

---

# Tracking time in the transcriptome of a developing organ.

Coraline Petit\*<sup>1</sup>, Marie Sémon<sup>1</sup>, and Sophie Pantalacci<sup>1</sup>

<sup>1</sup>Institut de Génomique Fonctionnelle de Lyon (IGFL) – CNRS : UMR5242, Institut national de la recherche agronomique (INRA) : UA1288, Université Claude Bernard - Lyon I (UCBL), École Normale Supérieure (ENS) - Lyon – Ecole Normale Supérieure de Lyon 46 allée d'Italie 69364 Lyon CEDEX07, France

## Résumé

During development, a large cohort of genes change their expression. It has recently been shown whole organism transcriptomic samples taken along development time carry a strong temporal signal (Yanai *et al.*, 2014), supported by a large number of genes. It seems contradictory that despite so many changes happening during development there is nevertheless an overall coherence of the transcriptome bearing a temporal signal.

Therefore our team is interested in the source of temporal information in transcriptomes, using mouse molar development as a model. Molar development involves the sequential addition and maturation of cusps (hills at the surface of the molar crown) from the buccal to the lingual side. Our team has shown that the temporal signal carried by the whole tooth germ, at both small and large time scales, could be explained by the increase cusp epithelium proportion throughout development. Development is to be considered in terms of changes through time and also changes through space.

I have been working on the transcriptome of tooth germs dissected along the bucco-lingual axis (at embryonic day 15.0, when the first cusp is patterned) and, surprisingly, we found that these transcriptomes also carry a temporal signal. We found that the buccal side is developmentally “older” than the lingual side. This temporal signal could be accounted for by differences in tissue proportions, the proportion of cusp epithelium in particular. The age difference between buccal and lingual side is consistent with the fact that, at this stage, there is a cusp patterned on the buccal side only. Moreover, cusp epithelium proportion enable us to find that the cusp location, along the bucco-lingual axis, differed between upper and lower molars.

Our work shows that changes in tissue proportion plays a role in temporal signal detected at the whole organ and sub-organ level. We will discuss to what extent tissue proportions are related to temporal signal in other developing organs.

---

\*Intervenant