Phylogenomic insights into the evolution of subterranean Coleoptera

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Abstract

Subterranean specialization is often accompanied by dramatic phenotypic changes epitomized by regressive evolution (e.g. loss or reduction of eyes and pigmentation). Nevertheless, the genetic underpinnings underlying these changes have been largely unexplored. The beetle tribes Leptodirini (Leiodidae), Hydroporini and Bidessini (Dytiscidae) represent ideal systems for exploring the genomic basis of adaptation to life in subterranean habitats, as both are represented by epigean and hypogean species including numerous lineages that independently colonized terrestrial and freshwater underground habitats respectively (Cooper et al. 2002, Ribera et al. 2010). We investigated gene repertoire evolutionary dynamics in both surface-dwelling and subterranean Coleoptera in lineages that underwent six independent underground colonization events. We generated highly complete transcriptomes for eight aquatic and fourteen terrestrial beetles including epigean and hypogean species and explored the evolution of their gene repertoire through a phylogenomic approach. Our results indicated that gene loss was a major force facilitating adaptation to an underground lifestyle. In contrast, we also observed that gene gain and duplication were also remarkable drivers for subterranean adaptation. Gene families experiencing contractions were involved in carbohydrate metabolism, response to starvation, wing disk development, rhodopsin and ommochrome biosynthetic processes and response to hypoxia, among many other examples. Conversely, gene families significantly expanded in subterranean lineages including those related to the regulation of apoptosis, alcohol metabolism, cell redox homeostasis, chitin-based cuticle development, larval instar development, oogenesis, and negative regulation of TORC1 signaling. Moreover we found that some gene families had experienced a more complex evolutionary dynamic encompassed by both expansion and contraction events, such as those involved in regulation of transcription, nervous system development, lipid metabolism, eye development, DNA repair and chemosensation,

indicating that these gene families underwent an in-depth reshaping throughout the evolutionary time. At a lineage-specific level, we did not observe many differences between the gene repertoire of the hypogean and epigean Leptodirini species in terms of gene gain and loss. Nonetheless, Hydroporini and Bidessini stygobitic species showed more disparity in their gene repertoire compared to their surface-dwelling relatives. Our results thus indicate that genomic exaptation may have facilitated underground colonization in Leptodirini prior to the diversification of the tribe, while in Hydroporini and Bidessini recent gene family turnover (dominated by gene loss) may have been guiding the surface-to-groundwater transition. These findings shed light towards understanding how the genomic toolkit has been reshaped in hypogean fauna from a macroevolutionary perspective.

Keywords

phylogenomics, gene repertoire evolution, Coleoptera, troglobitic and stygobitic fauna

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Author contributions

PBG conceived the study, generated and processed data, analyzed data, interpreted the results and prepared the presentation. SP collected some key species and provided knowledge about their ecological and taxonomic features. PBH analyzed data. TB generated and processed data. SC conceived the study, generated data and provided resources. RF conceived the study, provided resources, generated data, assisted in the data analyses and interpretation and supervised the project. All the authors approved the abstract and accepted the contents of the presentation.

Conflicts of interest

No conflicts of interest

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