



INSTITUTIONEN FÖR BIOLOGI OCH MILJÖVETENSKAP

# Evolutionary Genetics and Consequences of Inbreeding in Sand Lizards (*Lacerta agilis*)

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Akademisk avhandling för filosofie doktorsexamen i naturvetenskap, inriktning biologi, som med tillstånd från Naturvetenskapliga fakulteten kommer att offentligt försvaras fredagen den 28 maj 2021 kl. 10:00 i Hörsalen, Botanhuset, Institutionen för biologi och miljövetenskap, Carl Skottsbergs gata 22, Göteborg.  
Opponent är Professor Lukas Keller, Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland.

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## Abstract

Inbreeding is a well-known phenomenon in evolutionary and conservation biology. In the 19th century, Charles Darwin demonstrated the detrimental effects of inbreeding in plants, followed by over a century of extensive research including various animal and plant taxa. The effects of consanguineous matings are particularly pronounced in fitness-determining traits, such as life-history and sexually selected traits. Accordingly, a large body of literature has developed on traits that are directly associated with fitness, such as survival and reproductive output. Sexually selected traits have however received less attention. Due to its detrimental effects on fitness, inbreeding is often associated with the evolution of inbreeding avoidance mechanisms. This logical expectation is, however, not always met, with a number of studies reporting an absence of inbreeding avoidance in populations affected by inbreeding depression. The inconsistency in reports of inbreeding avoidance among studies is likely due to a balance between the costs and benefits of inbreeding, rendering predictions exceedingly difficult.

I used long-term data (collected over a decade) from a Swedish population of sand lizards (*Lacerta agilis*) to measure the effects of inbreeding on two key ontogenetic stages, embryonic development and first year post-hatching, survival, and a trait expressed in adult males, the intra-sexually selected green badge. The badge is developed laterally by males during the mating season, and varies in size and pigment saturation among individuals. This area of green nuptial coloration functions as a signal of fighting ability during male-male interactions, for access to females. I studied the mating pattern in the population, for signs of inbreeding avoidance. In addition, I evaluated the role of the major histocompatibility complex (MHC) as a cue of kinship. Inbreeding significantly affected hatching success, but not first year survival. Both structural and pigmentary components of the badge were affected by individual-level heterozygosity (size, pigment saturation, and brightness). Finally, no evidence of inbreeding avoidance was found, but parental pairs were more dissimilar at the MHC than expectations under random mating. Thus, parental pair similarity at the MHC does not appear to reliably reflect genome-wide similarity, in the Asketunnan population.

The effects of inbreeding in natural populations are difficult to measure. Traditionally, survival and reproductive success have been used to measure inbreeding depression. However, the results of these approaches can be confounded by various factors, such as environmental heterogeneity and parental effects. Moreover, the magnitude of inbreeding depression may vary according to the considered ontogenetic stage. Thus, an alternative would be to measure inbreeding depression using cellular function, which should reflect the accumulation of stress experienced by an individual over long periods of time. Telomeres offer this possibility, as their attrition rate is linked to somatic stress. Thus, one would expect inbred individuals to have short telomeres, relative to less inbred conspecifics. Surprisingly, no such effect was found in the study population. The only significant effect of inbreeding on telomere length that was found is a deviation from the mean maternal heterozygosity that is associated with shorter hatchling telomeres, suggesting stabilizing selection.

The final objective of the thesis was to estimate the additive genetic variance, and heritability, of badge size. The impetus for this work is the “lek paradox” theory, which predicts the erosion of additive genetic variance in fitness-determining traits, due to strong directional selection. In addition, the importance of genic capture for maintaining additive genetic variance in badge size was assessed by estimating additive genetic variance in body condition. The results of these analyses show a significant estimate of additive genetic variance in badge size, but not in body condition, which appears to be environmentally determined. This suggests that age and sex-dependent selection, combined with a complex genetic architecture that underlies multiple colour components, may explain the persistence of additive genetic variance in badge size in the sexually dichromatic sand lizard.