Persson, Stamatakis et al. 2002). Gli1 serves primarily as an activator of transcription and works through amplification of the activated state (Park, Bai et al. 2000).

Evidence Supporting this KER

Biological Plausibility

SMO signaling is dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). It has been shown that SMO localization to the tip of the primary cilia is essential for the SHH signaling cascade via the GLI transcription factors(Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Rohatgi, Milenkovic et al. 2009)

Empirical Evidence

- In vitro
 - NIH 3T3 clones with stable HA-Gli2 expression were created and a line with low HA-Gli2 expression was selected for further study. The reporter activity was induced by ShhN and fully inhibited by cyclopamine. When stimulated with ShhN, antibody staining was used to verify that Gli2 accumulates at the tip of the primary cilia. Immunostaining was also used to find that Gli2 accumulated in the nucleus of cells treated with ShhN. Using nuclear extracts of unstimulated cells HA-Gli2R was predominantly localized in the nucleus while in stimulated cells HA-Gli2 increased and HA-Gli2 decreased. Cells treated with Shh agonist SAG also had SMO accumulation in the primary cilia and increased HA-Gli2A in the nucleus (Kim, Kato et al. 2009).
 - NIH 3T3 cells were used to study whether the oxysterols and/or cholesterol are required for SHH signaling. Cells were depleted of sterols via incubation with methyl- β -cyclodextrin (MCD). Fluorinated sterols were added back as soluble components and the cells were stimulated with Shh ligand. Assays were performed for recruitment of endogenous SMO to the primary cilia and for pathway activation using a transcriptional reporter assay. Sterol depletion blocked relocation of SMO to the cilia and SHH activation. Cholesterol and 25-fluorocholesterol both rescued sterol depleted cells and restored SHH pathway activation (Huang, Nedelcu et al. 2016).
 - MMS1 (human myeloma) cells were used to study whether activation of Gli1 is required for its' translocation to the nucleus. Forskolin (FSK) which acts by blocking GLI1 access to PKA was added to culture for 24h at 10 μ m. The nuclear localization of GLI1 was significantly decreased in the presence of FSK (Blotta, Jakubikova et al. 2012).
- In vivo
 - none identified

Uncertainties and Inconsistencies

While we know that entry to the cilia is tightly controlled, the exact mechanism of SMO ciliary trafficking is not fully understood. The PC is separated from the plasma membrane by the ciliary pockets and the transition zone which function together to regulate the movement of lipids and proteins in and out of the organelle (Goetz, Ocbina et al. 2009, Rohatgi and Snell 2010). The SHH receptor PTCH contains a ciliary localization sequence in its' carboxy tail. Localization of PTCH to the PC is essential for inhibition of SMO as deletion of the CLS in PTCH prevents PTCH localization as well as inhibition of SMO (Kim, Hsia et al. 2015) (53). SMO also contains a CLS, but only accumulates in the PC upon ligand binding (Corbit, Aanstad et al. 2005). The entry of SMO into the PC is thought to occur either laterally through the ciliary pockets or internally via recycling endosomes (Milenkovic, Scott et al. 2009). Once inside the PC, SMO can diffuse freely, however it will usually accumulate in specific locations depending upon its' activation state. Inactive SMO will accumulate more at the base of the PC while active SMO will accumulate in the tip of the PC (Milenkovic, Weiss et al. 2015).

Quantitative Understanding of the Linkage

The data presented in support of this KER includes in vitro studies. The in vitro work offers data that SMO relocates to the tip of the primary cilium and that this plays a role in the translocation of the GLI transcription factors to the nucleus. The quantitative understanding of this linkage is low as studies including dose-response and time-course were not found.

Time-scale

Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation(Arensdorf, Marada et al. 2016). No data was found with regards to GLI1/2 translocation.

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[Relationship: 2721: Decrease, GLI1/2 translocation leads to Decrease, GLI1/2 target gene expression](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Low	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus	High	NCBI
human	Homo sapiens	Low	NCBI

Life Stage Applicability

Life Stage	Evidence
Embryo	High

Sex Applicability

Sex	Evidence
Unspecific	

All presented evidence for the relationship is performed in mice. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question.

Key Event Relationship Description

The Glioma-associated oncogene (Gli) family of zinc finger transcription factors (Gli1, Gli2, Gli3) are the primarily downstream effectors of the Hedgehog (HH) signaling cascade. When HH ligand binds to Patched (PTCH), its' inhibition on SMO is relieved. SMO this then able to accumulate to the tip of primary cilium in its' active form (Corbit, Aanstad et al. 2005, Rohatgi, Milenkovic et al. 2007, Kim, Kato et al. 2009). SMO causes the GLI family to become dislodged from their complex with the negative regulator of HH signaling, Suppressor of Fused (Sufu) (Kogerman, Grimm et al. 1999, Pearse, Collier et al. 1999, Stone, Murone et al. 1999, Tukachinsky, Lopez et al. 2010). The GLI-Sufu complex maintains retention of Gli in the cytosol allowing for exposure to phosphorylation via protein kinase A (PKA) which inhibits downstream signal transduction (Tuson, He et al. 2011). When SMO is activated, the GLI2/3-Sufu complex is dismantled allowing for retrograde transport of GLI back into the nucleus (Kim, Kato et al. 2009). This relocation then leads to signaling to effectors resulting in the activation of the GLI transcription factors and the subsequent induction of SHH target gene expression (Alexandre, Jacinto et al. 1996, Von Ohlen and Hooper 1997)

The GLI family is found in both a long activator form (GliA) or a proteolytically cleaved repressor form (GliR). Current understanding is that Gli3 functions primarily as a repressor while Gli1 and Gli2 function mainly as activators of the pathway and that recruitment of SMO to the cilium leads to an increase in the ratio of GliA:GliR (Hui and Angers 2011, Liu 2016). Downstream transcription is primarily activated by Gli2 and repressed by Gli3 (Wang, Fallon et al. 2000, Bai, Auerbach et al. 2002, Persson, Stamatakis et al. 2002). Gli1 serves primarily as an activator of transcription and works through amplification of the activated state (Park, Bai et al. 2000).

Evidence Supporting this KER

The evidence presented for this KER is low. The relationship between GLI1/2 translocation and a decrease in GLI1/2 target gene expression relocation has been shown indirectly in multiple mouse models through disruption of SHH signaling at the level of SMO. From our understanding of the SHH pathway, we can infer that disruption of the SHH signaling pathway at the level of SMO is causing a decrease in GLI1/2 translocation and it is this that is causing the altered gene expression. While clear evidence that disruption of SHH signaling leads to altered gene expression especially those of the Fox family, insufficient evidence exists for the direct relationship between GLI1/2 translocation and SHH target gene expression. The evidence also lacks direct human applicability as all presented work was

performed *in vitro* on murine models or *in vitro* on murine cell lines.

Biological Plausibility

SHH signaling is well established to be essential for proper embryonic development in vertebrates including mice and humans. Activation of the pathway results in a downstream signaling cascade resulting in the relocation of GLI to the nucleus and subsequent gene transcription (Carballo, Honorato et al. 2018).

Empirical Evidence

- In vitro
 - A mouse cNCC line (09-1) with the expression signature (AP-2alpha (Tfap2a, Twist1, Sox9, Cd44) was used to study whether foxf2 is a target of SHH signalling. Addition of SHH ligand (0.4µg/ml) was found to upregulate both GLI1 and Foxf2. This upregulation was completely blocked by the addition of vismodegib (120nm)(Everson, Fink et al. 2017).
 - To determine if SHH pathway inhibition was downstream for GANT 61 and GANT 58, a Sufu-null MEF cell line was used. Treatment of cells with either GANT at 10µm led to a significant reduction of SHH target genes GLI1 and Hip1 as determined by qPCR. As expected, cyclopamine was unable to inhibit signalling in this system as activation occurs downstream of SMO. GANT 61 is believed to act through addition of the modification to GLI1 that compromises its' ability to properly bind DNA (Lauth, Bergström et al. 2007).
 - GLI activators bind to the GACCACCA motif to promote transcription of GLI1, PTCH1, PTCH2, HHIP1, MYCN, CCND1, CCND2, BCL2, CFLAR, FOXF1, FOXL1, PRDM1 (BLIMP1), JAG2, GREM1, and Follistatin (Katoh and Katoh 2009)
 - Using a 3D microphysiological model loaded with 3T3 SHH lightII and GMSM-K GFP SHH cells a gradient of PTCH1 correlating with the distance from the epithelium secreting SHH ligand (Johnson, Vitek et al. 2021).
- In vivo
 - In situ hybridization was used to determine expression of GLI1 in C57BL/6J mice to better understanding temporal SHH signalling. At GD 9.0 no difference was found between control and embryos exposed to cyclopamine (120mg/kg/day). GLI1 was downregulated in the ventral frontonasal prominence (FNP) of clomipramine exposed embryos by GD 9.25. FNP tissue was micro dissected and cDNA microarray analysis was performed. 210 genes were found to be dysregulated including a significant enrichment to the forkhead box (Fox) family. RT-PCR confirmed significant down regulation of the SHH target genes GLI1 and PTCH1 as well as nine Fox members: Foxa2, Foxb2, Foxc1, Foxc2, Foxd1, Foxe1, Foxf1, Foxf2, Foxl1. Two members of the fox family, Foxm1 and Foxo1 were not found to differentially expressed in either the cDNA microarray or RT-PCR (Everson, Fink et al. 2017).
 - Using mutant Osr2-IresCre;Smo^{C/C} mice Foxf2 and Foxf1 were found to be positively regulated by SHH-SMO signalling. Expression of Osr2 was found to be reduced by E13.5 in the mutants. Expression of Osr1, Pax9, Tbx22 were not found to be altered (Lan and Jiang 2009).
 - To study whether SHH signaling regulates the developmental fate of the ecto-mesenchyme via regulation of gene activity in the facial primordia, Wnt1-Cre;Smon/c, (removal of SHH signaling) and Wnt1-Cre;R26SmoM2 (activation of SHH signaling). Positive regulation from SHH activity was found for Foxc2, Foxd1, Foxd2, Foxf1, and Foxf2. The Fox genes were found to be dissimilar in expression pattern with spatial activation even with uniform activation of the SHH pathway. Foxc2 and Foxd1 were found to be expressed ubiquitously in the MNA except at the midline, while Foxf1 is expressed at the lateral ends. Foxd2 and Foxf2 are both expressed along the mediolateral axis with Foxd2 having an increasing gradient from medial to lateral and Foxf2 having an opposing gradient (Jeong, Mao et al. 2004). These data support that disrupting GLI1/2 translocation via disruption of the SHH signaling pathway disrupts transcription of Foxc2, Foxd1, Foxd2, Foxf1, and Foxf2.

Uncertainties and Inconsistencies

None identified

Quantitative Understanding of the Linkage

The quantitative understanding for this KER is low. Studies to investigate response-response relationship as well as time scale have not been conducted or were not found in the literature review. The empirical evidence presented establishes that disruption of SHH signaling results in the altered gene expression of SHH target genes. There is a need for more studies to address the dose-response and time course relationship of this linkage.

Known Feedforward/Feedback loops influencing this KER

Positive feedback loop of gene expression from GLI1 and negative feedback loop for PTCH1, PTCH2, HHIP1(Katoh and Katoh 2009)

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[Relationship: 2731: Decrease, GLI1/2 target gene expression leads to Decrease, SHH second messenger production](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
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AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Low	Low
Decrease, GLI1/2 target gene expression leads to orofacial clefting	adjacent	Low	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus	High	NCBI
human	Homo sapiens	Low	NCBI

Life Stage Applicability

Life Stage Evidence

Embryo High

Sex Applicability

Sex Evidence

Unspecific High

The relationship between a decrease in GLI1/2 target gene expression and a decrease in secondary messenger production has been shown in mouse models. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question.

Key Event Relationship Description

Activation of the Sonic Hedgehog (SHH) pathway results in a downstream signaling cascade resulting in the relocation of GLI to the nucleus and subsequent gene transcription (Carballo, Honorado et al. 2018). This gene expression drives secondary messenger signaling for the pathway. The following genes are believed to be regulated by GLI as a component of SHH signaling: FGF10, BMP2, BMP4.

Evidence Supporting this KER

Biological Plausibility

SHH signaling is well established to be essential for proper embryonic development in vertebrates including mice and humans. Activation of the pathway results in a downstream signaling cascade resulting in the relocation of GLI to the nucleus and subsequent gene transcription (Carballo, Honorado et al. 2018). SHH cross talks with other developmental pathways including FGF and BMP.

Empirical Evidence

- In *Osr2-IresCre;Smoo^{c/c}* (SHH pathway inactive) mutant mice *Fgf10* mRNA was found to be significantly reduced in the anterior palatal mesenchyme. The expression of *Fgf10* correlated with a downregulation of *PTCH1* (Lan and Jiang 2009).
- To determine if SHH can induce *Fgf10*, SHH overexpressing cells were implanted in the anterior region of the wing bud of chick embryos. By 27 hours, the expression of *Fgf10* had significantly increased and expanded from the anterior mesenchyme to the bifurcating wing bud (Ohuchi, Nakagawa et al. 1997).
- To investigate whether *MSX-1* is in the same pathway as *Fgf10*, *MSX-1* expression was examined in *Fgf10-/-* mice and *Fgf10* expression was examined in *Msx-1-/-* mice. No change in expression was found and it is concluded that *MSX-1* is not a downstream target of *Fgf10* (Alappat, Zhang et al. 2005).
- SHH expression is reduced in the palatal epithelium of both *Fgf10-/-* and *Fgfr2b -/-* mutants. Exogenous *Fgf10* induced SHH in WT palatal epithelium (Rice, Spencer-Dene et al. 2004).
- BMP2 and BMP4 is downregulated in the anterior palate of *Osr2-IresCre;Smoo^{c/c}* (SHH pathway inactive) mutant mice (Lan and Jiang 2009).
- Upregulation of mesenchymal BMP4 by SHH via *Foxf1* or *Foxl1* (Katoh and Katoh 2009).

Uncertainties and Inconsistencies

The relationships and feedback/feedback loops that exist between SHH and its' secondary messengers primary *Fgf10* and *BMP4* is not well understood. Some evidence exists that expression of both *Fgf10* and *BMP4* correlates with that of SHH. The state of evidence is lacking and no dose response data was found.

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[Relationship: 2732: Decrease, SHH second messenger production leads to Decrease, Cell proliferation](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Low	Low
Decrease, GLI1/2 target gene expression leads to orofacial clefting	adjacent	Low	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus		NCBI
chicken	Gallus gallus		NCBI

Life Stage Applicability

Life Stage Evidence

Embryo High

Sex Applicability

Sex Evidence

Unspecific

The relationship between a decrease in SHH secondary messengers and a decrease in cellular proliferation translocation has been demonstrated in both mouse and chick models. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question.

Key Event Relationship Description

SHH is a mitogen that regulates cell proliferation during development. SHH regulation of proliferation works at least in part through regulation of cyclin D1 (ccnd 1) and cyclin D2 (Ccnd 2) (Kenney and Rowitch 2000, Ishibashi and McMahon 2002, Lobjois, Benazeraf et al. 2004, Mill, Mo et al. 2005, Hu, Mo et al. 2006). The regulation of ccnd 1 and ccnd 2 by SHH is not fully understood but is believed to be in part by regulation via SHH signaling and its signaling to SHH secondary messengers, namely the fibroblast growth factor family and GLI. GLI1 has been shown to directly bind and regulate ccnd1 and ccnd2 (Yoon, Kita et al. 2002). This signaling is largely comprised of a network between bone morphogenic protein (BMP), Fibroblast growth factor (Fgf), and SHH (SHH) (Zhang, Song et al. 2002, Rice, Spencer-Dene et al. 2004). The SHH signaling cascade results in the expression of secondary messengers. Proper Msx1 activity in the mesenchyme is required for the expression of SHH in the overlying epithelium (Zhang, Song et al. 2002). Maintenance of SHH expression in the epithelium is believed to be dependent on Fgf10 expression in the mesenchyme and its' signaling through Fgfr2b in the epithelium (Rice, Spencer-Dene et al. 2004).

Evidence Supporting this KER

-

Biological Plausibility

The SHH pathway is well known to be associated with cellular proliferation. There is a high biological probability that this proliferation results through regulation of SHH secondary messengers.

Empirical Evidence

- In vitro
 - Mouse cerebellar granule cells exposed to cycloheximide and SHH did not promote upregulation of ccnd 1, ccnd 2, or ccn3 mRNA. This supports that there is a protein intermediate between the SHH pathway and regulation of the G1 cyclins(Kenney and Rowitch 2000).
 -
- In vivo
 - In mouse palate explants application of SHH was found to induce proliferation in the palatal mesenchyme as measured by BrdU (Rice, Spencer-Dene et al. 2004).
 - In CD-1 WT and MSX-1-/-, SHH soaked beads were able to induce proliferation in palatal mesenchyme explants at 24hr but not after 8hr suggesting the induction of proliferation is through an indirect mechanism (Zhang, Song et al. 2002).
 - IHC staining for Ccnd-1 and Ccnd-2 in Osr2-IresCre Smoc/c (SHH inactive) and control embryos was used to determine if expression patterns differed between the mesenchyme and epithelium in mutants. Expression for both Ccnd-1 and Ccnd-2 was found to be reduced in the mesenchyme for mutants. mRNA was found to be reduced for both Ccnd-1 and Ccnd-2 in the palatal mesenchyme (Lan and Jiang 2009).
 - In Osr2-IresCre;Smoc/c (SHH pathway inactive) mutant mice Fgf10 mRNA was found to be significantly reduced in the anterior palatal mesenchyme. The expression of Fgf10 correlated with a downregulation of PTCH1 (Lan and Jiang 2009).
 - SHH expression is reduced in the palatal epithelium of both Fgf10-/- and Fgfr2b -/- mutants. Exogenous Fgf10 induced SHH in WT palatal epithelium (Rice, Spencer-Dene et al. 2004).
 - Decreased proliferation correlating with downregulation of GLI1 and PTCH1 was found in E10.25 mouse embryos treated with cyclopamine (Everson, Fink et al. 2017).

Uncertainties and Inconsistencies

The relationship between a decrease in SHH secondary messenger production and a decrease in cellular proliferation is plausible and data is shown that supports a decrease in ccnd 1 and 2 in correlation with the Fgf and SHH pathways. Further studies are needed to further out understanding of the regulation of proliferation by SHH.

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[Relationship: 2724: Decrease, Cell proliferation leads to Decrease, facial prominence outgrowth](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Low	Low
Decrease, GLI1/2 target gene expression leads to orofacial clefting	adjacent	Low	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus	High	NCBI

Life Stage Applicability

Life Stage	Evidence
Embryo	High

Sex Applicability

Sex	Evidence
Unspecific	

The relationship between a decrease in cellular proliferation and a decrease in outgrowth has been demonstrated in both mouse and chick models. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question.

Key Event Relationship Description

SHH is a mitogen that regulates cell proliferation during development. SHH regulation of proliferation works at least in part through regulation of cyclin D1 (ccnd 1) and cyclin D2 (Ccnd 2) (Kenney and Rowitch 2000, Ishibashi and McMahon 2002, Lobjois, Benazeraf et al. 2004, Mill, Mo et al. 2005, Hu, Mo et al. 2006). The regulation of ccnd 1 and ccnd 2 by SHH is not fully understood but is believed to be in part by regulation via SHH signaling and its signaling to SHH secondary messengers, namely the fibroblast growth factor family. A network of reciprocal growth factor signaling between the epithelium and mesenchyme is required for proper growth and patterning of the early palatal shelves.

The development of the face occurs early in embryogenesis and involves precise coordination of multiple tissues. The oropharyngeal membrane appears early in the 4th week of gestation and gives rise to the frontonasal process and the 1st pharyngeal arch. The frontonasal process is derived from the neural crest and in turn gives rise to two medial nasal process and two lateral nasal processes that later fuse and form the intermaxillary process. The pharyngeal arch is derived from mesoderm and the neural crest. It gives rise to two mandibular process and two maxillary processes (Som and Naidich 2013). These processes are comprised of mesenchymal cells from neural crest migration and the craniopharyngeal ectoderm and are coated in an epithelium (Ferguson 1988). The upper lip is formed during weeks 5-7 when the maxillary processes grow towards the midline and fuse intermaxillary process that have formed the philtrum and columella (Warbrick 1960, Kim, Park et al. 2004). The palate develops between week 6-12 from a median palatine process and a pair of lateral palatine processes. The primary palate is formed from the posterior extension of the intermaxillary process. The lateral palatine processes arise as medial mesenchymal processes from both maxillary processes. These processes initially grow inferiorly until the tongue is pulled downwards by the elongation of the maxilla and mandible. Once above the tongue, the lateral processes grow medially until they make contact and fuse (Som and Naidich 2014). For normal facial development and growth coordinated multivariate signaling is required. For example, retinoic acid, BMP, FGF, and SHH signal together to control facial growth (Liu, Rooker et al. 2010). SHH is an important modulator of epithelial-mesenchyme interaction (EMi) during development. SHH has been shown to regulate growth and formation of the palatal shelves prior to elevation and fusion (Rice, Connor et al. 2006). During development, SHH ligand is secreted by the epithelium into the underlying mesenchyme. This causes a gradient of signaling where mesenchyme proximal to the epithelium is exposed to higher concentrations of SHH than more distal cells (Cohen, Kicheva et al. 2015). Disruption of SHH during critical windows of development is believed to work in an EMi dependent, but epithelial-mesenchyme transition (Emt) independent manner. OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015).

Evidence Supporting this KER

Biological Plausibility

The SHH pathway is well known to be associated with cellular proliferation and growth of the facial prominences. There is a high biological probability that disruption to proliferation of the facial prominences disrupts outgrowth.

Empirical Evidence

- In vitro
 - None identified
- In vivo
 - To investigate how SHH might regulate early pharyngeal arch (PA1) development SHH-/ embryos were generated. At E9.5, the mutant embryos were thinner with hypoplasia on PA1. Morphometrics of PA1 of mutant vs. control showed a significant decrease in size in the mutant ($P<0.05$) for both the dorsal-ventral and the anteroposterior axis. Hypoplasia was quantified using a Pax3-Cre/R26R transgenic mouse line marked with LacZ and stained with X-gal (Yamagishi, Yamagishi et al. 2006).
 - SHH expressed in thickened palatal epithelium prior to palatal shelf outgrowth (E13.0-14.5) (Rice, Connor et al. 2006)
 - Using Wnt1-Cre;Smn/c embryos, a significant decrease in the growth of the mandibular arch in both the proximodistal and dorsoventral (D-V) axes. This supports that observation that the wild type, but not the mutants undergo rapid growth in the D-V axis around E11.5 (Jeong, Mao et al. 2004).
 - SHH is expressed in oral epithelium and shown as a key signal for palatal shelf outgrowth in explant culture (Lan and Jiang 2009)

Uncertainties and Inconsistencies

The regulation of proliferation by SHH has been shown but questions to the exact mechanism of regulation remain. Evidence exists that there is likely an intermediate between SHH and regulation of ccnd 1 and ccnd 2. Some evidence exists that the intermediate could be a member(s) of the Fgf family. The relationship between a decrease in cellular proliferation and a decrease in outgrowth is plausible and data is shown that supports that disruption of the SHH pathway leads to decrease in palatal outgrowth. Further studies are needed to further out understanding of the regulation of proliferation by SHH and its subsequent impact on outgrowth of the facial prominences.

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[Relationship: 2726: Decrease, facial prominence outgrowth leads to orofacial cleft](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Moderate	Low
Decrease, GLI1/2 target gene expression leads to orofacial clefting	adjacent	Moderate	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus	High	NCBI

Life Stage Applicability

Life Stage	Evidence
Embryo	High

Sex Applicability

Sex	Evidence
Unspecific	

The relationship is biologically plausible in human, but to date no specific experiments have addressed this question.

The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs). For this reason, this KER is applicable to the embryonic stage with a high level of confidence.

Key Event Relationship Description

Orofacial clefts (OFCs) are one of the most common human birth defects and occur in approximately 1 in 700 live births (Mossey, Little et al. 2009, Dixon, Marazita et al. 2011) Formation of the upper lip and palate requires the orchestrated proliferation and fusion of embryonic facial growth centers and is dependent on paracrine intercellular signaling through multiple pathways. Genetic and chemical disruption of the Sonic Hedgehog (SHH), Transforming growth factor-beta (Tgf- β), bone morphogenic protein (BMP), epidermal growth factor (EGF) etc. pathways have been shown to cause OFCs (Jiang, Bush et al. 2006, Bush and Jiang 2012, Lan, Xu et al. 2015) Early orofacial development involves epithelial ectoderm derived SHH ligand driving tissue outgrowth through an induced gradient of SHH dependent transcription in the underlying mesenchyme, which is thought to drive mesenchymal proliferation (Lan and Jiang 2009, Kurosaka 2015).

The development of the face occurs early in embryogenesis and involves precise coordination of multiple tissues. The oropharyngeal membrane appears early in the 4th week of gestation and gives rise to the frontonasal process and the 1st pharyngeal arch. The frontonasal process is derived from the neural crest and in turn gives rise to two medial nasal process and two lateral nasal processes that later fuse and form the intermaxillary process. The pharyngeal arch is derived from mesoderm and the neural crest. It gives rise to two mandibular process and two maxillary processes (Som and Naidich 2013). These processes are comprised of mesenchymal cells from neural crest migration and the craniopharyngeal ectoderm and are coated in an epithelium (Ferguson 1988). The upper lip is formed during weeks 5-7 when the maxillary processes grow towards the midline and fuse intermaxillary process that have formed the philtrum and columella (Warbrick 1960, Kim, Park et al. 2004). The palate develops between week 6-12 from a median palatine process and a pair of lateral palatine processes. The primary palate is formed from the posterior extension of the intermaxillary process. The lateral palatine processes arise as medial mesenchymal processes from both maxillary processes. These processes initially grow inferiorly until the tongue is pulled downwards by the elongation of the maxilla and mandible. Once above the tongue, the lateral processes grow medially until they make contact and fuse (Som and Naidich 2014). For normal facial development and growth coordinated multivariate signaling is required. For example, retinoic acid, BMP, FGF, and SHH signal together to control facial growth (Liu, Rooker et al. 2010). SHH is an important modulator of epithelial-mesenchyme interaction (EMi) during development. SHH has been shown to regulate growth and formation of the palatal shelves prior to elevation and fusion (Rice, Connor et al. 2006). During development, SHH ligand is secreted by the epithelium into the underlying mesenchyme. This causes a gradient of signaling where mesenchyme proximal to the epithelium is exposed to higher concentrations of SHH than more distal cells (Cohen, Kicheva et al. 2015). Disruption of SHH during critical windows of development is believed to work in an EMi dependent, but epithelial-mesenchyme transition (Emt) independent manner. OFCs caused by disruption to SHH are believed to be due to a reduction in epithelial induced proliferation and the subsequent decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015).

Evidence Supporting this KER

Biological Plausibility

The SHH pathway is well known to be associated with development of the face including the lip and palatal. Disruption of SHH at critical periods of development has been shown to cause OFCs.

Empirical Evidence

- In vitro
 - None identified
- In vivo
 - ~85% of K14-Cre;Shh^{c/n} mice had cleft palate with rudimentary palatal shelves spaced apart without contact suggesting that the cleft is due to insufficient outgrowth of the shelves (Rice, Spencer-Dene et al. 2004).
 - 100% (n=22) Osr2-IresCre;Smoc^{c/c} had a cleft palate. At E14.5 the palatal shelves were underdeveloped and had not grown out to make contact compared to control littermates that had met and initiated fusion. This supports that disruption of SHH signalling impairs palatal shelf outgrowth and can lead to cleft palate (Lan and Jiang 2009)

Uncertainties and Inconsistencies

The quantitative understanding of this relationship is low. No studies were found to exist to address dose response or time-scale data. Further work is needed to address these questions and create a better understanding of this relationship.

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AOP460

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[Relationship: 2792: Apoptosis leads to Decrease, facial prominence outgrowth](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Low	Low
Decrease, GLI1/2 target gene expression leads to orofacial clefting	adjacent	Low	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term Scientific Term Evidence Links

mouse *Mus musculus* High [NCBI](#)

Life Stage Applicability

Life Stage Evidence

Embryo High

Sex Applicability

Sex Evidence**Unspecific**

The relationship between an increase in apoptosis and a decrease in palatal shelf outgrowth has been shown in mice models as detailed in the empirical evidence section. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question. The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs). For this reason, this KER is applicable to the embryonic stage with a high level of confidence.

Key Event Relationship Description

The development of the face occurs early in embryogenesis and involves precise coordination of multiple tissues. The oropharyngeal membrane appears early in the 4th week of gestation and gives rise to the frontonasal process and the 1st pharyngeal arch. The frontonasal process is derived from the neural crest and in turn gives rise to two medial nasal process and two lateral nasal processes that later fuse and form the intermaxillary process. The pharyngeal arch is derived from mesoderm and the neural crest. It gives rise to two mandibular process and two maxillary processes (Som and Naidich 2013). These processes are comprised of mesenchymal cells from neural crest migration and the craniopharyngeal ectoderm and are coated in an epithelium (Ferguson 1988). The upper lip is formed during weeks 5-7 when the maxillary processes grow towards the midline and fuse intermaxillary process that have formed the philtrum and columella (Warbrick 1960, Kim, Park et al. 2004). The palate develops between week 6-12 from a median palatine process and a pair of lateral palatine processes. The primary palate is formed from the posterior extension of the intermaxillary process. The lateral palatine processes arise as medial mesenchymal processes from both maxillary processes. These processes initially grow inferiorly until the tongue is pulled downwards by the elongation of the maxilla and mandible. Once above the tongue, the lateral processes grow medially until they make contact and fuse (Som and Naidich 2014). For normal facial development and growth coordinated multivariate signaling is required. For example, retinoic acid, BMP, FGF, and SHH signal together to control facial growth (Liu, Rooker et al. 2010). SHH is an important modulator of epithelial-mesenchyme interaction (EMi) during development. SHH has been shown to regulate growth and formation of the palatal shelves prior to elevation and fusion (Rice, Connor et al. 2006). During development, SHH ligand is secreted by the epithelium into the underlying mesenchyme. This causes a gradient of signaling where mesenchyme proximal to the epithelium is exposed to higher concentrations of SHH than more distal cells (Cohen, Kicheva et al. 2015). Disruption of SHH during critical windows of development is believed to work in an EMi dependent, but epithelial-mesenchyme transition (Emt) independent manner. OFCs caused by disruption to SHH are believed to be due to a decrease in cellular proliferation and an increase in apoptosis leading to a decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015). In mice, zones of apoptosis within the fusing epithelium of the medial nasal process and the lateral nasal process have been identified (Gaare and Langman 1977). These regions have been shown to be nonproliferative and are actively undergoing apoptosis (Jiang, Bush et al. 2006, Song, Li et al. 2009, Ferretti, Li et al. 2011). These studies demonstrate the importance of apoptosis in orofacial development and indicate that dysregulation of this process could result in OFC formation.

Evidence Supporting this KER**Biological Plausibility**

There is a high biological plausibility that increased apoptosis would lead to decreased facial prominence outgrowth.

Empirical Evidence

- In vitro
 - None found in search
- In vivo
 - Wnt1-Cre;Smoo^{n/c} have increased apoptosis in the mandibular arch compared to wild type at E9.5, E 10.5. This is combination with a decrease in proliferation at E11.5 leads to a decrease in outgrowth of the process (Jeong, Mao et al. 2004).
 - Chick embryos exposed to 200ul of 10% ethanol with an additional 20ul of 1% ethanol at stage 9-10 display a reduction in the growth of the frontonasal prominence, hypoplastic branchial arches, and increased apoptosis in cranial neural crest cells. Treatment with antibodies that block SHH signalling had the same impact as ethanol exposure supporting that ethanol exposure reduces shh signalling (Ahlgren, Thakur et al. 2002).

Uncertainties and Inconsistencies

Further studies are needed to expand our understanding of the role that apoptosis plays in orofacial development and cleft formation.

Quantitative Understanding of the Linkage

The quantitative understanding of this relationship is low. No studies were found to exist to address dose response or

time-scale data. Further work is needed to address these questions and create a better understanding of this relationship.

Response-response relationship

Insufficient evidence

Time-scale

Insufficient evidence

Known modulating factors

Modulating Factor (MF) MF Specification Effect(s) on the KER Reference(s)

Insufficient evidence

Known Feedforward/Feedback loops influencing this KER

Insufficient evidence

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[Relationship: 2882: Decrease, GLI1/2 target gene expression leads to Apoptosis](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	adjacent	Low	Low

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus	High	NCBI

Life Stage Applicability**Life Stage Evidence**

Embryo High

Sex Applicability**Sex Evidence**

Unspecific

The relationship between a decrease in cellular proliferation and a decrease in outgrowth has been demonstrated in both mouse and chick models. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question.

Key Event Relationship Description

The GLI transcription factors are the main transcription factors of the Sonic Hedgehog (SHH) pathway. Sonic Hedgehog is a major developmental pathway involved in embryonic development. Disruption of SHH during critical windows of development can cause birth defects (ex. Orofacial clefting (OFCs)). OFCs caused by disruption to SHH are believed to be due to a decrease in cellular proliferation and an increase in apoptosis leading to a decrease in tissue outgrowth and the failure of the facial processes to meet and fuse (Lipinski, Song et al. 2010, Heyne, Melberg et al. 2015). This increase in apoptosis is believed to be due to a decrease in GLI1/2 target gene expression.

Evidence Supporting this KER**Biological Plausibility**

There is a high biological probability that disruption of GLI1/2 target gene expression leads to an increase in apoptosis.

Empirical Evidence

- In vitro
 - None found
- In vivo
 - Decreased GLI1/2 expression found using in situ hybridization was found on E9.5 embryos of all-trans RA (E 8.5 25mg/kg oral gavage) exposed pregnant dams. An increase in apoptosis of CNCC was also found in the E9.5 embryos. A rescue experiment with SAG (SMO agonist) dosed in combination with RA reduced the incidence of CP and CNCC apoptosis (Wang, Kurosaka et al. 2019).
 - Chick embryos exposed to 200µl of 10% ethanol with an additional 20µl of 1% ethanol at stage 9-10 display saw decreased GLI and SHH expression in the head. These embryos also display a reduction in the growth of the frontonasal prominence, hypoplastic branchial arches, and increased apoptosis in cranial neural crest cells. Treatment with antibodies that block SHH signalling had the same impact (Ahlgren, Thakur et al. 2002).

Uncertainties and Inconsistencies

The relationship between GLI1/2 target gene expression and increased apoptosis has a high biological plausibility although there is currently lack of studies that address this relationship.

Quantitative Understanding of the Linkage

The quantitative understanding of this relationship is low. No studies were found to exist to address dose response or time-scale data. Further work is needed to address these questions and create a better understanding of this relationship.

Response-response relationship

Further work is needed to increase the understanding of this relationship and its' response-response relationship.

Time-scale

Further work is needed to increase the understanding of this relationship and its' time scale.

Known modulating factors

Modulating Factor (MF)	MF Specification	Effect(s) on the KER	Reference(s)
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Modulating Factor (MF)	MF Specification	Effect(s) on the KER	Reference(s)
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Further work is needed to increase the understanding of this relationship and its' modulating factors.

Known Feedforward/Feedback loops influencing this KER

Further work is needed to increase the understanding of this relationship and shed light on what other feedback/forward loops are at play.

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List of Non Adjacent Key Event Relationships

[Relationship: 2894: Antagonism Smoothened leads to orofacial cleft](#)

AOPs Referencing Relationship

AOP Name	Adjacency	Weight of Evidence	Quantitative Understanding
Antagonism of Smoothened receptor leading to orofacial clefting	non-adjacent	High	Moderate

Evidence Supporting Applicability of this Relationship

Taxonomic Applicability

Term	Scientific Term	Evidence	Links
mouse	Mus musculus	High	NCBI

Life Stage Applicability

Life Stage	Evidence

Life Stage Evidence

Embryo High

Sex Applicability**Sex Evidence**

Unspecific

The nonadjacent relationship between antagonism of SMO and orofacial clefting (OFCs) has been shown repeatedly in mice models as detailed in the empirical evidence section. The relationship is biologically plausible in human, but to date no specific experiments have addressed this question. The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs). For this reason, this KER is applicable to the embryonic stage with a high level of confidence.

Key Event Relationship Description

The Smoothened (SMO) receptor is Class F G protein coupled receptor involved in signal transduction of the Sonic Hedgehog (SHH) pathway. It includes distinct functional groups including ligand binding pockets, cysteine rich domain (CRD), transmembrane helix (TM), extracellular loop (ECL), intracellular loop (ICL), and a carboxyl-terminal tail (C-term tail) (Arensdorf, Marada et al. 2016). SMO signaling is dependent upon its relocation to a subcellular location. This relocation occurs in the primary cilium (PC) in vertebrates (Huangfu and Anderson 2005). Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation (Arensdorf, Marada et al. 2016).

In the absence of SHH ligand, the Patched (PTCH) receptor suppresses the activation of SMO. When HH ligand binds to PTCH, suppression on SMO is released and SMO can relocate, accumulate, and signal to intracellular effectors (Denef, Neubüser et al. 2000, Rohatgi and Scott 2007). It has been shown that SMO localization to the tip of the primary cilia is essential for the SHH signaling cascade in vertebrates (Corbit, Aanstad et al. 2005, Rohatgi, Milenovic et al. 2007, Rohatgi, Milenovic et al. 2009). This relocation then leads to signaling to effectors resulting in the activation of the GLI transcription factors and the subsequent induction of HH target gene expression (Alexandre, Jacinto et al. 1996, Von Ohlen and Hooper 1997). Antagonism of SMO disrupts the downstream signaling cascade of SHH and if disrupted during critical periods of development can lead birth defects including OFCs.

Evidence Supporting this KER**Biological Plausibility**

There is high biological plausibility of this relationship. The SHH pathway is well understood to be fundamental to proper embryonic development and that aberrant SHH signaling during embryonic development can cause birth defects including orofacial clefts (OFCs).

Empirical Evidence

- *In vitro*- It should be noted that OFC cannot be evaluated *in vitro*. The evidence presented below is intended to further support the *in vivo* evidence and offers support of which stressors might cause an OFC and their possible mechanism.
 - A small molecule screen of 10,000 compounds identified six inhibitors of SHH signaling, four of which bind directly to SMO (SANT1-4). Screening was conducted using NIH 3T3 SHH Light2 cells cultured in media conditioned from HEK 293 transfected to stably express Shh-N. Cells were dosed with the compound library at 0.714ug/ml and SHH activity was quantified at 30h using Renilla luciferase activity. A fluorescent binding assay using BODIPY-cyclopamine was used to verify binding to SMO for the SANT compounds. Dose response reported as IC50 for the inhibition of SHH signaling was conducted in NIH 3T3 SHH light2, NIH 3T3 SmoA1-Light2, P2 Ptch1-/- (mouse embryonic fibroblasts) (Chen, Taipale et al. 2002).

Compound/Cell	SHH-Light2 (nM)	SmoA1-Light2 (nM)	Ptch1-/- (nM)
SANT-1	20	30	20
SANT-2	30	70	50
SANT-3	100	80	80
SANT-4	200	300	300

- Direct binding of cyclopamine to SMO was verified using a photoaffinity form of cyclopamine (PA-cyclopamine). PA-cyclopamine had previously been shown to inhibit SHH signaling in NIH 3T3 Shh-Light2 cells with similar IC50 values to cyclopamine (300nm and 150nm respectively) (Taipale, Chen et al. 2000). Binding to SMO was verified using a COS-1 (fibroblast, monkey) line transfected to over express SMO. The location of cyclopamine binding was further investigated using BODIPY- cyclopamine and COS-1 cells modified to lack either a N-terminal, extracellular cysteine-rich domain, or the cytoplasmic C terminal of SMO. The findings support that cyclopamine does not require these domains and instead binds directly to

the heptahelical domain (Chen, Taipale et al. 2002).

- **In vivo**
 - The presence of critical periods for disruption of SHH was investigated using C57BL/6J mice. Vismodegib was suspended at 3mg/ml in 0.5% methyl cellulose and 0.2% tween. Pregnant dams were administered 40mg/kg vismodegib at GD7.0, 7.25, 7.5, 7.75, 8.0, 8.25, 8.5, 8.625, 8.75, 8.875, 9.0, 9.25, 9.5, 9.75, and 10.0. Cyclopamine was dosed at 120mg/kg/d via subcutaneous infusion between GD8.25-9.375. Pregnant dams were euthanized at GD17 and fetal specimens were collected and fixed for imaging. The control group consisted of fetuses exposed to 0.5% methyl cellulose and 0.2% tween at GD7.75, 8.875, or 9.5. Acute exposure to vismodegib resulted in a peak incidence of lateral cleft lip and palate at GD8.875 (13%). Exposure at GD9.0 and 10.0 resulted in clefts of the secondary palate only (34%). A higher penetrance (81%) was found for cyclopamine exposure (Heyne, Melberg et al. 2015).
 - Timed pregnant C57B1/6J mice were treated with cyclopamine from GD 8.25-9.5 by subcutaneous infusion (160mg/kg/d) or at GD 8.5 with AZ75 (potent cyclopamine analog) via oral gavage (40 or 80mg/kg). Exposure to cyclopamine resulted in lateral cleft lip and cleft palate defects attributed to a deficiency of midline and lower medial nasal prominence tissue. Both drugs infrequently resulted in an intermediate phenotype of median CLP. Cyclopamine caused gross facial malformations in 5/14 litters with an intra-litter penetrance of clefting of 50%. AZ75 dosed at 80mg/kg caused all embryos to resorb. At 40mg/kg AZ75 caused gross facial malformations in 6/7 litters (Lipinski, Song et al. 2010).
 - Timed pregnant C57B1/6J mice were administered cyclopamine via micro osmotic pumps (120mg/kg/d) surgically implanted at GD 8.25. Dams were euthanized on GD 17. 25/45 of the cyclopamine exposed fetuses presented with a cleft compared to 0/39 for the control group (Lipinski, Holloway et al. 2014).
 - Pregnant Sprague Dawley rats were dosed with 240mg/kg of cyclopamine (oral gavage once daily) from GD 6.0-9.0. Craniofacial malformations were noted including cebophthalmia, microcephaly, hydrocephaly, exencephaly, and anencephaly. Parallel experimentation in golden hamsters found that 170mg/kg of cyclopamine was sufficient to cause malformations including cleft lip and palate (Keeler 1975).
 - C57BL/6J and A/J mice were dosed with single doses of jervine (70, 150, 300mg/kg gavage) on either GD 8, 9, 10. A dose response pattern of CLP was seen for both strains with dosing on GD 8. A dose response pattern for CP was found for C57BL/6J for treatment on GD 9 or 10 but not at GD 8 (Omnell, Sim et al. 1990).

Quantitative Understanding of the Linkage

Response-response relationship

Further work is needed to address these questions and create a better understanding of this relationship.

Time-scale

Relocation of SMO to the PC typically occurs within ~20 minutes of agonist stimulation (Arensdorf, Marada et al. 2016). No data was found on how fast antagonism of SMO will stop its' relocation to the primary cilia. Further work is needed to increase the understanding of this relationship and its' time scale

Known modulating factors

Modulating Factor (MF)	MF Specification	Effect(s) on the KER	Reference(s)
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Further work is needed to increase the understanding of this relationship and its' modulating factors.

Known Feedforward/Feedback loops influencing this KER

Further work is needed to increase the understanding of this relationship and shed light on what other feedback/forward loops are at play.

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