Historical human activity shapes the genomic landscape of urban and forest túngara frogs

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Abstract

Urbanisation is rapidly altering ecosystems, leading to profound biodiversity loss. To mitigate these effects, we need a better understanding of how urbanisation impacts dispersal and reproduction. Two contrasting population demographic models have been proposed which predict that urbanisation either promotes (facilitation model) or constrains (fragmentation model) gene flow and genetic diversity. Which of these models prevails likely depends on the strength of selection on specific phenotypic traits that influence dispersal, survival or reproduction. Here, we examine the genomic impact of urbanisation on the Neotropical túngara frog (Engystomops pustulosus), a species known to adapt its reproductive traits to urban selective pressures. Using whole-genome resequencing for multiple paired urban and forest populations we examined genomic diversity, population connectivity and demographic history. Contrary to both the fragmentation and facilitation models, urban populations did not exhibit substantial changes in genomic diversity or differentiation compared to forest populations and genomic variation was best explained by geographic distance rather than environmental factors. Moreover, both urban and forest populations appear to have undergone population declines which are coincident with extensive human-activity around the Panama Canal during the last few centuries rather than recent urbanisation. Overall, our study underscores the importance of considering the historical context in urban evolution studies as anthropogenic effects may be extensive and impact non-urban areas on both recent and older timescales. Failure to take this into account when interpreting comparisons between urban and non-urban areas may underestimate the impact of urbanisation.

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