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This document is part of a collection that serves two purposes. First it is a public archive for data and documents resulting from evolutionary, ecological, and behavioral research conducted by the Ketterson-Nolan research group. The focus of the research is an abundant North American songbird, the dark-eyed junco, *Junco hyemalis*, and the primary sources of support have been the National Science Foundation and Indiana University. The research was conducted in collaboration with numerous colleagues and students, and the objective of this site is to preserve not only the published products of the research, but also to document the organization and people that led to the published findings. Second it is a repository for the works of Val Nolan Jr., who studied songbirds in addition to the junco: in particular the prairie warbler, *Dendroica discolor*. This site was originally compiled and organized by Eric Snajdr, Nicole Gerlach, and Ellen Ketterson.

### Context Statement

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# Flexibility in mate choice for MHC: a comparison of two ecologically distinct populations of Dark-eyed Juncos

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## Introduction

The major histocompatibility complex (MHC) is a gene family involved in immune function. Alleles code for peptides that detect pathogens, and greater variability allows resistance to a wider range of pathogens. Hypotheses for why animals may base their choice of mates on MHC include inbreeding avoidance and compatible genotypes. We evaluated mate choice in two populations of a songbird species, and tested whether an isolated population with few migrants employs a different mate choice strategy than a migratory, outbred population.

During the 1980s, the Dark-eyed Junco (*Junco hyemalis*) colonized a novel urban environment outside of the species' normal breeding range at the University of California San Diego (UCSD) campus (Fig. 1). This population has undergone changes in body size, plumage and behavior, and has ceased migrating. Population size is small (fewer than 100 breeding pairs) and genetic variation is decreased (Rasner et al 2004). We compared mating patterns with respect to MHC at UCSD to a population located in the ancestral breeding range at Laguna Mountain. We predicted that UCSD females would be more likely to avoid mating with MHC-similar males than Laguna Mountain females.



## Methods

### Bird capture and monitoring:

- 2006 and 2007 breeding seasons, 39 pairs at Laguna Mtn, 64 at UCSD
- Monitored nests, sampled nestlings

### MHC sequencing:

- Species-specific MHC Class IIB loci (JUHY1 and JUHY2) (Whittaker et al submitted)
- Direct sequencing
- Allele phases resolved with PHASE 2.1 (Stephens & Donnelly 2003)
- Amino acid distances between alleles calculated with PAUP\*4.0
- JUHY1 did not vary significantly between populations, no patterns observed with respect to mate choice; only JUHY2 reported here

### Paternity and relatedness testing:

- 8 microsatellite loci
- Paternity assigned with CERVUS 3.0
- Pairwise relatedness coefficients between adult males and females calculated with KINSHIP

### Statistics:

- Distances between social pairs: added together four amino acid distances (between female genotype AB and male genotype ab, distances are Aa, Ab, Ba, and Bb)
- All potential male mates ranked with respect to distance from each female: scale from 0 to 1, with 1 being the most different male
- SPSS 16.0 for statistical tests; significance tests reported here for ANOVA are one-tailed because hypotheses were directional

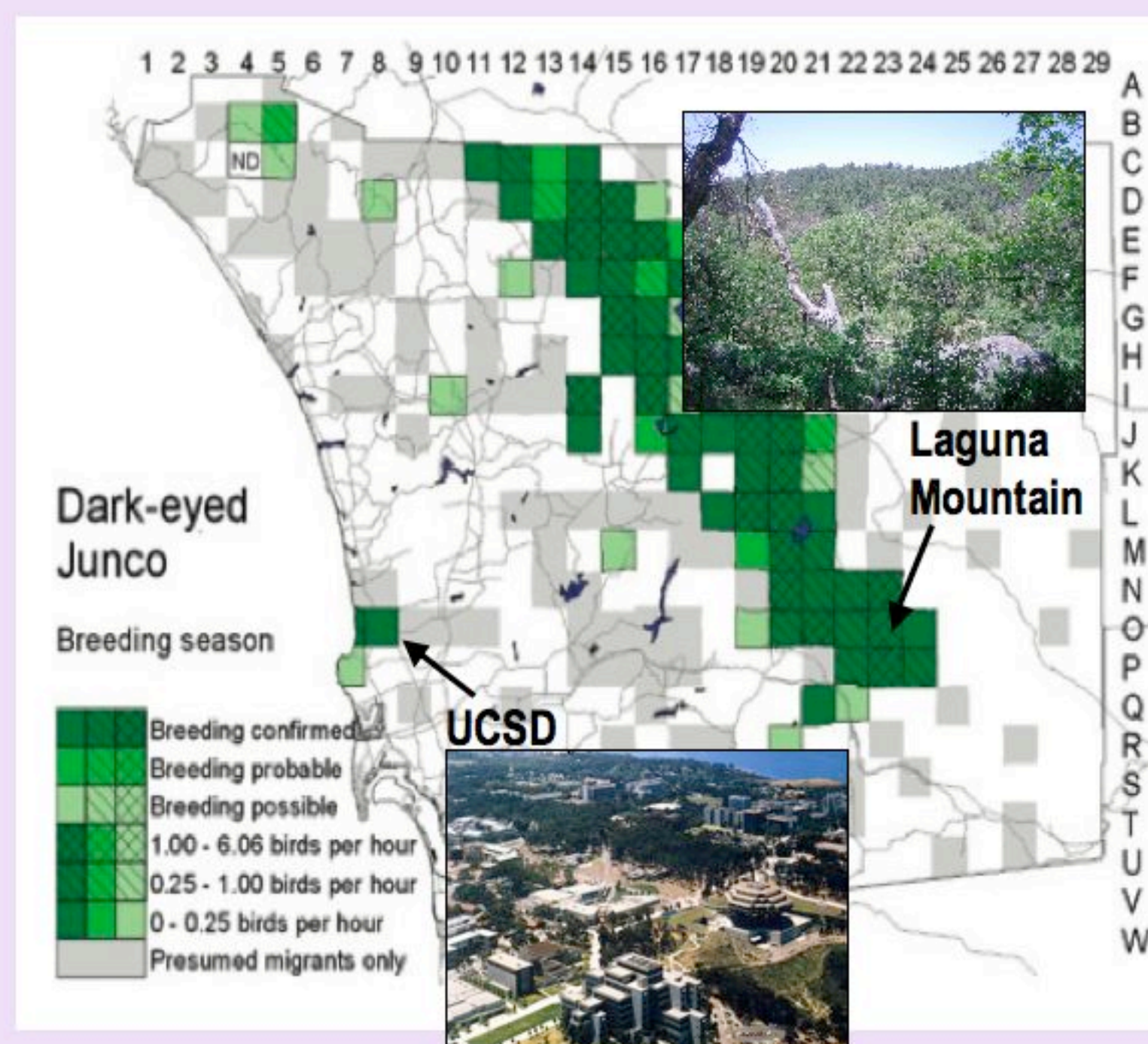


Figure 1. Map of junco breeding range and study sites in San Diego County (adapted from Unitt 2005).

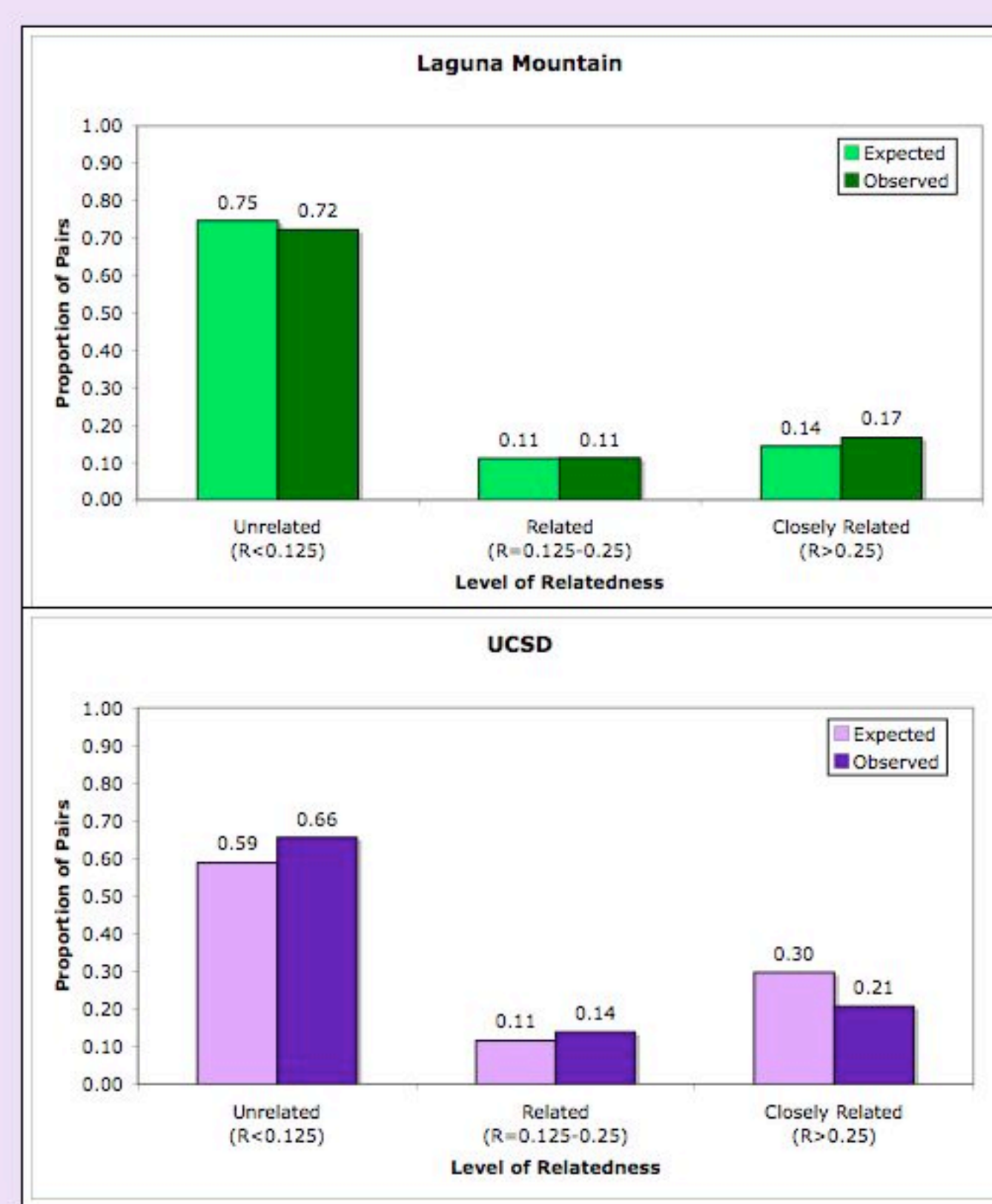


Figure 2. Observed and expected proportion of pairs that were unrelated, related, and closely related at Laguna Mountain and UCSD.

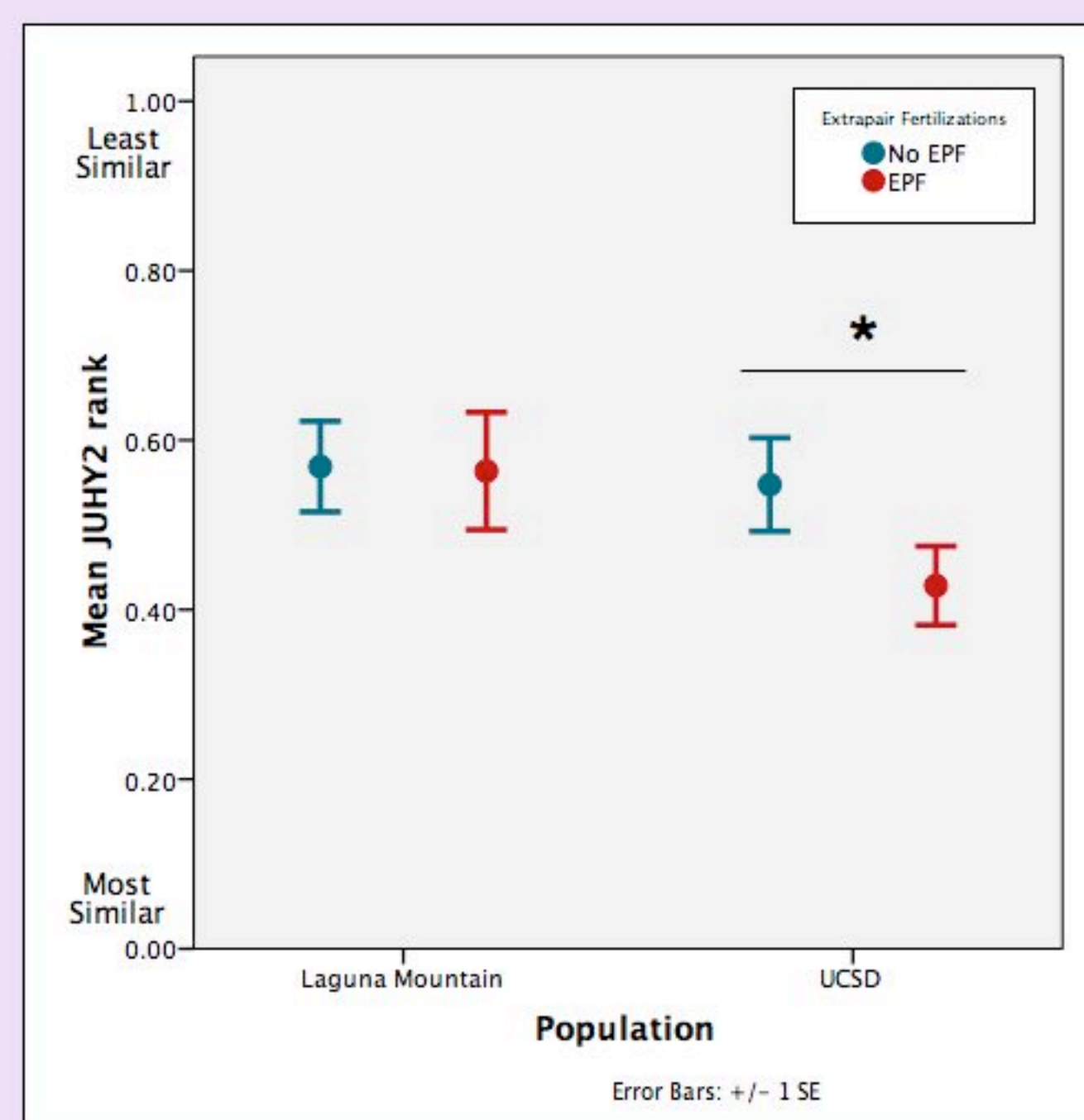


Figure 3. Mean rank of male social mates relative to other possible mates in pairs with and without extra-pair fertilizations in both populations. (ANOVA,  $p=0.05$ )

## References

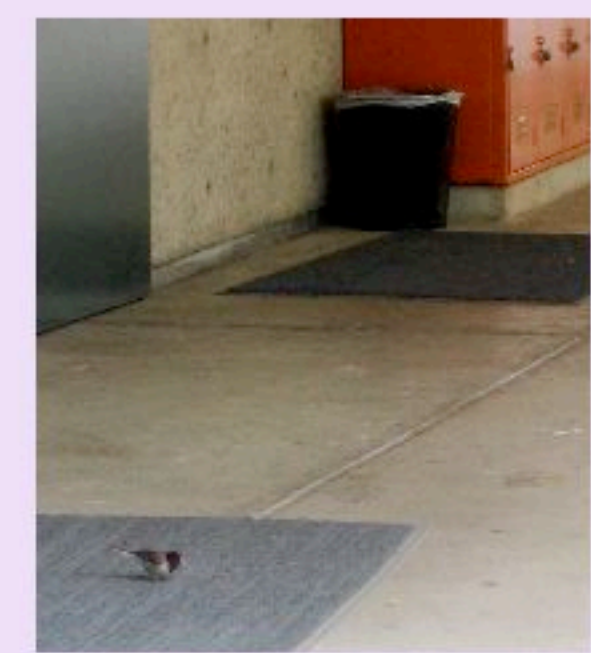
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## Results

UCSD pairs were significantly more MHC-similar to each other than pairs at Laguna Mountain (ANOVA,  $p=0.0015$ ). Overall, **all individuals at UCSD were more MHC-similar to each other**. Furthermore, **UCSD adults were more closely related to each other** (microsats) than Laguna Mountain adults.

**MHC distances between social mates at UCSD were significantly different from the set of all possible pairwise distances** (ANOVA,  $p=0.04$ ), while mate choice at Laguna Mountain did not differ from random ( $p=0.46$ ) (not shown). **UCSD adults avoided close relatives as social mates (chi-square,  $p=0.07$ )**, while mate choice with respect to relatedness did not differ from random at Laguna Mountain (Fig. 2).

Extra-pair paternity rates were as high as 40% of all offspring in both populations (Atwell et al in prep). **Pairs with EPFs were more MHC-similar than pairs with no EPFs ( $p=0.05$ ) – but only at UCSD** (Fig. 3). At Laguna Mountain, there was no difference in MHC distance between pairs with and without EPFs ( $p=0.48$ ).



## Discussion

In the migratory, outbreeding Laguna Mountain population, we find no evidence for MHC-based mate choice. Other factors, such as territory quality or morphological characteristics, may play a greater role. However, in the sedentary, isolated UCSD population, which has a greater proportion of close relatives, the juncos appear to be making mating decisions on the basis of MHC similarity. Females with mates who are more similar at MHC loci are more likely to engage in extra-pair copulations.

**These data suggest that birds may be able to adjust their mate choice behavior in response to the genetic environment.** In a population where inbreeding is a higher risk, genetic similarity becomes an important factor in choosing a mate. Interestingly, traits that are typically preferred by female juncos such as tail white and high serum testosterone levels are reduced in the UCSD population.

Future research will focus on 1) additional population comparisons and understanding the "inbreeding threshold" that leads to this switch in mate choice behavior and 2) the mechanisms by which birds may evaluate MHC genotype, primarily olfaction.

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