

Supplementary Legends

Table S1. Summary of microsatellite markers used in this study. Product size ranges filed with grey signify markers with allele-ranges not exceeding the limit for successful amplification in historical material.

Table S2. Genotypes and metadata of every individual included in the study.

Figure S1. Graphs showing genetic distance plotted against geographic distance in the (A) contemporary dataset and (B) combined dataset. Results of Mantels tests are summarized on top of each plot. Dependent variables are the same within each row and their distributions are illustrated in the histograms to the right. Independent variables are the same within each column and their distributions are illustrated in the histograms at the bottom.

Figure S2. A: Comparison of assumed number of populations (K) for the *Structure* analysis of the contemporary dataset. **B:** Comparison of assumed number of populations (K) for the *Structure* analysis of the combined dataset. **C:** Comparison of assumed number of populations (K) for the *Structure* analysis of the contemporary dataset using 4 loci.

Figure S3. Measures of genetic diversity of *P. alcon* populations in Denmark, the Netherlands and Belgium. Estimated from 13 microsatellite loci from the contemporary dataset and data from Vanden Broeck et al. (2017). The two datasets have 11 loci in common.

Supplementary Methods S1. Mapping the current and past distribution of the alcon blue butterfly and marsh gentian in Denmark