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Molecular characterization of human immature third molars: dental stem cells and their niches

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Introduction:

Tooth development is driven by a complex crosstalk between epithelium and neural crest-derived mesenchyme via signalling molecules, transcription factors and influences of the extracellular matrix. Despite knowledge of tooth development in rodents, the knowledge on gene expression important for a comprehensive tooth development in humans remains fragmentary. The aim of this study was to gain more insight into the molecular mechanisms that control differentiation of human tooth, and to clarify whether different compartments (niches) show inherent differences in their expression levels of stemness markers due to different cell populations.

Materials and Methods:

Human impacted third molars were divided into the operculum, periodontal ligament, developing pulp and ? as novel ? the pad like tissue beneath the pulp. We characterized the expression level of all compartments by real-time PCR of 16 different genes. In addition we performed whole genome expression arrays to clarify whether the coding of stem cells derived from different compartments is maintained in vitro.

Results:

The expression of Msx2 and HNK1 in all compartments confirms their ectomesenchymal origin. With regard to markers for ectomesenchyme and tooth development every single compartment held its own signature of gene expression. The expression of stemness markers such as nanog or Oct4 pointed to multipotent / pluripotent features. The differences in relative gene expression turned out to be dynamic along the progress in tooth development. In vitro, cell cultures derived from dental pulp and pad like tissue showed substantial differences in their respective gene expression profiles on a whole genome scale.

Discussion and Conclusion:

Concerning a set of 16 genes leads to the impression of dynamic opposed by rather quiescent compartments. Differences observed in cell cultures derived from pulp and pad like tissue may account to the fact that both compartments share in general the same cell populations but vary with respect to their
relative abundance. On the other hand, it is conceivable that cells of both compartments are committed due to instructive signalling of their respective niches. Is has to be explored in further experiments whether this is reflected by differences in e.g. differentiation capacities to other tooth derived stem cells.