TITLE: Molecular Diagnostics and *In Utero* Therapeutics for Orofacial Clefts

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DISCLOSURES: None for all authors

WORD COUNT: 4,000

REFERENCES: 60

KEYWORDS: Orofacial Clefts; Cleft Palate; Craniofacial; Signaling Molecules; Replacement Therapies

Abstract

Orofacial clefts and their management impose a substantial burden on patients, on their families, and on the health system. Under the current standard of care, affected patients are subjected to a life-long journey of corrective surgeries and multidisciplinary management to replace bone and soft tissues, restore esthetics and physiologic functions while restoring self-esteem and psychological health. Hence, a better understanding of the dynamic interplay of molecular signaling pathways at critical phases of palate development is necessary in order to pioneer novel prenatal interventions. Such pathways include transforming growth factor-beta (*Tgfβ*), sonic hedgehog (*Shh*), wingless-integrated site (*Wnt*)/β-catenin, bone morphogenetic protein (*Bmp*), fibroblast growth factor (*Fgf*) and its associated receptors, among others. Here, we summarize commonly used surgical methods used to coorect cleft defects postnatally. We also review the advances made in prenatal diagnostics of clefts through imaging and genomics and the various *in utero* surgical corrections that have been attempted thus far. An overview of how key mediators of signaling that drive palatogenesis is emphasized in the context of the framework and rationale for the development and testing of therapeutics in animal model systems as well as in humans is provided. The pros and cons of *in utero* therapies that can potentially restore molecular homeostasis needed for the proper growth and fusion of palatal shelves are presented. The theme advanced throughout this review is the need to develop pre-clinical molecular therapies that could ultimately be translated into human trials that can correct orofacial clefts at earlier stages of development.

Introduction

Orofacial clefts (OFCs) are the most common craniofacial birth defect in humans, arising early in pregnancy after a disruption or failure in the growth and fusion of craniofacial tissues. The most common OFCs are clefts of the lip alone (CL), cleft lip with palate (CLP) or cleft palate (CP) (Leslie and Marazita 2013). Multiple genes and environmental factors contribute to this group of complex disorders that present as isolated/non-syndromic defects or those that involve other organ systems as part of a syndrome. Non-syndromic clefts of the lip and/or palate (CL/P) show a distribution of prevelance across ethnic and geographic groups, with rates ranging from 1:500 to 1:2500 live human births. Since embryological origins are different for the upper lip and secondary palate, CL and CLP are viewed as variants of the same defect that differ in severity (Marazita 2012).

One-third of OFCs are part of syndromes, including DiGeorge, Van der Woude and Treacher-Collins syndromes, as well as the Pierre Robin sequence (Pereira et al. 2018). Among the known environmental associations are maternal smoking or passive smoke exposure (Sabbagh et al. 2015), viral infection (James et al. 2014), phenytoin and other anti-epileptic medication use (Veroniki et al. 2017), isotretinoin (Lammer et al. 1985) and deficiencies of zinc, folic acid and other micronutrients (Wehby and Murray 2010). A maternal history of diabetes mellitus, overweight and obesity, advanced maternal and/or paternal age and parental consanguinity have also been identified as factors that contribute to cleft development (Sabbagh et al. 2014). However, current evidence does not support the speculation that fetal exposure to alcohol early in development may be implicated in OFCs (Bell et al. 2014). The genetic origin of OFCs is supported by familial studies that show a 32-fold higher risk in the proband if first-degree

relatives are affected by CL/P (Sivertsen et al. 2008). Furthermore, genome-wide association studies (GWAS) have identified a range of DNA variants influencing the risk of OFCs (Leslie and Marazita 2013). Next-generation sequencing has allowed for the rapid discovery of cleft-associated genes for cases that are extremely rare, clinically heterogeneous or lack a strong family history (Weinberg et al. 2018). The recent use of a "cleft map" allowed the dissection and visualization of the contribution of shared genetic effects to phenotypic heterogeneity of OFCs and revealed that CL and CLP share GWAS loci (Carlson et al. 2019).

Postnatal Surgical Correction of Cleft Palate Defects

The current standard-of-care for patients affected by craniofacial cleft anomalies includes postnatal surgical interventions that are based upon a timeline that coincides with midfacial growth and development. A variety of well-established CL and palatoplasty techniques are available and are dictated by the severity of clefting in individuals. CP repair, in general, is dependent upon the principles of a tension-free and multilayered closure with repositioning of the velar muscle sling (Dao and Goudy 2016). The consensus for the optimum timing of intervention falls between 10-12 months of age (Liao and Mars 2006), but most customarily within 18 months. While closure of the palatal defect will facilitate feeding and speech, the benefits of early palate repair must be carefully weighed against concerns of negatively affecting the patient's midfacial growth (Liao and Mars 2006). A successful repair involves: (1) complete closure of the oral and nasal layers without fistula formation; (2) velopharyngeal competence with feeding and speech; (3) minimal impact on mid-facial growth; and (4) improved eustachian tube function.

While these initial goals can be achieved through velar muscle repositioning on first intervention, patients with a deficient or absent bone of the primary palate typically undergo a second surgical intervention (alveolar bone graft) during or prior to the mixed dentition stage, essential for the development of proper anatomical relationships of midface structures (Dao and Goudy 2016). Within the United States, pre- and post-surgical consultations involve a multi-disciplinary panel of care providers, including otorhinolaryngologists, oral and maxillofacial surgeons, speech therapists, audiologists, orthodontists, pediatric dental specialists and social workers.

Prenatal Approaches

Diagnostic Screening – At present, both invasive and non-invasive methods exist to collect fetal material for prenatal screening with a range of diagnostic approaches. For pregnancies arising from *in vitro* fertilization, it is possible to undertake pre-implantation genetic screening (Vermeesch et al. 2016). For natural pregnancies, routine invasive approaches involve harvesting fetal cells by real-time ultrasound-guided transabdominal aspiration of amniotic fluid (i.e. amniocentesis), typically at 16 weeks of gestation. Alternatively, placental cells (i.e. chorionic villus sampling (CVS)), retrieved between 10 to 13 weeks of gestation can be used (Ghidini 2019). Since CVS results can be initially reported within 48 hours of testing and final results from long-term culture available in 7 to 10 days, fetal anomalies may be detected as early as the eleventh gestational week. In contrast, amniocentesis usually only provides an answer after 17 weeks' gestation (Alfirevic et al. 2017).

Harvesting cell-free nucleic acids (cfDNA and cfRNA) from maternal blood is a more recent non-invasive approach to prenatal screening initially introduced to detect common fetal

autosomal and sex chromosome aneuploidies, now with the capacity to identify DNA microdeletions, CNVs and monogenic disorders (Ghidini et al. 2019). This approach has already been used to diagnose cleft-associated syndromes, such as DiGeorge syndrome (Wapner et al. 2015). Sampling maternal biofluids is advantageous as it obviates the risk of fetal loss that accompanies invasive sampling of fetal tissue directly (Bianchi 2012). Since a negative result in cfRNA/DNA analysis has upwards of 99% negative predictive value, there has been a 70% decrease worldwide in invasive testing, with an associated reduction in costs to the healthcare system (Ghidini et al. 2019). However, the mixture of fetal and maternal material does confer additional downstream analytic complexity.

While karyotyping and microarray-based cytogenic techniques can detect aneuploidy, microarray is preferred, as it avails additional genetic information (Vermeesch et al. 2016), providing higher sensitivity and shorter turnaround times than conventional metaphase karyotyping (Bianchi 2012). Recently, next-generation technologies have surpassed chromosomal microarray techniques for the diagnosis of genetic disease (Clark et al. 2018). Prenatal whole exome sequencing (WES) assists in the diagnosis of dysmorphic fetuses by identification of single nucleotide polymorphisms (SNPs) as well as insertion or deletion events (Thevenon et al. 2016). Cleft detection with fetal-parental-trio WES has recently been linked to enhanced detection of fetal structural anomalies relative to cytogenetic or microarray techniques (Lord et al. 2019). However, in recently published protocols, this technique follows ultrasound at approximately 11 weeks of gestation, as it relies on the triangulation of data to predict the pathogenicity of each molecular variant based on fetal phenotype. Notwithstanding, prenatal molecular diagnoses derived from similar protocols have arisen almost twice as frequently in fetuses with craniofacial

morphological abnormalities (46%) compared to those without (24%) (Normand et al. 2018). Thus, first-trimester molecular diagnoses may be made possible by advances in imaging technology that allow morphologic assessment earlier in development. Pertinent also is that some (Ghidini et al. 2019), but not all, published studies provided real-time molecular diagnoses during pregnancy. The clinical utility of sequencing modalities will be enhanced by the advent of more efficient techniques and the refinement of pathology workflows to accelerate the turnaround time of molecular testing. While studies that have implemented WES have derived fetal tissue via invasive methods that involve CVS, amniotic fluid or fetal blood, it remains to be investigated whether less invasive strategies for obtaining fetal tissue could also be employed to promptly detect dysmorphology in offspring via analysis of genetic aberrations in fetal cfDNA/RNA. Cell-free fetal transcriptomics may be a useful diagnostic tool in the future, but its implementation would necessitate the acquisition of reference data for the expression of key genes across a range of developmental stages and accurate determination of the gestational age.

In addition to exploration of DNA- and RNA-based methodologies, discernment of variation at the *protein level* may aid in prenatal diagnosis. For decades, alpha-fetoprotein in maternal blood samples has been routinely used to assist in the detection of developmental anomalies including Down Syndrome (Cheng et al. 1993) and neural tube defects (Milunsky et al. 1980). Proteomic approaches have since arisen to better diagnose a range of chromosomal aberrations (Narasimhan et al. 2013). More recent advances in prenatal diagnostics have involved putative protein biomarkers to discriminate normal pregnancies from those with congenital heart defects, with changes in protein levels having been identified from as early as 8 weeks' gestation (Chen et al. 2016). Interestingly, studied cardiac structural anomalies were polygenic in nature, which

foreshadows that the diagnosis of clefts with diverse genetic diagnoses may be possible by appraisal of a handful of biomarkers from known cleft-associated pathways. Conversely, analysis of these prenatal samples may enable us to glean a deeper understanding of the molecular events underpinning craniofacial dysmorphogenesis.

In Utero Surgical Repair – Surgical interventions are currently undertaken for a subset of fetuses diagnosed with congenital anomalies linked to high mortality or severe morbidity if treatment is delayed. However, there is considerable debate about the practicality and efficacy of these high-risk approaches. The appeal of prenatal interventions for OFC repair stems from their promise to definitively restore form and function prior to birth, thereby mitigating the need for complex postnatal surgical manipulations and multi-disciplinary dental/maxillofacial treatments that often commit patients to ongoing care into their adult years of life. Significantly, prenatal surgery can circumvent scarring sequelae associated with postnatal interventions, namely secondary dentoalveolar and midfacial growth deformities (Moore et al. 2018). The distinct benefit to intervening surgically *in utero* is the nearly-scarless mechanism of wound healing prenatally (Longaker et al. 1991; Ozturk et al. 2001). This is particularly advantageous in the case of OFCs, as the resultant therapy is heavily reliant on the reconstructive, functional and aesthetic outcome, given the physical and psychological impact of midfacial developmental anomalies (Wojcicki and Drozdowski 2011). Furthermore, prominent scars form within integumentary tissues, with underlying fibrous banding and contraction in facial morphology post-surgically. Some postulate that the less-intense inflammatory response during fetal development is responsible for scarless mechanisms of fetal wound repair *in utero*; there are also

theories related to the impact of amniotic fluid sterility and richness in growth factors (e.g. hyaluronic acid) in promoting wound healing (Longaker et al. 1994; Ozturk et al. 2001).

Mucosal wounds and minor bone defects heal during the course of fetal development without the formation of tissue callus, the equivalent of scarring in integument (Stelnicki et al. 1999). Furthermore, maxillary growth restriction was not identified in early cleft treatment *in utero* in animal models. This is of particular clinical significance, as earlier repair of cleft anomalies during fetal development may allow for post-repair growth of midface morphology beyond that which can be achieved postnatally. Thus, earlier cleft repair *in utero* has a potential for CLP healing with minimal scar formation, lower or no restriction of mandibular/maxillary bone growth, and potential elimination for need of postnatal corrective procedures. However, there are important barriers that must be overcome in order to consider *in utero* surgical correction of OFCs clinically feasible. As false-positive results during prenatal morphological screening can lead to unnecessary, risk-provoking intervention for mother and fetus, it is critical that prenatal diagnostic techniques are first developed and optimized in larger animal models.

Targeted Molecular Therapeutics - Evidence of the efficacy of molecular agents to restore palatal morphogenesis in the prenatal period is also emerging. Beyond the environmental and stochastic factors known to influence palatogenesis, precision therapies can target genetic defects of craniofacial development. Precision therapies for Mendelian diseases, such as those that replace deficient proteins, directly target disease-associated pathways, or influence expression of disease-relevant genes, are clinically available for a number of conditions, such as lysosomal storage disorders, cystic fibrosis, tuberous sclerosis and spinal muscular atrophy (Dugger et al.

2018). While these approaches have historically been applied to monogenic conditions, there is scope for their extrapolation to conditions for which there is genetic heterogeneity but pathway homogeneity. Hence, while a range of causative mutations are implicated in CLP, targeting inter-related pathways may be of therapeutic benefit to cleft patients with a range of genetic etiologies. The most significant among the barriers that currently exist for the effective translation and application of biologically driven therapies to human OFCs is the underlying complexity of cleft genetics itself. While the molecular basis of an individual cleft condition is genetically heterogenous, known variants account for a minority of the estimated heritability. Hence, new gene discoveries along with the knowledge of interacting signaling pathways are critical for the advancement of the field.

In contrast to inherited metabolic diseases, that require chronic treatments with repeated infusion of replacement proteins or other bioactive molecules (Hughes 2018), therapies able to impact non-reversible developmental fate decisions can produce permanent effects in response to short term treatments. Such transient therapies have potential benefits over longer-acting gene therapy approaches that risk incorporation of transgenic products into maternal or filial DNA. Known cleft-associated genetic aberrations represent potential targets for appropriately timed precision gene product replacement therapies to restore the delicate molecular equilibrium required for normal embryonic development. The efficacy of such therapies at various timepoints in animal models has advanced contemporary knowledge of when the activity of key proteins peaks during palatogenesis. Trialed preclinical interventions and their outcomes are discussed below.

184 *TGF-β3 Rescue* - Given its role in medial edge epithelial fusion of the left and right palatal
185 processes, transient, high-level expression of Tgfβ3 is critical to murine palatogenesis (Funato et
186 al. 2015). To remedy the cleft phenotype of Tgfβ3-null mice, Spivak et al. pioneered a virally
187 mediated intra-amniotic Tgfβ3 gene transfer therapy and showed palatal fusion without adverse
188 effects in 100% of pups followed injections at E12.5 and E13.5 (Spivak et al. 2007). Another
189 group tested delayed timing of therapy at E14.5 and E15.5 resulting in 82% and 75% palatal
190 closures, respectively (Wu et al. 2012). Since TGFβ3 polymorphisms are also associated with
191 non-syndromic clefts in humans (Zhu et al. 2010), successful translation into human fetuses was
192 hypothesized to yield successful outcomes between gestational weeks 8 and 10 (Spivak et al.
193 2007). Promising results from murine palatal cultures foreshadow the potential versatility of
194 TGFβ3-based therapies for CP attributed to environmental causes, including dioxin exposure
195 (Thomae et al. 2005). In 2019, a group of researchers were able to rescue a core binding factor β
196 (Cbfb) (a cofactor of the Runx1 family of transcription factors) -deficiency-induced anterior CP
197 phenotype through the in vitro administration of folic acid (Sarper et al. 2019). In these mutants,
198 TGFβ3 expression is disrupted in the area of failed anterior palatal fusion and affects the
199 phosphorylation of Stat3, a downstream effector molecule of cellular proliferation, migration,
200 and apoptosis. This reversal of CP using folic acid highlights the obligatory function of the
201 Runx1/Cbfb-Stat3-TGFβ3 signaling axis in anterior palatal fusion.
202
203 *Activation of Shh signaling* - The intestinal cell kinase (ICK) gene encoding for a mitogen-
204 activated protein (MAP) kinase involved in activating Shh signaling during development is down
205 regulated during endocrine-cerebro-osteodysplasia (ECO), a syndrome that includes CP. As the
206 first study to attempt prenatal pharmaceutical activation of Shh signaling, Shin et al., in 2019

injected a small-molecule agonist for Smoothened (SAG) intraperitoneally into pregnant *Ick*$^{tm1a/+}$ mice at various stages (Shin et al. 2019). Although success in palatal closures showed variable efficacy, the highest efficiency was achieved at E11.25, indicating that developmental windows are critical for restoring molecular homeostasis in Shh-mediated actions.

Modulation of the Wnt signaling pathway – The importance of Wnt signaling and related pathway genes in palate formation is elegantly reviewed by Reynolds et al., 2019 b. The first Wnt pathway intervention study was performed on mice deficient in glycogen synthase kinase-3β (GSK-3β), a key mediator of canonical Wnt signaling. Subcutaneous rapamycin was administered every 12 hours to pregnant dams at E13.5 to E15 in order to stabilize the recombinant FRB-tagged Gsk-3β protein. Complete and partial alleviation of the cleft phenotype was subsequently reported in 5/9 and 1/9 treated pups, respectively (Liu et al. 2007). Rescue was not observed with later injection regimens, which attests to the developmental window during which Gsk-3β functions in palatogenesis. While an elegant proof-of-concept of targeted Wnt pathway manipulation, the clinical utility of this study is limited by its development in a conveniently inducible transgenic system that *cannot* be clinically reproduced in humans.

Another set of approaches target the activities of dickkopf-related (Dkk) proteins that are extracellular antagonists of Wnt signal transduction and function by high-affinity binding to Wnt co-receptors Lrp5/6. *In situ* application of dickkopf1 (Dkk1) to the maxillary processes of chick embryos via protein-impregnated beads elicits downregulation of osteochondrogenic targets of Wnt signaling, including *Bmp4, Tbx22, Sox9 and Barx1,* thereby hindering growth of the maxillary and palatine bones (Shimomura et al. 2019).

Small-molecule inhibitors of Dkk1 and Dkk2 are now known to share a functional molecular relationship with the paired box domain-containing transcription factor, Pax9. *Pax9* hemizygosity in humans led to a decreased level of Wnt signaling and concurrent increased level of Dkks, suggesting that *Pax9* deficiency-related phenotypes could be mitigated with direct Dkk antagonism (Schuffenhauer et al. 1999). Researchers have subsequently revealed the potential linkages between *Pax9* and CP in cases from America, Japan, Korea, and China (Song et al. 2013). The controlled delivery of a small-molecule WAY-262611 that has been shown to potentiate downstream Wnt-β-catenin signaling via Dkk1 antagonism (Pelletier et al. 2009), faithfully reversed secondary CPs in *Pax9*-deficient mice *in utero* (Jia et al. 2017) (see Figure 1). However, WAY-262611 could not rescue the expression of *Msx1* and *Bmp4*, which appear restricted to the anterior palatal mesenchyme. Jia *et al.* also trialed another Dkk inhibitor, IIIc3a (Li et al. 2012), via tail vein injections and showed complete closure of secondary palate in 80% (12/15) of embryos (Jia et al. 2017). Maternal intraperitoneal injections at E12.5, E13.5 and E14.5, also resulted in resolution of the cleft defect in middle and posterior regions of 7/11 *Pax9*-deficient palates as shown in independent studies by Li et al., 2017.

Since Wnt signaling pathway is critical for organogenesis and is also implicated in tumorigenesis (particularly bone tumors), it is crucial to perform thorough toxicology analyses. Jia et al. in 2017 performed MRI imaging on mothers injected intraperitoneally with Wnt agonist small-molecule therapies, along with surviving wild-type and heterozygous progeny, showing no toxic effects or tumor development up to 18 months following the last injection.

253 ***Challenges and Considerations for a Way Forward***

254 Prior to the translation of prenatal intervention for the correction of human OFCs, a number of
255 barriers remain to be overcome. The implementation of *in utero* therapies is constrained by the
256 inability of contemporary approaches to identify structural anomalies in the first trimester of
257 pregnancy. Since the primary and secondary palates form between 6 to 7 weeks and 8 to 10
258 weeks of gestation, respectively (Yu et al. 2017), cleft detection prior to or during this window
259 would be essential for maximum therapeutic effect. Clearly, more research is needed on whether
260 therapies can indeed operate retroactively and if intervention times can be targeted later in
261 palatogenesis.

262

263 Whereas the maxillary lip and alveolar ridge can be confidently evaluated with conventional
264 ultrasonography, isolated clefts of the secondary palate have historically gone undetected. While
265 conventional screening protocols subject to initial ultrasound can identify cleft phenotypes at
266 week 20, high-frequency ultrasonic technology can accurately visualized structures as early as 13
267 weeks' gestation (Maarse et al. 2010). Novel two- and three-dimensional ultrasound techniques
268 have ameliorated detection rates of secondary CP, but are largely implemented in the latter stage
269 of pregnancy. In spite of reports of first-trimester diagnoses with select ultrasound techniques,
270 these novel approaches have yet to be widely adopted in routine screening. Similarly, while MRI
271 has higher positive predictive value than ultrasound for posterior CPs, it is not typically
272 employed until weeks 20-39 (Tian et al. 2019).

273

274 The potential for earlier OFC identification through screening of prospective parents for
275 pathogenic mutations that could induce palatal dysmorphogenesis in their offspring is an exciting

forefront in precision medicine. Current diagnostic panels only include genes known to cause lethal and/or debilitating diseases. Non-syndromic OFCs and those that are part of syndromes (i.e. *WNT7A* and *MKS1*) are not captured in routine screening panels and will be overlooked prior to pregnancy. Even as panels are updated with more genes definitively linked to birth defects, preconception screening is limited by the inability to detect *de novo* mutations. The latter are causative in 3.5-fold more cases of fetal structural anomalies detected *in utero* than inherited genetic abnormalities (Lord et al. 2019). Importantly, these methods of screening would not be effective in detecting environmentally induced OFCs (i.e. those due to factors such as vitamin deficiencies and teratogenic exposures), and they depend upon *a priori* knowledge of specific single SNPs, insertion or deletion events and CNVs. This necessitates prenatal screening to adequately determine whether a developing fetus harbors a molecular aberration that can lead to disordered morphogenesis and be considered for targeted putative therapies.

Current strategies for prenatal correction of OFC phenotypes in the animal models discussed have focused solely on single-gene mutations but offer valuable proof-of-concepts for replacement therapy aproaches that restore molecular homeostasis during critical stages of development. It is also important to consider the potentially undesirable developmental implications or delayed pathological outcomes of therapies, given that many palate-specific molecular targets function within signaling cascades with diverse molecular outcomes. For example, beyond its developmental roles, Wnt signaling also orchestrates tumorigenesis in several organ systems (Zhan et al. 2017). Notwithstanding, the controlled dosage of agonist or antagonist drugs that target discrete ligand-receptor complexes can be effective as pathologic levels are likely modulated by cellular regulatory mechanisms (Komiya and Habas 2008).

Targeted drug delivery systems must be optimized in order to drive translation of preclinical methodologies. Due to variability in the transplacental passage of therapeutic agents administered systemically to pregnant women, this route of delivery is considered suboptimal (Hermes et al. 2014). In primates, less than 1% of maternal serum concentrations of a protein tagged with the Fc portion of an IgG1 reached the fetus following maternal systemic delivery (Schneider et al. 2018). Thus, to compensate, mothers would be exposed to large quantities of exogenous molecules with potentially detrimental effects. However, no signs of maternal or fetal drug-related toxicity have been demonstrated in primates at the maximum dose administered in humans to remedy ectodermal dysplasia.

Although it is believed that lower quantities of molecules administered intra-amniotically are needed (as amniotic fluid may serve as a reservoir promoting targeted drug uptake), drug kinetics must be measured to rule out toxicity and side effects to both mother and fetus (Hermes et al. 2014). While fetal and maternal outcomes may be compromised by invasive injection protocols, less invasive ultrasound-guided injections have been employed in mice and humans (Schneider et al. 2018). In murine models, even fetuses in high-dose cohorts survived intra-amniotic injection and were born without complications (Hermes et al. 2014). Of the three human babies born following intra-amniotic EDA therapy, the twins were born prematurely, as is common of multiple pregnancies, but the single pregnancy was carried for a normal gestational term. Consequently, more studies are required to determine whether an association exists between premature births and *in utero* therapy and whether this has clinically significant implications.

With the dawn of direct-to-consumer genomic analysis assays, a high propensity for misinterpretation of test results will persist, further reinforcing the need for effective communication between knowledgeable provider and responsive patient. The International Fetal Transplantation and Immunology Society's *In Utero* Gene Therapy Consensus Statement dictates prenatal intervention should only be considered when both a reliable molecular diagnosis *and* a strong genotype-phenotype correlation exists (Almeida-Porada et al. 2019). Multiple barriers presently preclude the widespread adoption of genomics into prenatal clinical practice, compromising shared decision-making processes in prenatal diagnostics and management. The advent of CRISPR/Cas9 technology to readily generate craniofacial disease models with specific human mutations should aid in the translation of new technologies (Neben et al. 2016). The 1998 UK Gene Therapy Advisory Committee recommends that *in utero* treatment should be reserved for cases that confer a clear advantage over postnatal intervention (Kingdom. 1998). While precision medicine gives rise to a range of other ethical conundrums, we believe that the promise of precision-driven approaches for early diagnosis and therapy for the treatment of orofacial clefts is an essential step forward.

ACKNOWLEDGEMENTS

This work was supported by the National Institute of Health/National Institute of Dental and Craniofacial Research Grants DE019471 and DE027255 (RDS) and supported in part by the American Cleft Palate-Craniofacial Association (SJ) and a Ph.D. training stipend from the Department of Biomedical Engineering, University of Utah to JDO. PS is supported by the Swiss National Science Foundation [Grant 310030A - 176356]. We would also like to acknowledge Russell Hendrycks for his assistance in generating Figure 1.

AUTHOR CONTRIBUTIONS

Author 1 (JDO): Contributed to conception and design; Contributed to acquisition, analysis, or interpretation; Drafted the manuscript; Critically revised the manuscript; Gave final approval.

Author 2 (ECT): Contributed to conception and design; Contributed to acquisition, analysis, or interpretation; Drafted the manuscript; Gave final approval.

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CONFLICT OF INTEREST STATEMENT

None of the authors have any conflicts of interest to disclose.

REFERENCES

Alfirevic Z, Navaratnam K, Mujezinovic F. 2017. Amniocentesis and chorionic villus sampling for prenatal diagnosis. Cochrane Database of Systematic Reviews. (9).

Almeida-Porada G, Waddington SN, Chan JKY, Peranteau WH, MacKenzie T, Porada CD. 2019. In utero gene therapy consensus statement from the ifetis. Molecular Therapy. 27(4):705-707.

Bell JC, Raynes-Greenow C, Turner RM, Bower C, Nassar N, O'Leary CM. 2014. Maternal alcohol consumption during pregnancy and the risk of orofacial clefts in infants: A systematic review and meta-analysis. Paediatr Perinat Epidemiol. 28(4):322-332.

Bianchi DW. 2012. From prenatal genomic diagnosis to fetal personalized medicine: Progress and challenges. Nature Medicine. 18(7):1041-1051.

Carlson JC, Anand D, Butali A, Buxo CJ, Christensen K, Deleyiannis F, Hecht JT, Moreno LM, Orioli IM, Padilla C et al. 2019. A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft gwas signals. Genet Epidemiol. 43(6):704-716.

Chen L, Gu H, Li J, Yang Z-Y, Sun X, Zhang L, Shan L, Wu L, Wei X, Zhao Y et al. 2016. Comprehensive maternal serum proteomics identifies the cytoskeletal proteins as non-invasive biomarkers in prenatal diagnosis of congenital heart defects. Scientific Reports. 6(1):19248.

Cheng EY, Luthy DA, Zebelman AM, Williams MA, Lieppman RE, Hickok DE. 1993. A prospective evaluation of a second-trimester screening test for fetal down syndrome using maternal serum alpha-fetoprotein, hcg, and unconjugated estriol. Obstet Gynecol. 81(1):72-77.

Clark MM, Stark Z, Farnaes L, Tan TY, White SM, Dimmock D, Kingsmore SF. 2018. Meta-analysis of the diagnostic and clinical utility of genome and exome sequencing and chromosomal microarray in children with suspected genetic diseases. npj Genomic Medicine. 3(1):16.

Dao AM, Goudy SL. 2016. Cleft palate repair, gingivoperiosteoplasty, and alveolar bone grafting. Facial Plast Surg Clin North Am. 24(4):467-476.

Dugger SA, Platt A, Goldstein DB. 2018. Drug development in the era of precision medicine. Nature Reviews Drug Discovery. 17(3):183-196.

Funato N, Nakamura M, Yanagisawa H. 2015. Molecular basis of cleft palates in mice. World J Biol Chem. 6(3):121-138.

Ghidini A, Bianchi DW, Levy B, Van Mieghem T, Deprest J, Chitty LS. 2019. In case you missed it: The prenatal diagnosis editors bring you the most significant advances of 2018. Prenatal Diagnosis. 39(2):61-69.

Hermes K, Schneider P, Krieg P, Dang A, Huttner K, Schneider H. 2014. Prenatal therapy in developmental disorders: Drug targeting via intra-amniotic injection to treat x-linked hypohidrotic ectodermal dysplasia. The Journal of investigative dermatology. 134.

James A, Oluwatosin B, Njideka G, Babafemi, Benjamin OG, Olufemi D, Leo R, Folorunso I, Phylis, Olusina O. 2014. Cleft palate in hiv-exposed newborns of mothers on highly active antiretroviral therapy. Oral Surg. 7(Suppl 1):102-106.

Jia S, Zhou J, Fanelli C, Wee Y, Bonds J, Schneider P, Mues G, D'Souza RN. 2017. Small-molecule wnt agonists correct cleft palates in pax9 mutant mice in utero. Development. 144(20):3819-3828.

Kingdom. HDotU. 1998. Gene therapy advisory committee: Report on the potential use of gene therapy in utero. Disease markers. 14(3):151-154.
Komiya Y, Habas R. 2008. Wnt signal transduction pathways. Organogenesis. 4(2):68-75.
Lammer EJ, Chen DT, Hoar RM, Agnish ND, Benke PJ, Braun JT, Curry CJ, Fernhoff PM, Grix AW, Jr., Lott IT et al. 1985. Retinoic acid embryopathy. N Engl J Med. 313(14):837-841.
Leslie EJ, Marazita ML. 2013. Genetics of cleft lip and cleft palate. Am J Med Genet C Semin Med Genet. 163C(4):246-258.
Li X, Shan J, Chang W, Kim I, Bao J, Lee HJ, Zhang X, Samuel VT, Shulman GI, Liu D et al. 2012. Chemical and genetic evidence for the involvement of wnt antagonist dickkopf2 in regulation of glucose metabolism. Proc Natl Acad Sci U S A. 109(28):11402-11407.
Liao YF, Mars M. 2006. Hard palate repair timing and facial growth in cleft lip and palate: A systematic review. Cleft Palate Craniofac J. 43(5):563-570.
Liu KJ, Arron JR, Stankunas K, Crabtree GR, Longaker MT. 2007. Chemical rescue of cleft palate and midline defects in conditional gsk-3beta mice. Nature. 446(7131):79-82.
Longaker MT, Chiu ES, Adzick NS, Stern M, Harrison MR, Stern R. 1991. Studies in fetal wound healing. V. A prolonged presence of hyaluronic acid characterizes fetal wound fluid. Ann Surg. 213(4):292-296.
Longaker MT, Whitby DJ, Ferguson MW, Lorenz HP, Harrison MR, Adzick NS. 1994. Adult skin wounds in the fetal environment heal with scar formation. Ann Surg. 219(1):65-72.
Lord J, McMullan DJ, Eberhardt RY, Rinck G, Hamilton SJ, Quinlan-Jones E, Prigmore E, Keelagher R, Best SK, Carey GK et al. 2019. Prenatal exome sequencing analysis in fetal structural anomalies detected by ultrasonography (page): A cohort study. The Lancet. 393(10173):747-757.
Maarse W, Berge SJ, Pistorius L, van Barneveld T, Kon M, Breugem C, Mink van der Molen AB. 2010. Diagnostic accuracy of transabdominal ultrasound in detecting prenatal cleft lip and palate: A systematic review. Ultrasound Obstet Gynecol. 35(4):495-502.
Marazita ML. 2012. The evolution of human genetic studies of cleft lip and cleft palate. Annu Rev Genomics Hum Genet. 13:263-283.
Milunsky A, Alpert E, Neff RK, Frigoletto FD. 1980. Prenatal diagnosis of neural tube defects. Iv. Maternal serum alpha-fetoprotein screening. Obstet Gynecol. 55(1):60-66.
Moore AL, Marshall CD, Barnes LA, Murphy MP, Ransom RC, Longaker MT. 2018. Scarless wound healing: Transitioning from fetal research to regenerative healing. Wiley Interdiscip Rev Dev Biol. 7(2).
Narasimhan K, Lin SL, Tong T, Baig S, Ho S, Sukumar P, Biswas A, Hahn S, Bajic VB, Choolani M. 2013. Maternal serum protein profile and immune response protein subunits as markers for non-invasive prenatal diagnosis of trisomy 21, 18, and 13. Prenat Diagn. 33(3):223-231.
Neben CL, Roberts RR, Dipple KM, Merrill AE, Klein OD. 2016. Modeling craniofacial and skeletal congenital birth defects to advance therapies. Hum Mol Genet. 25(R2):R86-R93.
Normand EA, Braxton A, Nassef S, Ward PA, Vetrini F, He W, Patel V, Qu C, Westerfield LE, Stover S et al. 2018. Clinical exome sequencing for fetuses with ultrasound abnormalities and a suspected mendelian disorder. Genome Medicine. 10(1):74.
Ozturk S, Deveci M, Sengezer M, Gunhan O. 2001. Results of artificial inflammation in scarless foetal wound healing: An experimental study in foetal lambs. Br J Plast Surg. 54(1):47-52.

458 Pelletier JC, Lundquist JT, Gilbert AM, Alon N, Bex FJ, Bhat BM, Bursavich MG, Coleburn
459 VE, Felix LA, Green DM et al. 2009. (1-(4-(naphthalen-2-yl)pyrimidin-2-yl)piperidin-4-
460 yl)methanamine: A wingless β-catenin agonist that increases bone formation rate. Journal
461 of Medicinal Chemistry. 52(22):6962-6965.
462 Pereira AV, Fradinho N, Carmo S, de Sousa JM, Rasteiro D, Duarte R, Leal MJ. 2018.
463 Associated malformations in children with orofacial clefts in portugal: A 31-year study.
464 Plast Reconstr Surg Glob Open. 6(2):e1635-e1635.
465 Reynolds K, Kumari P, Sepulveda Rincon L, Gu R, Ji Y, Kumar S, Zhou CJ. 2019. Wnt
466 signaling in orofacial clefts: Crosstalk, pathogenesis and models. Dis Model Mech. 12(2).
467 Sabbagh HJ, Ahmed Hassan MH, Innes NPT, Baik AA, Mossey PA. 2014. Parental
468 consanguinity and nonsyndromic orofacial clefts in children: A systematic review and
469 meta-analyses. The Cleft Palate-Craniofacial Journal. 51(5):501-513.
470 Sabbagh HJ, Hassan MHA, Innes NPT, Elkodary HM, Little J, Mossey PA. 2015. Passive
471 smoking in the etiology of non-syndromic orofacial clefts: A systematic review and meta-
472 analysis. PLoS One. 10(3):e0116963.
473 Sarper SE, Inubushi T, Kurosaka H, Ono Minagi H, Murata Y, Kuremoto KI, Sakai T, Taniuchi
474 I, Yamashiro T. 2019. Anterior cleft palate due to cbfb deficiency and its rescue by folic
475 acid. Dis Model Mech. 12(6).
476 Schneider H, Faschingbauer F, Schuepbach-Mallepell S, Korber I, Wohlfart S, Dick A,
477 Wahlbuhl M, Kowalczyk-Quintas C, Vigolo M, Kirby N et al. 2018. Prenatal correction
478 of x-linked hypohidrotic ectodermal dysplasia. N Engl J Med. 378(17):1604-1610.
479 Schuffenhauer S, Leifheit HJ, Lichtner P, Peters H, Murken J, Emmerich P. 1999. De novo
480 deletion (14)(q11.2q13) including pax9: Clinical and molecular findings. J Med Genet.
481 36(3):233-236.
482 Shimomura T, Kawakami M, Tatsumi K, Tanaka T, Morita-Takemura S, Kirita T, Wanaka A.
483 2019. The role of the wnt signaling pathway in upper jaw development of chick embryo.
484 ACTA HISTOCHEMICA ET CYTOCHEMICA. 52(1):19-26.
485 Shin JO, Song J, Choi HS, Lee J, Lee K, Ko HW, Bok J. 2019. Activation of sonic hedgehog
486 signaling by a smoothened agonist restores congenital defects in mouse models of
487 endocrine-cerebro-osteodysplasia syndrome. EBioMedicine. 49:305-317.
488 Sivertsen A, Wilcox AJ, Skjaerven R, Vindenes HA, Abyholm F, Harville E, Lie RT. 2008.
489 Familial risk of oral clefts by morphological type and severity: Population based cohort
490 study of first degree relatives. BMJ. 336(7641):432-434.
491 Song T, Wu D, Wang Y, Li H, Yin N, Zhao Z. 2013. Snps and interaction analyses of irf6, msx1
492 and pax9 genes in patients with nonsyndromic cleft lip with or without palate. Mol Med
493 Rep. 8(4):1228-1234.
494 Spivak RM, Endo M, Zajac A, Zoltick P, Ang B, Horn R, Flake A, Kirschner R, Nah H-D. 2007.
495 In utero gene delivery of adenovirus encoded tgf-beta3 restores physiologic palatal fusion
496 and rescues cleft palate in a tgf-beta3 knockout mouse. Journal of the American College
497 of Surgeons. 205(3, Supplement):S92.
498 Stelnicki EJ, Lee S, Hoffman W, Lopoo J, Foster R, Harrison MR, Longaker MT. 1999. A long-
499 term, controlled-outcome analysis of in utero versus neonatal cleft lip repair using an
500 ovine model. Plast Reconstr Surg. 104(3):607-615.
501 Thevenon J, Duffourd Y, Masurel-Paulet A, Lefebvre M, Feillet F, El Chehadeh-Djebbar S, St-
502 Onge J, Steinmetz A, Huet F, Chouchane M et al. 2016. Diagnostic odyssey in severe

neurodevelopmental disorders: Toward clinical whole-exome sequencing as a first-line diagnostic test. Clin Genet. 89(6):700-707.
Thomae TL, Stevens EA, Bradfield CA. 2005. Transforming growth factor-beta3 restores fusion in palatal shelves exposed to 2,3,7,8-tetrachlorodibenzo-p-dioxin. The Journal of biological chemistry. 280(13):12742-12746.
Tian M, Xiao L, Jian N, Wei X, Liu S, Zhao H, Li G, Zhang S, Liang W, Lin N et al. 2019. Accurate diagnosis of fetal cleft lip/palate by typical signs of magnetic resonance imaging. Prenatal Diagnosis. 39(10):883-889.
Vermeesch JR, Voet T, Devriendt K. 2016. Prenatal and pre-implantation genetic diagnosis. Nat Rev Genet. 17(10):643-656.
Veroniki AA, Cogo E, Rios P, Straus SE, Finkelstein Y, Kealey R, Reynen E, Soobiah C, Thavorn K, Hutton B et al. 2017. Comparative safety of anti-epileptic drugs during pregnancy: A systematic review and network meta-analysis of congenital malformations and prenatal outcomes. BMC Medicine. 15(1):95.
Wapner RJ, Babiarz JE, Levy B, Stosic M, Zimmermann B, Sigurjonsson S, Wayham N, Ryan A, Banjevic M, Lacroute P et al. 2015. Expanding the scope of noninvasive prenatal testing: Detection of fetal microdeletion syndromes. American Journal of Obstetrics and Gynecology. 212(3):332.e331-332.e339.
Wehby GL, Murray JC. 2010. Folic acid and orofacial clefts: A review of the evidence. Oral diseases. 16(1):11-19.
Weinberg SM, Cornell R, Leslie EJ. 2018. Craniofacial genetics: Where have we been and where are we going? PLoS Genet. 14(6):e1007438.
Wojcicki P, Drozdowski PH. 2011. In utero surgery--current state of the art--part ii. Med Sci Monit. 17(12):RA262-270.
Wu C, Zhou Y, Fan W, Han P, Chang J, Yuen J, Zhang M, Xiao Y. 2012. Hypoxia-mimicking mesoporous bioactive glass scaffolds with controllable cobalt ion release for bone tissue engineering. Biomaterials. 33(7):2076-2085.
Yu K, Deng M, Naluai-Cecchini T, Glass IA, Cox TC. 2017. Differences in oral structure and tissue interactions during mouse vs. Human palatogenesis: Implications for the translation of findings from mice. Front Physiol. 8:154.
Zhan T, Rindtorff N, Boutros M. 2017. Wnt signaling in cancer. Oncogene. 36(11):1461-1473.
Zhu J, Hao L, Li S, Bailey LB, Tian Y, Li Z. 2010. Mthfr, tgfb3, and tgfa polymorphisms and their association with the risk of non-syndromic cleft lip and cleft palate in china. American journal of medical genetics Part A. 152a(2):291-298.

FIGURE LEGEND

Figure 1. Small-molecule inhibitors of Dkk1 and Dkk2 (inhibitors of LRP5/6) allow for the activation of Wnt/B-catenin signaling transduction. Several different molecules have been described (e.g. WAY262611; IIIc3a) and trialed to rescue the phenotype of murine cleft models in which Dkk1/2 are upregulated in the posterior palate to the detriment of Wnt signaling.

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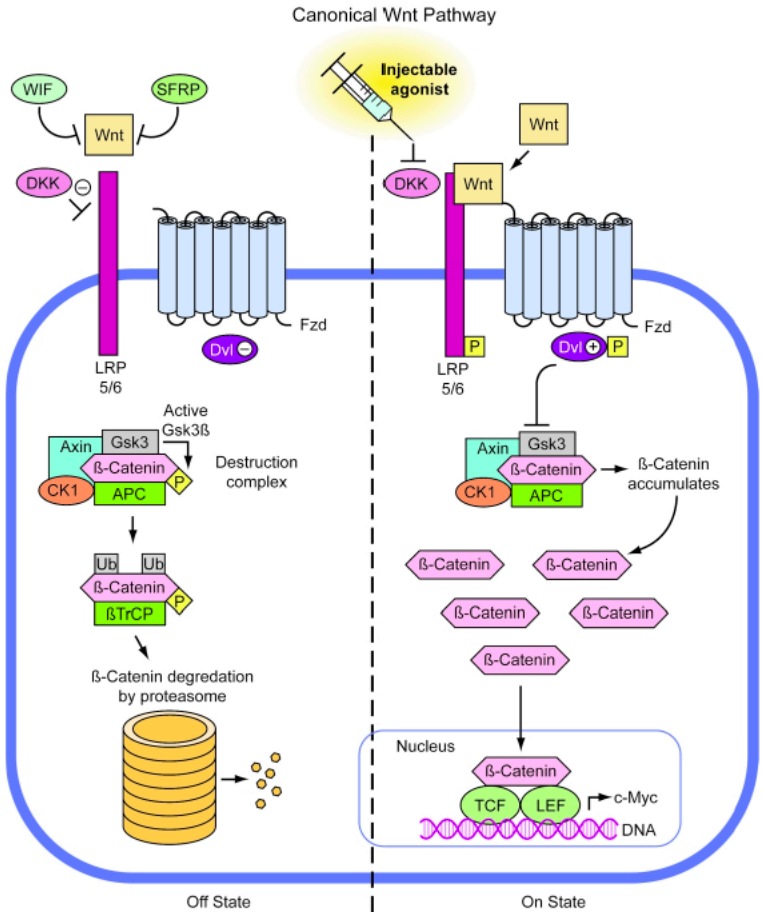
Canonical Wnt Pathway
Injectable agonist
WIF
SFRP
Wnt
DKK
Fzd
Dvl
LRP 5/6
P
Active Gsk3ß
Axin
Gsk3
ß-Catenin
CK1
APC
Destruction complex
Ub
ßTrCP
ß-Catenin degredation by proteasome
ß-Catenin accumulates
Nucleus
TCF
LEF
c-Myc
DNA
Off State
On State