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Data Article

Gene expression profile data for mouse facial development

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ABSTRACT

This article contains data related to the research articles "Spatial and Temporal Analysis of Gene Expression during Growth and Fusion of the Mouse Facial Prominences" (Feng et al., 2009) [1] and "Systems Biology of facial development: contributions of ectoderm and mesenchyme" (Hooper et al., 2017 In press) [2]. Embryonic mammalian craniofacial development is a complex process involving the growth, morphogenesis, and fusion of distinct facial prominences into a functional whole. Aberrant gene regulation during this process can lead to severe craniofacial birth defects, including orofacial clefting. As a means to understand the genes involved in facial development, we had previously dissected the embryonic mouse face into distinct prominences: the mandibular, maxillary or nasal between E10.5 and E12.5. The prominences were then processed intact, or separated into ectoderm and mesenchyme layers, prior analysis of RNA expression using microarrays (Feng et al., 2009, Hooper et al., 2017 in press) [1,2]. Here, individual gene expression profiles have been built from these datasets that illustrate the timing of gene expression in whole prominences or in the separated tissue layers. The data profiles are presented as an indexed and clickable list of the genes each linked to a graphical image of that gene's expression profile in the ectoderm, mesenchyme, or intact prominence. These data files

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E-mail address: trevor.williams@ucdenver.edu (T. Williams).<http://dx.doi.org/10.1016/j.dib.2017.05.003>2352-3409/© 2017 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

will enable investigators to obtain a rapid assessment of the relative expression level of any gene on the array with respect to time, tissue, prominence, and expression trajectory.

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Specifications Table

Subject area	<i>Developmental Biology</i>
More specific subject area	<i>Mouse craniofacial development</i>
Type of data	<i>html pages</i>
How data was acquired	<i>Affymetrix Mouse430v2.0 and Affymetrix MoGene-1.0-st-v1 microarrays</i>
Data format	<i>Analyzed</i>
Experimental factors	<i>Samples for microarray analysis were pooled microdissected facial prominence as described in [1,2]. Ectoderm was separated from mesenchyme by 'peeling' after dispase treatment, as described in Li and Williams [3].</i>
Experimental features	<i>Gene expression data was compared across age, prominence and tissue layer.</i>
Data source location	<i>University of Colorado School of Dental Medicine, Aurora, CO</i>
Data accessibility	<i>The raw data (.cel files) and normalized expression data are available at GEO (www.ncbi.nlm.nih.gov/geo) under accession numbers GSE7759 [1] and GSE62214 [2] and at FaceBase (www.facebase.org) under accession FB00000803.</i>
Related research article	<i>[1,2]</i>

Value of the data

- The data is a statistically robust and extensively verified multidimensional gene expression resource for mouse facial development.
- By comparing the transcriptome across age, prominence and tissue layer, the data provide a valuable tool for studying the complex process of craniofacial development.
- The data could contribute to interpretation of gene expression data in mouse mutants.
- The data could contribute to interpretation of clinical genetic data pertaining to facial development, morphology and orofacial cleft pathogenesis.

1. Data

The data are contained in the folder "Trev HTMLs" and within this folder are three items: two folders and an Index.html (see [Supplementary material](#)). The data are designed to be uncompressed in a single location, where hyperlinks use relative file path names to navigate the set of files. Clicking on the top-level Index.html link will provide information concerning the two datasets. This sheet provides an overview, using color-coded boxes for each named gene, to illustrate the gene expression profile found within each of the datasets (Fig. 1). Hyperlinks are also available to access details for each gene in the Whole Prominence or Ectoderm/Mesenchyme datasets. The two folders, Whole-Prominence and EctoMesen, contain expression profiles and database annotations for every named gene available as.html pages, indexed by gene name for the two studies. Again, within each folder

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