Recurring phenotypic loss: Repeatability of genome and regulatory evolution

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The loss of phenotypes represents a type of evolutionary innovation and is a widespread phenomenon. Like phenotypic gain, it can be adaptive and lead to new life histories. However, compared to phenotype gain, it is less well studied. A particularly interesting case for evolutionary studies is the repeated loss of the same phenotype in independent lineages, because this allows for investigating the repeatability, and to some extent predictability, of evolution. Here we propose to study the genomic basis of repeated phenotypic loss using pollen collecting structures as example. These structures, called scopae, have evolved in several independent bee lineages and facilitated the evolutionary success of these lineages as pollinators. As typically only female bees engage in foraging, scopae are sexually dimorphic. Interestingly, scopae have been lost in more than a dozen independent lineages of kleptoparasitic bees, along with certain behaviors and pilosity. Using a genome-wide comparative approach, we aim to reveal the genomic underpinnings that lead to the repeated evolution of that loss.
To this end, we will take advantage of existing high quality bee genomes and produce another 21 new high quality bee genomes of species with critical positions in the phylogenetic tree. This will provide us with more than 100 genomes as foundation for comprehensively studying genomic differences at all levels to reveal the emergence of that phenotypic loss within a phylogenetic framework. Using forward phylogenomic genotype to phenotype mapping and comparative genomics we will investigate genomic changes associated with phenotypic loss, in particular loss of genes and regulatory elements, including the evolution of gene families. As scopae are a sexually dimorphic trait that seems to be gained and lost dynamically during evolution, we hypothesize that gene regulatory changes play an important role in achieving such phenotypic plasticity that can eventually get fixed in the genome. Hence, in addition to genomes, we will also produce transcriptomes and ATAC-Seq data from six species, precisely three pairs of host and kleptoparasitic species having gained or lost scopae, respectively, from males and females during development. With this setup, we will test whether similar changes are involved in plastic as well as evolutionary loss of scopae. We will integratively analyze these new OMICs data using state-of-the-art computational methods to reveal the role of coding versus regulatory changes, transposable elements in genome architecture and regulation, gene family evolution and sequence changes with a focus on gene regulatory factors. We will further study how the genomic elements and factors are interacting in regulatory networks and how these networks have changed during evolution. In addition, we will investigate shifts in selective pressures acting on coding and non-coding sequences to understand how they might have conveyed the repeated loss of scopae.