On the efficacy of natural selection in the Iberian hare, *Lepus granatensis*, from transcriptome-level sequencing data

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The nearly neutral theory of evolution predicts that the efficacy of natural selection is positively correlated with the long term effective population size (N_e), because in small populations there is an increased probability of fixation of deleterious variants or loss of advantageous mutations due to drift. Here, we analyzed transcriptome sequence data from hares and inferred that i) the proportion of adaptive substitutions driven to fixation by positive selection (α) was ~21%, and ii) the proportion of effectively neutral new amino acid changes was ~15%. When interpreted in light of the results in other mammalian taxa our estimates indicate that the efficacy of both positive and negative selection is intermediate in *Lepus* (mice>hares>humans), fitting the expectations given the inferred N_e of each species [mice (500,000) > hares (100,000) > humans (10,000)]. Our results contribute to the growing list of examples suggesting N_e as a strong predictor of the efficacy of natural selection.

Poster presentation

session 2