BACKGROUND: Sexual selection plays an essential role in shaping the evolution and adaptation of species to their natural environment, with individuals more proficient in securing mates achieving higher fitness.1,2,3 Previous research has been disproportionately focused on the evolution and maintenance of male secondary sexual traits in species with polygynous mating systems and pronounced sexual dimorphisms (SDs), where sexual selection plays an obvious role.4,5 This has led to a persistent gap in our understanding of how sexual selection operates within and between the sexes in species with little apparent dimorphism. Further, the evolution of SD is seen as a potential resolution of intra-locus sexual conflict (IASC)—wherein the sexes differ in their phenotypic optima for a shared trait—which may be especially strong in species with weak or subtle SDs6. It is still unclear whether IASC represents a transient or permanent constraint on the adaptive divergence of the sexes, with genetic constraints potentially preventing sex-specific optimal trait expression. The aim of my PhD thesis is to address the importance of IASC with the Alpine swift (*Tachymarptis melba*), a species with little apparent sexual dimorphism.

Alpine swifts are long-lived aerial insectivorous birds who provide biparental care to their offspring.7,8,9 Although they appear monomorphic to human observers, subtle dimorphisms exist in addition to within sex variation: the characteristic white throat patch is 1% larger in females than in males, while the fork is 7% longer in males than in females. Forked tails may confer an advantage during aerial courtship displays, and as such have been considered a classical example of sexual selection in swifts and swallows.10,11 The Swiss population I study has been monitored at the individual level for 20+ years, resulting in an outstanding database detailing reproductive success, morphology, pairing decisions, and relatedness (i.e., complex social pedigree required for quantitative genetic analyses12), which I will build upon (2022, 2023 field seasons).

OBJECTIVES: To understand the evolution of SD and IASC in both sexes, I will investigate the relative contributions of environment and genetics and whether these effects and their fitness consequences are sex specific. My aims, corresponding to each chapter of my PhD thesis, are to: 1) quantify the existing subtle SD by assessing the sex-specific allometric slopes13 of morphometric (body mass, skeletal size, wing, tail, and fork length) and coloration (breast patch melanization and achromatic throat patch size) traits; 2) investigate the fitness consequences of variation and sexual conflict over body mass; 3) assess the presence of IASC over fork depth; and 4) study the adaptive advantages of divorce (vs. mate retention) and of assortative (vs. non- assortative) pairing decisions in both sexes.

The analyses for my first chapter are well underway and will be completed after additional molecular sexing of swifts,14 as ~200 individuals to be considered in that chapter are currently of unknown sex. My second chapter is completed and has been submitted to the Journal of Animal Ecology, and my third chapter is well underway with most analyses completed.

METHODS: To investigate the evolution of SD and IASC as well as the relative contributions of environmental and genetic effects, I will use state of the art quantitative genetic analyses. These multivariate mixed effects models linked to a pedigree (animal models12) will allow for statistical inferences about the additive genetic variance (heritability) of traits expressed in both sexes as well as the genetic correlation(s) between the sexes and between traits. To assess the fitness consequences of these effects and whether they are sex-specific, selection models (linear (LMM) and generalized (GLMM) linear mixed effects models) will be fit for a series of fitness proxies (yearly and lifetime reproductive success, overwinter survival). In all models, individual identity and year will be included as random effects to account for repeated measures and non-independence between years, respectively.

SIGNIFICANCE: This study will shed new light on the evolution of SD and IASC as well as the genetic basis of pairing decisions in both sexes of a wild population. Given the importance of sexual selection in shaping population dynamics, and the relative scarcity of long-term studies able to answer such questions using quantitative genetics, this study fills an important gap in our understanding of how sexual selection operates within and between the sexes in nature.

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