Widespread species have been able to colonize many regions that make different demands on them. A species can manage these varying selection regimes by changing its traits in response to the environment (plasticity), or through changes in the frequency of gene variants in the population over generations (local adaptation).

Our study aims to determine how the widespread butterfly *Melanitis leda* has colonized its range and adapted to varying climates and habitats. This will shed light on how species may respond to climate and habitat change: will they have appropriate plastic responses, or are they able to adapt to the new environment?

Most climates are seasonal, so selection pressures vary over time in predictable ways. In response, most species have evolved mechanisms that use environmental cues to predict the coming season to develop a fitting appearance (adaptive seasonal phenotypic plasticity). Regions will differ in the optimal cues, because these environmental cues vary in their detectability and predictive value among regions. For example, temperate species often use changes in day length, while in tropical areas, the variation in day length is so small that species respond to other environmental cues. We have shown that in *M. leda*, temperature, host plant quality, and possibly humidity during larval development, determine the later seasonal colour form of the adult. Because the use of such cues tends to change slowly over evolutionary time, butterflies might produce wing colour patterns that do not fit the current season in some regions.

As a species colonizes different regions, it will also encounter repeated habitat contrasts, such as forest versus grassland. These different habitats will select for particular color patterns and life history traits such as body size. Some species show a wide variety of colour patterns within a population. Such polymorphic colour patterns may make it difficult for predators to search for prey: what colour pattern to look for? This benefit of looking different will be greater when the population density is higher. Therefore, such polymorphic species provide easy-to-measure traits that can be linked to genetic lineages, habitat, and the species' local abundance.

To reconstruct how and when *M. leda* spread across the range, estimate genetic connectivity among populations, and determine the nature of repeated adaptation to forest vs grassland habitats, we will sequence genomes of individuals from throughout the range (spanning Australia, Japan, Liberia, South Africa). To obtain complementary phenotype data, we will analyse photographs and perform specimen sampling from various regions and contrasting habitats. This will provide insight into geographic variation in wing color pattern traits, and the expression of phenotypic plasticity in the wild under various climates. To further study local adaptations, we will perform common garden experiments in which individuals from different populations will be tested simultaneously under the same conditions. Offspring of each individual will be split over two temperature- and host plant treatments, and each individual larva will be reared at a fixed temperature and fed a single plant species. In one such experiment, we will compare populations from three contrasting climate zones, and in two we will compare populations from different habitats within regions. We will measure traits such as egg-laying behavior, body size, larval coloration, and effects of temperature and host plant on wing color pattern. With these data, we will trace how the *M. leda* has spread while adapting to climates and habitats, which will help predict to what extent species can cope with rapid climate and habitat change.