

Tiedekunta — Fakultet Matemaattis-luonnontieteellinen		Laitos — Institution Ekologian ja systematiikan laitos, populaatiobiologian osasto	
Tekijä — Författare Maaria Kankare			
Työn nimi — Arbetets titel Genetic variation between alternate-year cohorts of <i>Xestia tecta</i> (Lepidoptera: Noctuidae) in Lapland			
Oppiaine — Läroämne Morfologis-ekologinen eläintiede			
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Tiivistelmä — Referat Several species within the genus <i>Xestia</i> exhibit alternate-year flight; with different cohorts flying in alternate years. Typically one cohort is abundant and other one rare. The population dynamics and typical 2-year life cycle of the two cohorts indicate that they are more or less isolated in time. The common flight year is an even year in western Lapland and an odd year in eastern Lapland. Knowledge of the extent of isolation is important to fully understand the population dynamics and evolution of the alternate-year flight of these species. Quantifying the genetic mixing among the cohorts by ecological methods would be difficult and time-consuming. Molecular markers can be used to estimate gene flow and migration among and between the cohorts. The aim of this study was to quantify the amount of gene flow among and between the different cohorts of <i>Xestia tecta</i> , in the same geographical area, as well as between cohorts in different geographical areas. The methods used were allozyme electrophoresis and mitochondrial genome sequencing. Individuals from three different cohorts of <i>Xestia tecta</i> (Värriö common, Värriö rare and Olos common cohorts) were sampled for the genetic analysis. Thirtyfour enzyme loci were screened with several different buffer systems and running times. A preliminary survey revealed 6 enzyme loci which stained well but were monomorphic, and 6 polymorphic loci of which only 4 (PepA GPI, PGM, MPI) were consistently scorable. Molecular variation in <i>Xestia tecta</i> provides limited evidence of genetic differentiation and isolation between the even and odd year cohorts in eastern Finnish Lapland, and between the populations in western Lapland. F_{ST} values quantifying the degree of genetic differentiation between populations, calculated over all the loci, do not indicate any significant genetic differentiation between the different cohorts ($F_{ST} = 0.006$). The exact test of genic differentiation applied to the two loci with the lowest levels of polymorphism (PepA and GPI) does not indicate any significant differentiation ($p = 0.662, 0.571$). However, at the other two, more polymorphic loci (PGM and MPI), it indicates a highly significant (PGM, $p = 0.005$) and significant differentiation (MPI, $p = 0.034$) between the cohorts. In the mitochondrial DNA, all the individuals representing the three different cohorts were identical over about 550 bp sequence of the COI gene. In the control region, which is a non-coding and therefore relatively mutable region in the mtDNA, there are two differences between the cohorts. In the tRNAile gene, which is located between the AT-rich region and ND2 gene region, there is one difference between the cohorts. Two of the three observed differences occur in the homopolymers (T ₂₀ and A ₇) in the non-coding region. Four different haplotypes were found in the entire 3249 bp sequence of <i>Xestia tecta</i> mtDNA from the three different cohorts. The fact that the three sequence differences occur in mutational 'hot spots' provides strong evidence that all the mitochondria in the sample share a very recent common ancestor. One hypotheses to explain low levels of differentiation between the three cohorts of <i>Xestia tecta</i> may be that substantial gene flow occur between the cohorts. Gene flow between the Värriö rare and Olos common cohorts may occur as individuals from these cohorts reach maturity in the same year. Individuals from the Värriö common cohort fly in the intervening year. Gene flow between the Värriö common and Värriö rare or between Värriö common and Olos common cohorts is possible if some larvae have an exceptional three-year life cycle, maturing in the third summer of their life span and mating with adults with the usual two-year development time. A three-year life cycle has been observed in a laboratory rearing of <i>Xestia tecta</i> at University of Oulu, but it is not known whether it also occurs in nature. Another hypothesis is that the current <i>Xestia tecta</i> populations are isolated remnants of a much larger ancestral population, and that they have become isolated from each other so recently that there has not been enough time for substantial differentiation to develop, through genetic drift and mutation, particularly if effective population size is large. It has been suggested that the <i>Xestia</i> species living in the boreal forests survived the last glaciation in refugia in Beringea, and then expanded with coniferous trees to Scandinavia. Both the allozyme data and the mitochondrial data seem consistent with this recent common ancestor hypothesis. The overall low levels of genetic variation it has not been possible to establish conclusively the degree of genetic isolation between contemporary cohorts of <i>Xestia tecta</i> in Finland. Further molecular and ecological studies with more polymorphic markers will be necessary in order to fully explain the observed lack of genetic variation between different cohorts of <i>Xestia tecta</i> and to better quantify the extent of isolation among the cohorts.			
Avainsanat — Nyckelord <i>Xestia tecta</i> , alternate-year flight, cohorts, allozymes, mtDNA, gene flow, recent common ancestor			
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