Comparative genomics reveals miRNAs that give identity to developing mid-facial tissues

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Abstract

Defects in mid-face development, including cleft lip/palate, account for the largest number of birth defects annually. Understanding the molecular genetic mechanisms that lead to human clefting remains a challenge because the development of the palate involves many interacting genes and craniofacial disease may involve slight modulation of these genes rather than total abrogation. MicroRNAs (miRNAs) are short, non-protein-encoding RNAs that modulate gene expression post-transcriptionally in numerous developmental and physiological processes.

Hypothesis: miRNA sub-populations drive palatal development by giving identity to mid-facial tissues

1. Do different regions of the developing craniofacial complex get their identity through the action of microRNAs (miRNAs)?

2. Identifying mid-facial tissue miRNAs by miRNAseq

3. Bioinformatics reveal tissue-specific enrichment of mid-facial miRNAs

4. Future directions
   a) Refine bioinformatic pipeline (see Batzel et al. poster)
   b) “Genetic dissection” of zebrafish FNP
   c) Testing function of enriched miRNAs by injecting miRNA duplexes in zebrafish (see Ding et al. poster)

5. FishFace Atlas

Also interested in teleost craniofacial morphology? Check out another FaceBase project (from Kimmel lab)