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## 2022 Finalist

### Single-cell genomics and evolution of cell type regulatory networks

*»I am an evolutionary biologist interested in how genome sequence and its regulation translate into specific cellular phenotypes and, in particular, how this genotype-cell phenotype link evolves.*

*Cell types are the basic functional units of multicellular organisms. Distinct cell type transcriptional programs are deployed by regulatory mechanisms that control the differential access to genetic information in each cell. This genome regulation ultimately results in specific cellular phenotypes. However, the origin, diversity, and evolution of cell types and genome regulation remain largely unexplored.*

*What are the regulatory mechanisms linked to the origin of cell differentiation?*

*When did major animal cell types such as neurons emerge and did they evolve more than once? How do animal cell type gene regulatory networks evolve?*

*And how these genetic changes translate into cellular novelties?*

*To answer these and related questions, in my group we combine chromatin profiling, proteomics, and single-cell technologies with computational genomics in order to dissect and compare cell type programs and genome regulatory architectures in phylogenetically diverse systems. This study has two major potential impacts. First, by systematically characterizing cell type diversity we advance our understanding of organismal evolution, function, and adaptation. Beyond that, the comparative study of these animal cell type programs can offer transformative insights linking classical models of molecular evolution with an intermediate molecular phenotype: cell type gene regulatory networks. Second, by studying genome function in non-traditional model species we can reveal fundamental, shared principles that govern cell biological systems and the associated molecular mechanisms of genome regulation.«*

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