



Molecular signatures associated with ecological adaptation in desert beetles

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Tenebrionid beetles (Insecta, Coleoptera) are one of the most species-rich families of animals, comprising about 20,000 species worldwide. They evolved before the split of the supercontinent Pangaea about 175 million years ago. Unique among beetles, distinct tenebrionid species independently colonized arid ecosystems in Africa (Namib desert) and in South America (Atacama desert) while closely related sister species did not enter the desert.

We used this unique setting to explore the genetic history of the dry-adapted phenotype. We assembled the transcriptomes of 20 tenebrionid species with (18) and without (2) adaptation to arid climate. In addition, we included in the dataset 59 transcriptomes from a broad range of non-tenebrionid species, summing up to a total of 5,425,713 sequences from 83 species with an average transcriptome completeness of 82.44 % (according to the BUSCO pipeline).

In previous work, we established methods to faithfully cluster orthologous genes and detect lineage-specific genes. Applied to the beetle dataset, these methods will allow us to uncover genes that were born in the ancestor of tenebrionid beetles and are correlated with their unique potential to survive in dry climate. By comparison of orthologous genes between dry-adapted and non-desert beetles, the dataset will also allow us to find molecular signatures associated with the adaptation to dry climate.

We will present the first results revealed by our computational pipeline.