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The role of *Irf6* in tooth epithelial invagination

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Abstract

Thickening and the subsequent invagination of the epithelium are an important initial step in ectodermal organ development. *Irf6* has been shown to play a critical role in controlling epithelial

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growth, since *Ikka* mutant mice show protrusions (evaginations) of incisor tooth, whisker and hair follicle epithelium rather than invagination. We show here that mutation of the Interferon regulatory factor (*Irf*) family, *Irf6* also results in evagination of incisor epithelium. In common with *Ikka* mutants, *Irf6* mutant evagination occurs in a NF- κ B-independent manner and shows the same molecular changes as those in *Ikka* mutants. *Irf6* thus also plays a critical role in regulating epithelial invagination. In addition, we also found that canonical Wnt signaling is upregulated in evaginated incisor epithelium of both *Ikka* and *Irf6* mutant embryos.

Keywords

Ikka; Irf6; Wnt; Incisor; Invagination; Epithelium; Tooth development

Introduction

Many organs (e.g. lung, liver, kidney, glands, eyes, hair) develop through reciprocal epithelial–mesenchymal interactions and share similar signaling pathways such as Bmp, Shh, Fgf, Wnt and Tgf at early stages of their development. At the early stages, these organs also show similar morphological features, consisting of a thickening and subsequent invagination of the epithelium. Teeth arise from a series of reciprocal interactions between the oral epithelium and underlying neural crest-derived mesenchyme (for reviews, see Thesleff, 2006; Tucker and Sharpe, 2004). The first morphological sign of tooth development is a narrow band of thickened epithelium on the developing jaw primordia and subsequent localized invagination into underlying mesenchyme to form buds. The bud epithelium progressively takes the form of the cap and bell configurations as differentiation proceeds. Epithelial cells and mesenchymal cells (dental papilla) then differentiate into enamel-producing ameloblasts and dentin-producing odontoblasts, respectively.

The nuclear Factor *kappa* B (NF- κ B) pathway plays a major role in many physiological and pathological process including immune response to infection and cancer (for review see Chariot, 2009; Häcker and Karin, 2006; Li and Verma, 2002; Sanz et al., 2010). In mammals, 12 NF- κ B homo- or hetero-dimers are formed among the five proteins NF- κ B1 (p50, generated from p105), NF- κ B2 (p52, generated from p100), RelA (p65), RelB and c-Rel. NF- κ B exists in the cytoplasm as an inactive form that is associated with inhibitory proteins termed Inhibitor of κ B (I κ B). Activation of the NF- κ B pathway results in nuclear translocation of NF- κ B proteins, and can proceed either through classical/canonical, alternative/noncanonical or hybrid pathways. Classical NF- κ B activation is usually a rapid and transient response to a wide range of stimuli. In nonstimulated cells, I κ B acts to retain NF- κ B in the cytoplasm by masking the nuclear localization sequence. Exposure to stimuli results in rapid phosphorylation of I κ B that leads to site-specific ubiquitination and degradation. The resulting free NF- κ B dimers translocate to the nucleus and regulate target gene transcription. The protein kinase that phosphorylates I κ B in response to stimuli is a multiprotein complex, I κ B kinase (IKK), composed of two catalytic subunits, IKK α and IKK β , and a regulatory subunit, IKK γ (also called NEMO). The alternative pathway involves slow activation of NF- κ B leading to prolonged activation of NF- κ B targets genes. NF- κ B inducing kinase (NIK) recruits IKK α that phosphorylates p100, promoting p100

polyubiquitination and subsequent proteasomal processing to p52, generating RelB/p52 dimers which facilitates full activation of the pathway. In addition, *Ikkα* is also known to function outside of the IKK complex in an NF-κB-independent manner. *Ikkα* is a critical regulator of keratinocyte differentiation by an NF-κB-independent manner, although the exact mechanism through which *Ikkα* acts is unclear. Taut undifferentiated epidermis, limb truncation, cleft palate, abnormal molar cusp shape and adhesion of oral epithelium are also observed in *Ikkα* mutant mice (Hu et al., 1999; Li et al., 1999; Takeda et al., 1999). In addition to these phenotypes, incisor tooth epithelium of *Ikkα* mutant mice fails to invaginate into the underlying mesenchyme and instead evaginates into the oral cavity, suggesting that *Ikkα* has a regulatory role in guiding directionality of developing tooth germs. This role of *Ikkα* is independent of the NF-κB (Ohazama et al., 2004).

Interferons (IFNs) play critical roles in many biological processes including the homeostasis and function of immune systems (Bonjardim et al., 2009; Hertzog et al., 2011). Irf regulatory factor (*Irf*) genes regulate the transcription of interferons, proteins produced in response to the presence of pathogens, and function as an integral part of the immune system (Platanias, 2005). The *Irf* family is comprised of nine members (*Irf1–Irf9*) that share a highly conserved N-terminal, penta-tryptophan, helix-turn-helix DNA-binding domain and a less well-conserved protein-binding domain (Taniguchi et al., 2001). Many members of *Irf* family are known to activate the canonical NF-κB pathway (Hiscott, 2007; Taniguchi et al., 2001). *Ikkα* is also involved in Toll-like receptor (TLR)7- and TLR9-mediated IFNα induction in plasmacytoid dendritic cells via *Irf7* phosphorylation as NF-κB independent manners (Hoshino et al., 2006). Mutation in *IRF6* has previously been shown to cause Van der Woude syndrome (VWS) and popliteal pterygium syndrome (PPS; Kondo et al., 2002). VWS is an autosomal dominant disorder of facial development that is characterized by cleft lip and palate and is the most common form of syndromic orofacial clefting (Van der Woude, 1954). PPS has a similar orofacial phenotype to VWS, but includes popliteal webbing, pterygia, oral synchia, adhesions between the eyelids, syndactyly and genital anomalies (Bixler et al., 1973; Froster-Iskenius, 1990). *Irf6* mutant mice show cleft palate, adhesion of oral epithelium, limb truncation and taut undifferentiated epidermis, all phenotypes also seen in *Ikkα* mutants (Hu et al., 1999; Ingraham et al., 2006; Li et al., 1999; Richardson et al., 2006; Takeda et al., 1999).

Thickening and the subsequent invagination of the epithelium is an important initial step in tooth development. Although several new insights have recently been revealed, the molecular mechanisms regulating epithelial invagination still remain unclear (Charles et al., 2011; Munne et al., 2009). We show here that null mutation of the *Irf6* results in identical incisor phenotypes (evagination of incisor epithelium) and similar molecular changes to those in *Ikkα* mutants. Despite these shared phenotypes and associated molecular changes, crosses between *Ikkα* and *Irf6* mutants failed to reveal any evidence of a genetic interaction in regulating tooth epithelial invagination.

Materials and methods

Production and analysis of transgenic mice

The production of mice with mutation of *Ikka*, *Irf6*, *Jagged2* (*Jag2*), *Rip4* and *Stratifin* (*Sfn*; *Sfn*^{Er/Er}) has previously been described (Guenet et al., 1979; Holland et al., 2002; Hu et al., 1999; Jiang et al., 1998; Richardson et al., 2006). Mice overexpressing *Ikka* under keratin (K) 5 promoter (*K5-Ikka*) have been described previously (Lomada et al., 2007). Production of the NF- κ B reporter [(*Ig κ*)₃*conalacZ*] and *Axin2* reporter (*Axin2*^{lacZ}) mice has also previously been described (Lustig et al., 2002; Schmidt-Ullrich et al., 1996). The *Irf6* hypomorph allele (*Irf6*^{neo}) was created as an intermediate step toward the construction of an *Irf6* conditional knockout targeting vector. In addition to loxP sites, we inserted the neomycin resistance gene (*neo*), under the control of a constitutive promoter, as a selectable marker for the insertion event. To create this construct, we screened a BAC library derived from 129/SV strain and identified clone RPCI22-516G. From this BAC, we subcloned a 1.8 kb *KpnI*–*Bam*HI fragment for the 5′-arm and a 3.9 kb *Bam*HI–*Hind*III fragment for the 3′-arm into the *Kpn*I and *Hind*III sites of pBluescript II SK(–) vector. The 3 kb *Bam*HI fragment, located between the 5′- and 3′-arms was cloned into the *Sal*I site in ploxP3NeopA vector (kind gift from Dr. Yagi and Dr. Hirabayashi, Osaka University). This vector was cut with *Xho*I, which liberated a 5.8 kb fragment that contained the floxed exons (3 and 4) and the *Pgk-neo* cassette, and was subcloned into the *Bam*HI site located at the junction of the 5′ and 3′ arms. This gene targeting vector was digested with *Not*I and electroporated into ES cells derived from 129/SV strain. We screened 384 ES clones by PCR. After G418 selection, four clones were positive. The positive ES cells were microinjected into C57BL/6 blastocysts, and we obtained nine male chimeras that were mated with C57BL/6 mice. Germline transmission was verified as previously described (Ingraham et al., 2006).

Embryonic day 0 (E0) was taken to be midnight prior to finding a vaginal plug. Embryos were harvested at the appropriate time and genotyped using PCR analysis of genomic DNA extracted from unused embryonic tissue. Embryonic heads were fixed in 4% paraformaldehyde (PFA), wax embedded and serially sectioned at 7 μ m. Sections were split over 5–10 slides and prepared for histology and radioactive in situ hybridisation.

In situ hybridisation

Radioactive in situ hybridisation with [³⁵S]UTP-labeled riboprobes was carried out as described previously (Ohazama et al., 2008). Decalcification using 0.5 M EDTA (pH 7.6) was performed after fixation of newborn mice. The radioactive antisense probes were generated from mouse cDNA clones that were gifts from T.A. Mitsiadis (*Notch1*, *Notch2*), A. McMahon (*Shh*) or were obtained from RZPD (*Irf1*, *Irf2*, *Irf3*, *Irf4*, *Irf5*, *Irf7*, *Irf8*, *Irf9*) or Geneservice (*Sfn*).

Immunohistochemistry

After deparaffinization, sections were treated by proteinase K and then incubated with antibody to phosphorylated Smad1, Smad5 and Smad8 (p-Smad1/5/8; Cell signaling Technology) or CD44 (Chemicon). As a negative control, normal rabbit or rat serum was

used instead of primary antibody. Tyramide signal amplification system was performed (Perkin Elmer Life Science or DAKO) for detecting primary antibody.

Apoptotic activity

For detecting apoptotic cells, we used the Apoptag plus fluorescein in situ apoptosis detection kit (Chemicon), according to manufacturer's protocol.

β -galactosidase staining

Embryo heads of lacZ-reporter and reporter-crossed mice were fixed for 1 h at 4 °C in 1% PFA and 0.2% glutaraldehyde in nuclease-free phosphate buffered saline (PBS). X-gal staining was performed at 37 °C in 4 mM potassium ferrocyanide, 4 mM potassium ferricyanide, 2 mM MgCl₂, and 400 μ g ml⁻¹ X-gal (4-chloro-5-bromo-3-indolyl- β -galactoside, Sigma) in 1x PBS for 4 h (*Axin2^{lacZ}* mice) or 27 h [(I γ κ)₃conalacZ mice]. Afterwards, embryo heads were washed several times in 1x PBS and post-fixed in 2.5% glutaraldehyde. The embryo heads were vacuum wax embedded and 10 μ m sections cut using a microtome. For analysis, sections were counterstained with eosin.

Scanning electron microscope (SEM) ultrastructure analysis

Heads were fixed with 2% glutaraldehyde in 0.1 M Na-cacodylate buffer with 0.1 M sucrose and postfixed with 1% osmium in 0.1 M coated Na-cacodylate buffer. After critical point drying, the samples were coated with gold and photographed using scanning electron microscopy.

Transmission electron microscope (TEM) ultrastructure analysis

Heads were fixed in 2.5% glutaraldehyde (phosphate buffer) overnight at 4 °C and postfixed in 2% osmium tetroxide (Millonigs buffer) for 90 mins at 4 °C after washing with phosphate buffer. Specimens were dehydrated through a graded series of ethanol and embedded in Epon 812-equivalent (TAAB Lab). Semi-thin sections (1 μ m) were stained with toluidine blue for light microscopy analysis. Ultra-thin sections (40–90 nm) were cut, stained with uranyl acetate and lead citrate and examined with a Hitachi H7600 transmission electron microscope.

Explants culture

Mandibles from *Axin2^{lacZ}* reporter or CD1 mouse embryos at E11.5 were dissected in D-MEM containing glutamax-1. The explants were cultured as previously described on membrane filters supported by metal grids (Ohazama et al., 2005). Explants were cultured in D-MEM including 10% FBS supplemented with 100 μ M γ -secretase inhibitor (DAPT; LY-374973, N-[N-(3,5-Difluorophenacetyl)-L-alanyl]-S-phenylglycine t-butyl ester; Sigma), DMSO, 20 mM LiCl or H₂O. After 1 day culture, the explants were fixed by 4% PFA and prepared for LacZ staining or protein was extracted from the explants.

Results

Irf6 expression in murine tooth development

In order to elucidate whether *Irf6* plays an integral role in tooth development, we first examined the *Irf6* expression pattern during murine tooth development. Radioactive in situ hybridisation revealed that *Irf6* was strongly expressed in dental and oral epithelium at all embryonic stages examined (Fig. 1). This included expression in both incisor and molar development.

To ascertain if other Irf members were involved in incisor tooth development, we analyzed the expression of genes at the late bud stage of odontogenesis. *Irf1*, *Irf2*, *Irf3*, *Irf4* and *Irf8* were weakly expressed in upper incisor tooth germs whereas weak *Irf1*, *Irf2*, *Irf3*, *Irf7* and *Irf8* expression were observed in lower incisor tooth germs (Supplementary Fig. 1).

Evagination of incisor tooth in Irf6 mutant mice

In order to investigate the role of *Irf6* in tooth development, we examined sections of heads from newborn *Irf6* null mutant mice. Newborn *Irf6* mutant mice showed abnormal enlarged anterior extents of their incisors that were prematurely exposed to oral cavity compared to the incisors of wild-types that were covered with alveolar bone and connective tissue (Figs. 1A-D). Mutant incisor tooth germs thus lacked connective tissue, alveolar bone, oral epithelium, and dental lamina (epithelium which connect tooth germs to oral epithelium). To establish the timing of the first appearance of the incisor tooth anomalies, sections of mutant embryos from E10.5 to 14.5 were examined. The first distinguishable abnormalities were observed as abnormal protrusions of epithelium in presumptive incisor regions at E13.5 while wild-type incisors showed invaginating epithelium (Figs. 2E-H). Mutant molars showed invaginated epithelium at the stage (data not shown). Expression of the primary enamel knot marker gene, *Shh* normally seen in the center of invaginated incisor epithelium (Fig. 2I), was localized at the outermost tip of the mutant protruded incisor epithelium (Fig. 2J). These results suggest that mutant incisor epithelium does not invaginate into the underlying mesenchyme but rather evaginates outward into the developing oral cavity as seen in *Ikka* mutants (Ohazama et al., 2004).

We previously identified changes in *Notch1* and *Notch2* expression in incisors of *Ikka* mutant embryos (Ohazama et al., 2004). In *Irf6* mutants, *Notch1* and *Notch2* expressions were also downregulated in incisor tooth germs (Figs. 2K-N). The *Ikka* mutant incisor phenotype has previously been shown to occur independently of the NF- κ B pathway (Ohazama et al., 2004). Members of Irf family are known to be involved in NF- κ B pathway, although interaction between *Irf6* and the NF- κ B pathway remains unclear (Hiscott, 2007). In order to investigate whether *Irf6* is involved in NF- κ B pathway in incisor tooth development, we crossed the *Irf6* mutants to an NF- κ B reporter mouse [(Ig κ)₃conalacZ]. LacZ positive cells were slightly expanded in mutant incisor epithelium (Figs. 2O-R). The expression domain of *Wnt7b* in *Ikka* mutant incisor epithelium was smaller than those in wild-types, consistent with the expansion of *Shh* expression, which were also observed in *Irf6* mutants (Supplementary Fig. 2; Ohazama et al., 2004). Incisor tooth epithelial domains were thus expanded in *Ikka* mutants, which was also observed in *Irf6* mutant mice. It still

however remains unclear how *Ikka/Irf6* regulates the size of tooth epithelium. *Irf6* mutants also showed no significant changes of *IκBα* gene expression which is known to be led by NF-κB activation (Supplementary Fig. 3). No significant down- or up-regulation of NF-κB activity was thus observed in the *Irf6* mutant embryo incisors, suggesting that, as with *Ikka* mutant mice, the incisor evaginating epithelium seen in *Irf6* mutant is likely to be independent of the NF-κB pathway (Figs. 2O-R). The *Irf6* mutant incisors were thus identical to those of *Ikka* mutant mice. No significant tooth anomalies could be detected in mice with null mutants of *Irf1*, *Irf2*, *Irf3*, *Irf5*, *Irf7* and *Irf9* (data not shown).

In order to determine whether epithelial invagination is controlled by dosage of *Irf6*, we generated a series of hypomorphic alleles. The evaginating incisor phenotype was absent in *Irf6^{neo/neo}* or *Irf6^{neo/-}* mice (Figs. 2S, T; data not shown). The adhesion of oral epithelium which is one of phenotypes in *Irf6* mutants also disappeared in *Irf6^{neo/neo}* or *Irf6^{neo/-}* mice. Analysis of this allelic series of *Irf6* mutants revealed that the evaginating incisor phenotype only occurs in the complete absence of *Irf6* activity.

It is known that Bmp signaling plays critical roles in regulating early stages of incisor tooth development (Tucker and Sharpe, 2004). In order to investigate whether impaired Bmp signaling results in epithelial evagination, phosphorylated Smad1, Smad5 and Smad8 (p-Smad1/5/8) were examined in *Irf6* mutants. Significant changes of p-Smad1/5/8 could not be detected in incisor tooth germs of *Irf6* mutant mice (Supplementary Fig. 4). In addition to growth factors, cell adhesion is also known to be important in regulating epithelial invagination (Schock and Perrimon, 2002). To understand whether the disruption of cell-adhesion results in evagination, CD44 (one of the epithelial cell-adhesion molecules) was examined in mutants (Goodison et al., 1999). CD44-positive cells were found in wild-type tooth epithelium, which were also observed in mutant evaginated epithelium (Supplementary Fig. 4). Highly coordinated cellular proliferation and apoptosis has been shown to be key factor for controlling early stages of incisor tooth development (Charles et al., 2011; Munne et al., 2009). Abnormalities of cellular proliferation or apoptosis could not be detected in mutants (Supplementary Fig. 4).

Tissue specificity in regulating epithelial invagination

Tooth formation requires epithelial–mesenchymal interaction throughout development. It has been shown that signaling from either epithelium or mesenchyme plays a critical role in controlling early stages of incisor tooth development (Charles et al., 2011; Munne et al., 2009). In order to determine whether incisor tooth invagination is regulated by epithelium and/or mesenchyme, we crossed *Ikka* mutants with mice over-expressing *Ikka* under the Keratin 5 (K5) promotor (*K5-Ikka*). *K5* is expressed in oral and dental epithelium from early stage of development (data not shown). *K5-Ikka* mice yielded no tooth phenotype or oral epithelial adhesion (one of the phenotypes of *Ikka* mutants) but it did completely rescue the incisor phenotype when crossed to *Ikka* mutant mice (Figs. 3E-H). Epithelial *Ikka* is thus required to control the direction of incisor tooth epithelial growth. In addition to evagination of incisor epithelium, the adhesion of oral epithelium were also rescued in *K5-Ikka*; *Ikka*^{-/-} mice, suggesting that the adhesion is also caused by the disruption of epithelial *Ikka* function (data not shown; Ohazama et al., 2004).

Since both *Ikka* and *Irf6* expressions in epithelium thus play critical roles in the development of incisors and oral mucosa development, we carried out further analysis on mutant epithelium. *Irf6* has previously been shown to be involved in the formation of periderm which is a superficial monolayer of embryonic epithelium (Thomason et al., 2010). Both *Ikka* and *Irf6* mutant mice showed no epithelial adhesion in anterior parts of the mouth, including incisor regions, which allowed us to perform SEM analysis on the surface of mutant incisor epithelium (Figs. 4A-D). SEM showed the presence of cobblestone-like structures on the surface of anterior regions of *Ikka* mutant mouth epithelium at E13.5, whereas these could not be detected at E10.5 or E11.5 or at birth (Figs. 4E-H, L; data not shown). To examine whether the cobblestone-like structures were cells, TEM assay was undertaken on mutant embryos. TEM showed that the cobblestone-like structures contained fragments of organelles, suggesting that these were disintegrated cells (Figs. 4J, K). The cobblestone-like cells were present only on the surface of the epithelium, not deeper inside. Similar cells were also observed in anterior regions of *Irf6* mutant mouth epithelium, although these cells retained more organelles than those in *Ikka* mutants (Figs. 4N-P). Cobblestone-like cells are known to be present along the medial epithelial edge of palatal shelves just before palatal fusion (Charoenchaikorn et al., 2009). It is possible that the anterior part of the mouth where incisors develop in *Ikka* and *Irf6* mutants shows initial signs of adhesion or fusion, but do not adhere.

In order to investigate the relationship between incisor epithelial evagination and epithelial adhesion, we examined mice that have previously been reported to have oral epithelial adhesion. Stratifin (*Sfn*; also known as 14-3-3 isoform σ) is known to have a pivotal role in cell cycle regulation and Receptor interacting protein 4 (*Rip4*; DIK, PKK) plays an important role during cellular stress (Hermeking and Benzinger, 2006; Janssens and Beyaert, 2003; Wang et al., 2000). Mice with mutation of either these molecules exhibit thickened epithelium, palatal cleft and adhesion of oral epithelium; identical phenotypes to those seen in *Ikka* and *Irf6* mutant mice (Bhr et al., 2000; Chen et al., 2001; Guenet et al., 1979; Holland et al., 2002). Evagination of incisor epithelium is characterized by abnormal enlargement of the anterior extent of incisors, a lack of associated dental lamina, alveolar bone and connective tissue, and displacement of enamel knot marker gene expression (Figs. 2, 5A-D; Ohazama et al., 2004). *Rip4* and *Sfn* mutant (*Sfn*^{Er/Er}) mice however did not show any of these incisor phenotypes (Figs. 5G-L). Both mutants revealed no significant abnormalities in molar tooth germs (data not shown). Although both *Rip4* and *Sfn* were expressed in tooth and oral epithelium, it is possible that null mutation of *Rip4* or *Sfn* is not enough to induce evagination of incisor epithelium. To address this question, we generated *Ikka*^{+/-};*Sfn*^{Er/Er} and *Irf6*^{+/-};*Sfn*^{Er/Er} compound mice but none presented with any obvious tooth anomalies (Figs. 5M-P; data not shown). *Sfn* expression showed no significant changes in incisors of *Irf6* or *Ikka* mutant mice while *Irf6* and *Ikka* expression were also normal in *Sfn*^{Er/Er} and *Rip4* mutant mice, suggesting that there is unlikely to be interaction between these molecules in incisor tooth development (Supplementary Fig. 5E-5R; data not shown). *Ikka*^{+/-};*Sfn*^{Er/Er} and *Irf6*^{+/-};*Sfn*^{Er/Er} compound mice showed no significant anomalies in molar tooth germs (data not shown).

Canonical Wnt signaling in incisor evagination

Wnt signaling is known to play a critical role in determining the direction of cell growth (Barth et al., 2008; Killeen and Sybingco, 2008). Conditional increased activation of the canonical Wnt pathway in epithelial tissues results in the abnormal enlarged anterior extents of incisors exposing to oral cavity; a similar phenotype to those observed in the *Ikka* and *Irf6* mutant embryos (Liu et al., 2008b). To investigate whether the incisor epithelial evagination is the result of aberrant canonical Wnt signaling, we crossed both the *Ikka* and *Irf6* mutant mice to reporter mice for canonical Wnt signaling, *Axin2^{lacZ}*. Strong activity was seen at E12.5 specifically in the incisor dental epithelium of both *Ikka* and *Irf6* mutant embryos (Figs. 6C-F; Supplementary Fig. 6). This suggests that canonical Wnt signaling may play a role in orienting the direction of tooth germ formation.

In addition to alteration of Wnt signaling, downregulation of *Notch1* and *Notch2* expressions was also observed in incisors of both *Ikka* mutant and *Irf6* mutant embryos (Fig. 3; Ohazama et al., 2004). In order to investigate the interaction between Notch and canonical Wnt signaling in incisor development at an early stage of development, we cultured E11.5 mandibles in the presence of γ -secretase inhibitor (DAPT), an inhibitor of cleavage of Notch1/2 to inhibit Notch signaling or GSK3 β inhibitor, LiCl to increase canonical Wnt signaling (Grosveld, 2009; Klein and Melton, 1996; Shih and Wang, 2007). Reduced Notch signaling led to no significant changes in *Axin2* reporter expression in DAPT-treated *Axin2^{lacZ}* mouse mandibles compared to those in control explants (Figs. 6G, H). Upregulation of Wnt signaling resulted in no significant changes of *Notch1* expression in LiCl treated explants compared to those seen in control explants (Figs. 6I, J). These results suggested that an obvious relationship between Notch and canonical Wnt signaling is unlikely to be present in incisor development.

Irf6 mutant incisors thus phenocopy those of *Ikka* mutants. Both *Ikka* and *Irf6* are expressed in the developing incisor epithelium (Fig. 1; Ohazama et al., 2004). In order to investigate potential genetic interactions between *Ikka* and *Irf6* in incisor tooth development, we intercrossed *Irf6* mutants with *Ikka* mutant mice. *Ikka^{+/-};Irf6^{+/-}* compound heterozygotes were viable (data not shown) but neither *Ikka^{+/-};Irf6^{-/-}* nor *Ikka^{-/-};Irf6^{+/-}* compound mice showed exacerbation or attenuation of the evaginating incisor phenotype (Figs. 7A-F). *Irf6* expression showed no significant changes in incisors of *Ikka* mice and *Ikka* expression was also normal in *Irf6* mice (Supplementary Fig. 5A-5D; data not shown). The results thus fail to show any evidence of direct genetic interaction between *Ikka* and *Irf6* in incisor development.

Discussion

Irf6 mutant mice show identical phenotypes including tooth, oral mucosa and skin to those described in *Ikka* mutants (Hu et al., 1999; Ingraham et al., 2006; Li et al., 1999; Ohazama et al., 2004; Richardson et al., 2006; Takeda et al., 1999). *Irf6* is a transcription factor that belongs to the Irf family which is known to be involved in the NF- κ B pathway (Taniguchi et al., 2001). Although other Irf family members are known to be related to the NF- κ B pathway, any interaction between the NF- κ B pathway and *Irf6* remains unclear. Since no change in NF- κ B pathway activity was observed in *Irf6* mutant embryos, in common with

Ikka mutants, the incisor evagination seen is likely to occur independently of the NF- κ B pathway (Fig. 2; Ohazama et al., 2004). Based on the phenotypes and common downstream molecular changes, one might predict that these proteins interact, either by *Ikka* phosphorylating *Irf6*, or *Irf6* transcriptionally regulating *Ikka*. *Ikka* has previously been shown to activate *Irf7* by phosphorylation (Hoshino et al., 2006). However, although it is feasible that *Ikka* could phosphorylate other members of the *Irf* protein family (including *Irf6*), the C-terminal protein-binding domains are less well conserved between members and only *Irf1*, *Irf3*, *Irf5* and *Irf7* are currently recognized as possessing phosphorylation sites (Lohoff and Mak, 2005). A lack of physical interaction between *Ikka* and *Irf6* functional proteins is supported by previous co-immunoprecipitation experiments (Ingraham et al., 2006). In addition, the loss of one gene does not appear to affect the expression of the other (Supplementary Fig. 5) and compound homozygote–heterozygotes show no exacerbation or attenuation of phenotype (Fig. 7). This is further supported by micro-array data that shows no change in *Ikka* gene expression in *Irf6* mutant skin (Ingraham et al., 2006). Identical phenotypes with the same downstream molecular changes but lack of direct evidence of genetic interaction in incisor tooth development between *Irf6* and *Ikka* mutants suggested that *Irf6* and *Ikka* are likely to function in separate (parallel) pathways involved in the same processes. Our data also show no link between the oral fusion and epithelial invagination phenotypes, suggesting that the invagination of incisor epithelium is unlikely to be regulated by the same molecular pathways as those in palate and oral mucosa development. *Irf6* and *Ikka* thus appear to be potentially involved in multiple pathways in epithelial cell biology.

All *Irf* proteins contain a carboxy (C)-terminal *Irf*-association domain, which facilitates homodimerization and heterodimerization between family members (Lohoff and Mak, 2005). Null mutations of *Irf* genes 1 to 9 are viable and fertile with the exception of *Irf6*, although cause of the differences still remained unclear (Holtschke et al., 1996; Honda et al., 2005; Kimura et al., 1996; Matsuyama et al., 1993; Mittrücker et al., 1997; Richardson et al., 2006; Sato et al., 2000; Takaoka et al., 2005). It is feasible that there is a level of redundancy within the *Irf*s and that in the null condition, other family members can compensate for the loss of one gene through heterodimerization. This possibility is obviously excluded in the case of *Irf6* mutant. The *Irf6* gene is thus unique within the *Irf* family and this is reflected not only in its expression pattern, but also in the severity of the phenotype.

Irf6 is also known to be responsible for Van der Woude syndrome that often features congenital missing teeth such as mandibular second premolars (Arangannal et al., 2002; Oberoi and Vargervik, 2005; Schneider, 1973). In addition to the hypodontia, taurodontism and dental pulp stones have also been shown in Van der Woude syndrome (Kantaputra et al., 2002; Nawa et al., 2008). Although crown shape is probably most affected by evagination of tooth epithelium, no significant anomalies of crown shape have been reported in Van der Woude syndrome. In mice, only incisor tooth epithelium was altered by *Irf6* mutation. Molecular mechanisms of epithelial invagination are thus likely to be different between humans and mice, possibly related to the continuous growth of mouse incisors.

Wnt signaling plays critical roles in many biological processes including development (Pellón-Cárdenas et al., 2011; Sylvie et al., 2011). Many Wnt signaling related molecules are known to be expressed during tooth development (Sarkar et al., 2000). We show strong

canonical Wnt activation in mutant evaginating incisor epithelium (Fig. 6). The conditionally increased activation of the canonical Wnt signaling pathway in epithelial tissues shows enlarged misshapen incisors which exposed to oral cavity, suggesting that Wnt signaling may regulate the direction of epithelial growth at early stages of tooth development (Liu et al., 2008b). *Ikka* has been shown to interact with canonical Wnt signaling to positively regulate β -catenin-dependent transcriptional activity by increasing the cytosolic levels of β -catenin (Albanese et al., 2003; Lamberti et al., 2001). *Ikka* has also been shown to physically interact with β -catenin, inhibiting Axin/APC/GSK-3 β and Siah-1 pathway-mediated β -catenin ubiquitination and subsequent degradation, a process that occurs independently of the NF- κ B pathway (Carayol and Wang, 2006). *P63* function is known to be required at early stages of tooth development, since *p63* mutant mice show no epithelial thickening of tooth epithelium which is accompanied by downregulation of *Notch1* expression (Laurikkala et al., 2006). *P63* has been shown to be associated with *Ikka* and *Irf6* in skin and palate, respectively (Candi et al., 2006; Ferretti et al., 2011; Thomason et al., 2010). Since the interaction of p63 with *Irf6* is known to be regulated by Wnt signaling, it is possible that *Ikka* and *Irf6* are involved in *p63* through Wnt signaling in tooth epithelial invagination (Ferretti et al., 2011; Thomason et al., 2010).

Wnt signaling is known to play a critical role in tooth initiation and Notch signaling is believed to regulate the direction of murine incisor rotation at early stages of tooth development (Järvinen et al., 2006; Liu et al., 2008a, 2008b; Mucchielli and Mitsiadis, 2000). Both *Ikka* and *Irf6* null mutant incisors showed alteration of Notch and Wnt signaling (Figs. 2, 6; Ohazama et al., 2004). Interactions between Wnt and Notch signaling have been reported in intestine, somatogenesis and keratinocytes (Dunty et al., 2008; Nicolas et al., 2003; van Es et al., 2005). Our results however showed no significant relationship between Notch and Wnt in incisor development. Regulating the direction of incisor epithelial invagination thus appears to involve multiple signaling networks.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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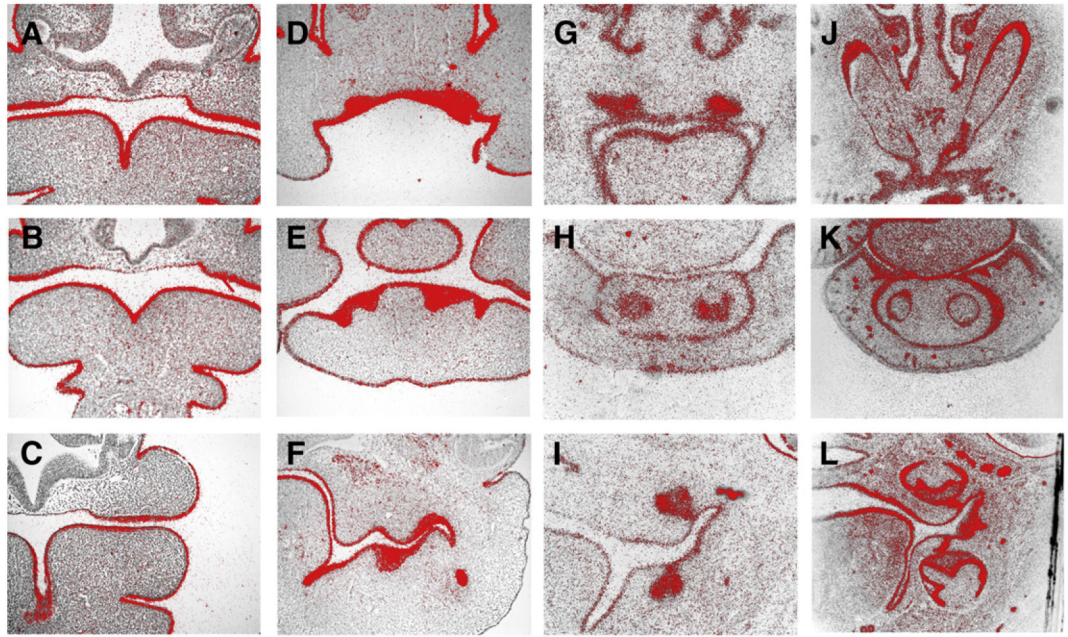


Fig. 1.
Irf6 expression in murine tooth development. In situ hybridisation of *Irf6* on frontal head sections at E10.5 (A–C), E12.5 (D–F), E14.5 (G–I) and E18.5 (J–L). Upper incisors (A, D, G, J); lower incisors (B, E, H, K); molars (C, F, I, L).

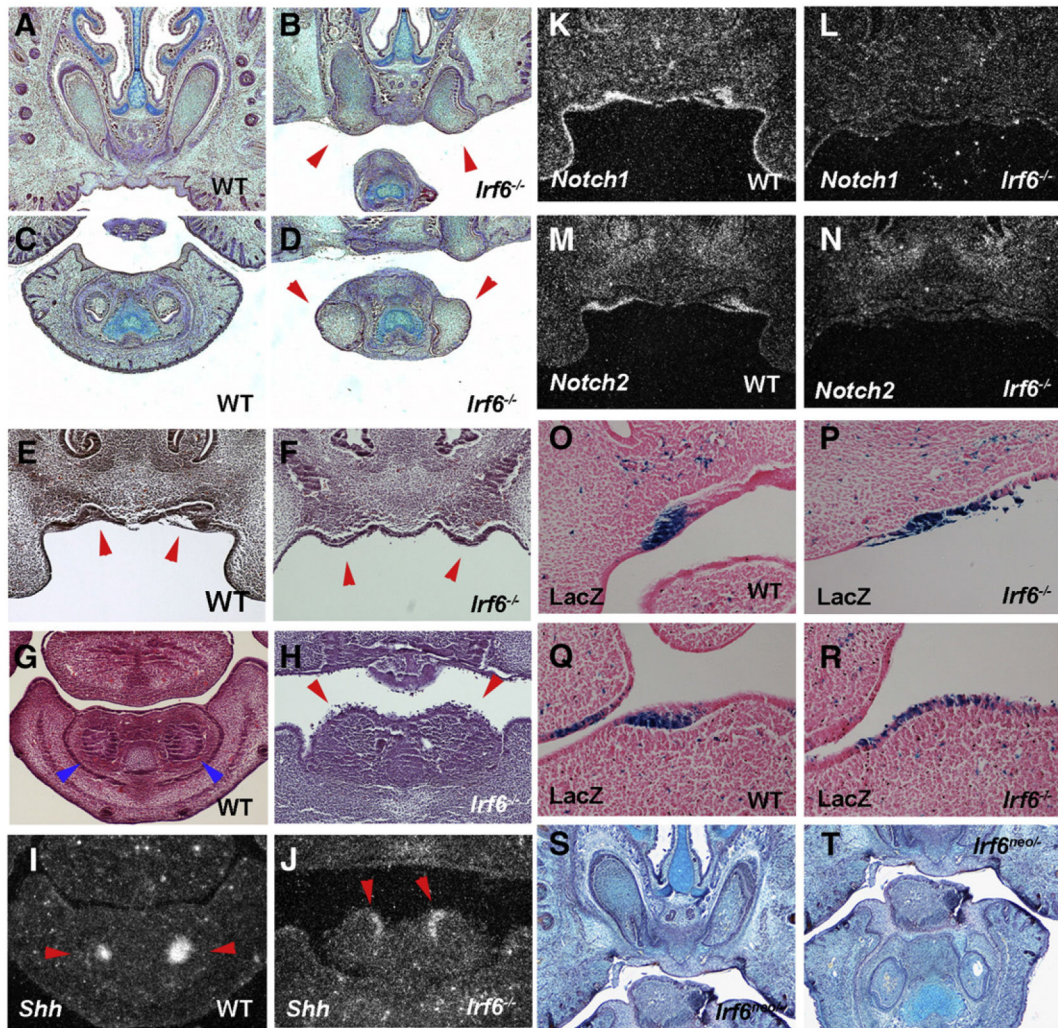


Fig. 2.

Incisor tooth development in *Irf6* mutant mice. Anterior extents of incisors are enlarged and exposed to the oral cavity in newborn *Irf6* mutants (arrowheads in B, D). Protrusion of incisor epithelium in *Irf6* mutants at E13.5 (arrowheads in F, H). Arrowheads indicating wild-type incisors (E, G). Expression of *Shh* at the outermost tip of evaginating epithelium of incisors in mutant (arrowheads in J) whereas *Shh* expression at the bottom of invaginating epithelium in wild-type (arrowheads in I). Downregulation of *Notch1* (L) and *Notch2* (N) in evaginating epithelium of mutant incisors. In situ hybridisation on frontal head sections at E13.5 (I–N). LacZ expression in incisor epithelium in $(Ig\kappa)_3conalacZ$ (O, Q) and *Irf6*^{-/-}; $(Ig\kappa)_3conalacZ$ (P, R) mice. Slight epithelial bulge and thickening were seen in mutant incisor (P, R). Incisors in *Irf6*^{neo/-} (S, T) on frontal sections at E18.5. Upper (A, B, E, F, K–N, O, P, S) and lower (C, D, G–J, Q, R, T) incisors.

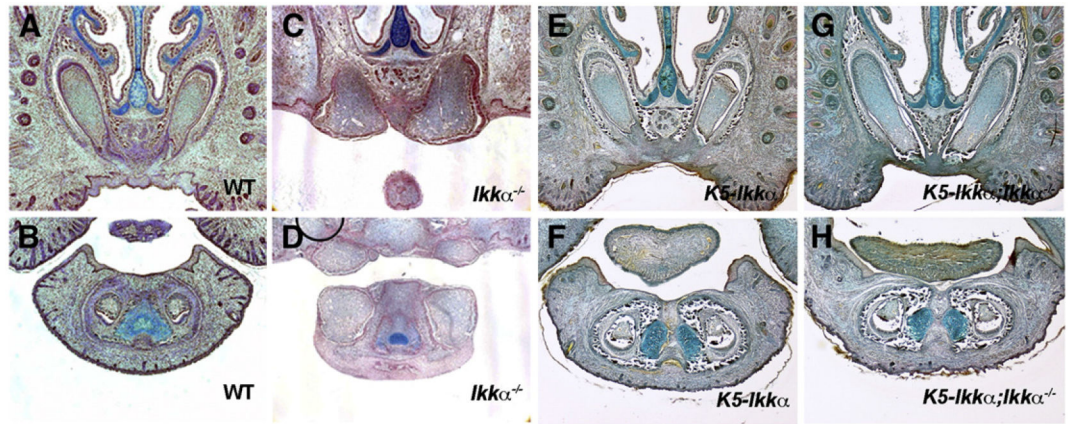


Fig. 3. Rescue of incisor epithelial evagination. Incisors in wild-type (A, B), *Ikka*^{-/-} (C, D), *K5-Ikka* (E, F) and *K5-Ikka;Ikka*^{-/-} (G, H) on frontal sections at E18.5. Upper (A, C, E, G) and lower (B, D, F, H) incisors.

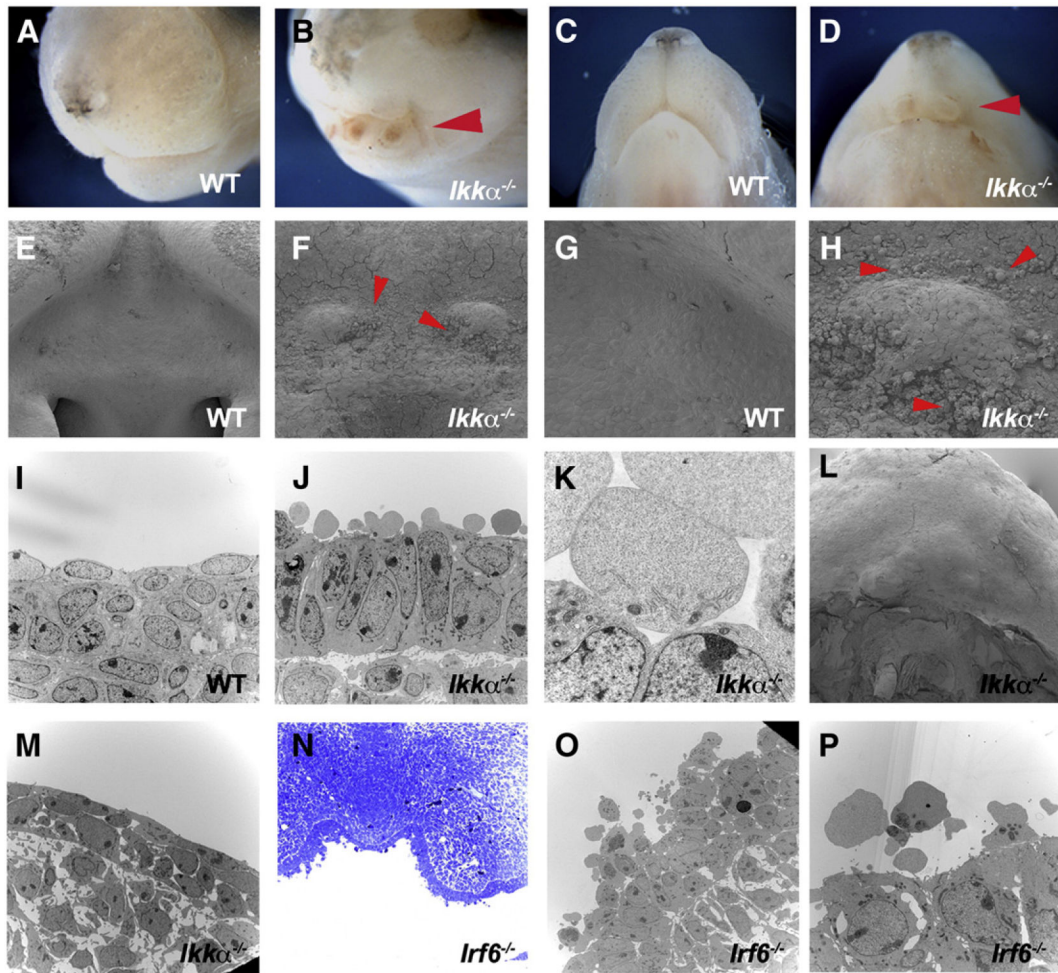


Fig. 4.

Ultrastructure of mutant epithelium. Anterior heads in wild-type (A, C) and *Ikka*^{-/-} (B, D) at E18.5 (A–D). Cobblestone-like cells in *Ikka*^{-/-} (arrowheads in F, H, J, K) and *Irf6*^{-/-} (N–P) at E13.5. No cobblestone-like cells in *Ikka*^{-/-} (L, M) at E18.5. SEM (E–H, L) and TEM (I–K, M, O, P).

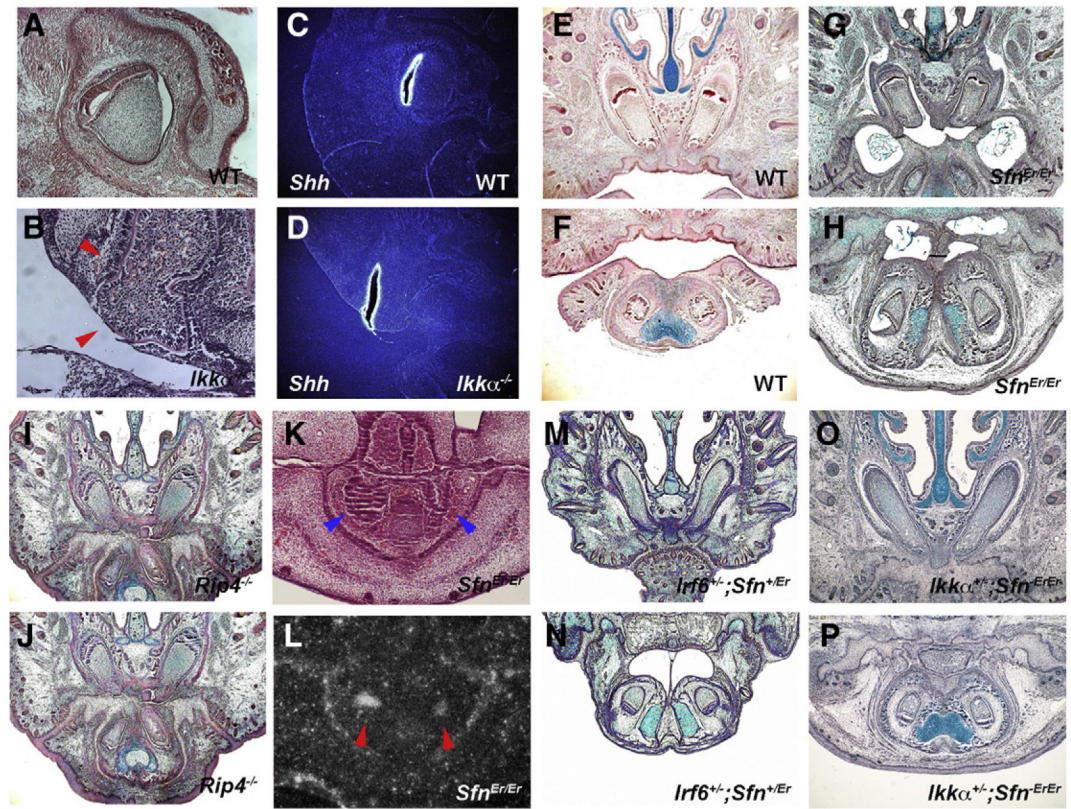


Fig. 5.

Incisors in mutant mice with oral epithelial adhesion. Sagittal sections of incisors in wildtype (A) and *Ikka*^{-/-} (B) mice. Arrowheads indicating evaginated incisor (B). In situ hybridisation of *Shh* on sagittal head sections at E18.5 in wildtype (C) and *Ikka*^{-/-} (D) mice. Incisors of wild-type (E, F), *Sfn*^{Er/Er} (G, H), *Rip4*^{-/-} (I, J), *Irf6*^{+/-};*Sfn*^{+Er} (M, N) and *Ikka*^{+/-};*Sfn*^{Er/Er} (O, P) mice. Arrowheads indicating incisor tooth germs in *Sfn*^{Er/Er} (K). In situ hybridisation of *Shh* on frontal head sections at E14.5 in *Sfn*^{Er/Er} mice (arrowheads in L). Upper (A–E, G, I, M, O) and lower (F, H, J–L, N, P) incisors.

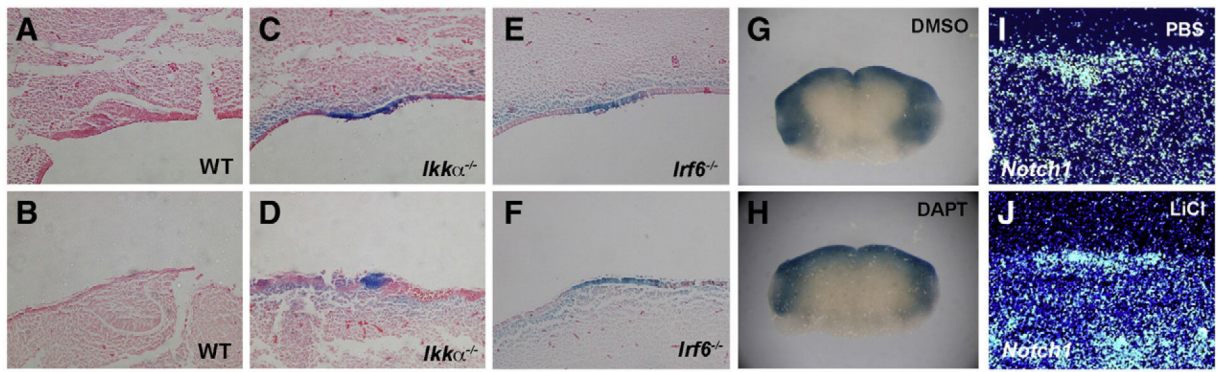


Fig. 6. Wnt and Notch signalling in evaginated incisor tooth germs. LacZ expression in thickened incisor epithelium in *Axin2*^{lacZ} (A, B), *Ikkα*^{-/-};*Axin2*^{lacZ} (C, D) and *Irf6*^{-/-};*Axin2*^{lacZ} (E, F) mice, and DMSO (G) and DAPT (H) treated mandible explants from *Axin2*^{lacZ} mice. *Notch1* expression in LiCl treated- (I) and nontreated- (J) mandible explants. Upper (A, C, E) and lower (B, D, F) incisors at E12.5.1 day cultured mandible from E11.5 (G–J).

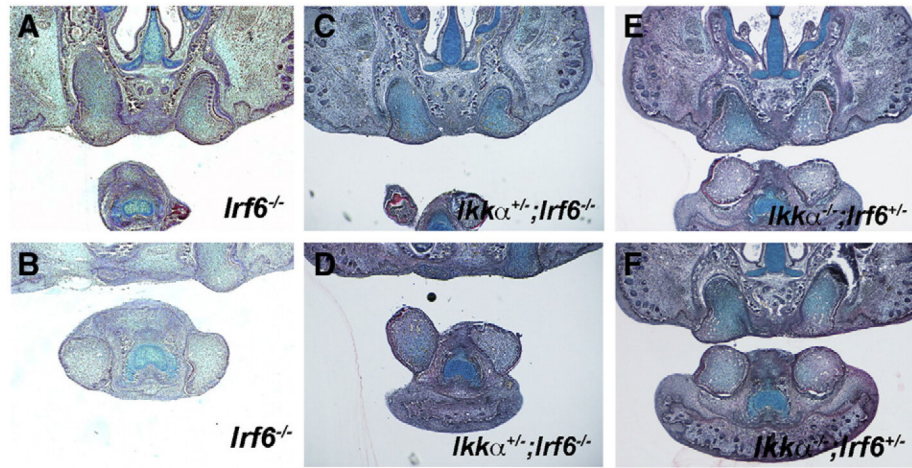


Fig. 7. Interaction between *Ikka* and *Irf6* in incisor tooth development. Incisors in *Irf6*^{-/-} (A, B), *Ikka*^{+/-};*Irf6*^{-/-} (C, D), *Ikka*^{-/-};*Irf6*^{+/-} (E, F) on frontal sections at E18.5. Upper (A, C, E) and lower (B, D, F) incisors.