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Microsatellite analysis in museum samples reveals inbreeding before the regression of *Bombus veteranus*

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Simulating the effects of bumblebee population decline on gene diversity

We observed no significant decrease of the genetic diversity in *B. veteranus* (see Results). So, we made simulations of how the genetic variation would be affected by an change (decline) in population size. And this in an equivalent data set and time periods like we found in our studied *B. veteranus* populations.

Therefore, we created models of populations that have sample sizes equivalent to our *B. veteranus* samples. For those created populations we constructed a simple model of decline in population size of 28 generations starting from a stable population. We used the program BayeSSC, a modification of the simulation program Serial SimCoal (Excoffier et al., 2000; Anderson et al., 2005), for coalescent simulations of data collected at multiple time points. We changed the negative growth factor (as for a decline) range from 0%, 1%, 2% and 5% over 28 generations and the ancestral effective population sizes (N_{Ae}) from 15000, 10000, 5000, 1000, 500 to 100. Other parameters we used were: a mutations probability for microsatellite loci of 5×10^{-4} per generation (average mutation rate, Selkoe and Toonen, 2006) according to a stepwise mutation model and a limit of 40 allele states per locus. We performed 7000 simulations for each population size combination or 1000 simulations for each microsatellite loci. To evaluated the loss of genetic diversity between the different time points we averaged the H_E estimates across loci and determined the drop in H_E .

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