

Southern introgression increases adaptive immune gene variability in northern range margin populations of Fire-bellied toad

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Abstract

Northern range margin populations of the European fire-bellied toad (*Bombina orientalis*) have rapidly declined during recent decades. Extensive agricultural land use has fragmented the landscape, leading to habitat disruption and loss, as well as eutrophication of ponds. In Northern Germany (Schleswig-Holstein) and Southern Sweden, this decline resulted in decreased gene flow from surrounding populations, low genetic diversity, and a putative reduction in adaptive potential, leaving populations vulnerable to future environmental and climatic changes. Previous studies using mitochondrial control region and nuclear transcriptome-wide SNP data detected introgressive hybridization in multiple northern *B. orientalis* populations after presumed illegal release of toads from Austria. Here, we determine the impact of this introgression by comparing the body conditions (as a proxy for fitness) of introgressed and non-introgressed populations, and the genetic consequences in two candidate genes for putative local adaptation (the MHC II gene as part of the adaptive immune system and the stress response gene HSP70 kDa). We detected regional differences in body condition. We observed significantly elevated levels of within individual MHC allele counts in introgressed Swedish populations, associated with a tendency towards higher body weight, relative to regional non-introgressed populations. These differences were not observed among introgressed and non-introgressed German populations. Genetic diversity in both MHC and HSP was generally lower in northern than southern populations. Our study sheds light on the potential benefits of translocations of more distantly related conspecifics as a means to increase adaptive genetic variability and fitness of struggling range margin populations without distortion of local adaptation.

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