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Accelerated evolution in transposable element islands in invasive Cardiocondyla obscurior

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Trait variation between populations is a result of selection, genetic drift or a combination of both. Adaptive evolution is based on selection of alternative phenotypes, implying heritable variation at the genotypic or epigenetic level. Genetic drift on the other hand results in a random distribution of genotypes drawn from a source population. We studied phenotypic differences and compared the genomes of two introduced populations of *C. obscurior* with very low effective population sizes to understand how variation is generated. In comparison to the other sequenced ants several subclasses of transposable elements (TEs) have selectively proliferated in *C. obscurior*. The genome is structured into low-density regions (LDR) and distinct TE islands that comprise 12.7% of the genome and range between 0.19 and 1.46 Mb. TE islands evolve faster than LDRs with regard to SNVs, gene/exon duplications/deletions, and degree of orthology. A non-random distribution of gene families, larvae/adult specific expression of genes located in TE islands and signs of stronger past methylation in TE islands compared to LDRs indicate different degrees of evolutionary rates and effective population sizes within the genome. We argue that TE islands have formed through genetic drift and have subsequently become adaptive because they generate a substantial proportion of the genetic diversity and thus provide additional leverage for selection. Our approach allows studying evolutionary genomic dynamics in response to drift and inbreeding in a species that successfully inhabits novel habitats.