

Newt transcriptome offers insight into tissue regeneration

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The transcriptome – the map of all [RNA molecules](#) – of the newt is published this week in [BioMed Central](#)'s open access journal [Genome Biology](#). *Notophthalmus viridescens* is a useful model in regenerative medicine, thanks to its ability to regenerate tissue, and this data gives insights into the mechanisms behind this process.

N. viridescens, the common newt, is native to North America, and an urodelian amphibian. Newt and salamander genomes are enormous; currently too big to sequence, but their potential to regenerate entire limbs, along with parts of the [central nervous system](#), has fascinated scientists for over 200 years. Thomas Braun, Thilo Borchardt at the Max Planck Institutes, Patagonis Tsonis at the University of Dayton and their colleagues sequenced a collection of healthy and regenerated tissues from newts, and converged them into one comprehensive transcriptome. Their analysis identified 826 proteins specific for urodeles, and several newly identified proteins that they believe may play important roles in regeneration process unique for urodeles. Their data also outline genes that appear only in regenerating, but not uninjured material, which will be of interest in regenerative medicine.

The transcriptome is not complete, but serves as a matrix for further analyses. The authors believe that their findings represent only the tip of the iceberg: 'Our data provide the groundwork for mechanistic experiments to answer the question whether urodeles utilize proprietary sets of genes for [tissue regeneration](#).' They continue: 'The newly established de novo transcriptome [...] will be an indispensable resource for a better understanding of regenerative events in newts and facilitate the identifications of molecules [...] that control this fascinating process.'

Provided by BioMed Central

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