

Poster F-1

Time-courses of gene expression during development of murine tooth germs by analysis of microarray data.



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Short Abstract: Analysis of microarray expression data from a series of microarrays, covering the duration of development of the murine tooth germ from 11.5-26.5dpc, has been used to describe time-courses of gene expression during development of this organ. Resulting data appears useful in assigning ontologies to observed, significant, changes in gene expression.

Long Abstract:

Current literature suggests that much remains to be learned regarding changes in gene expression occurring during maturation of the murine tooth germ. We have investigated gene expression in first mandibular molar tooth germs of CD1 mice embryos/pups at daily intervals, starting at 11.5dpc, ending at 26.5dpc. At each time-point total RNA was isolated from three separate tooth germs. These three samples were pooled and used for cDNA synthesis and Cy3 or Cy5 labelling (Genisphere 900 labelling kit). Microarray analysis was carried using triplicate 30K murine microarrays (NTNU Microarray Core Facility, Trondheim, Norway). Microarray data were analysed using Spotfire functional genomics software. The resulting microarray data (derived from 48 microarray slides) were combined into one data-file which was used for analysis of gene expression as a function of time of development. The net median fluorescence intensities were log2 transformed, and normalised by trimmed mean. ANOVA analysis was carried out, allowing selection of genes which were significantly differently expressed ($P \leq 0.015$) between any one to the time point included in the analysis (1295 genes). The resulting data presentation was far too complex to yield obvious trends, although SOM analysis of the 1295 genes suggested that many exhibited a cyclic pattern of change with time of development. Some genes had their expression profiles characterised using RT-PCR. These were found among the 1295 genes, and their expression profiles were utilized in carrying out profile searches. This analysis found families of genes exhibiting different time-courses of expression with respect to time of development. Genes involved in regulation of cell growth and division exhibited a cyclic time-course (541 genes); genes involved in formation of enamel exhibited low levels of expression prior to birth (236 genes). One family of genes, coding for proteins involved in tissue mineralization, were more highly expressed at 14.4-18.5dpc (118 genes). Further, PCA analysis suggested that birth represented a major component of variation.