Urbanization alters existing environmental conditions, resulting in a change in infection prevalence. The infection prevalence is calculated as the number of individuals infected divided by the total sample size. Haemoproteus and Plasmodium have different distributions in urban environments and nearby migratory populations of dark-eyed juncos (Junco hyemalis) were studied.

Two genera of Haemosporidian parasites (Haemoproteus and Plasmodium) infecting residential populations established in urban environments and nearby migratory populations of dark-eyed juncos (Junco hyemalis) were studied. This study aimed to determine: (1) whether there is a difference in infection prevalence between residential and migratory juncos, (2) the relative evolutionary relationship between the parasites and their avian hosts, and (3) the relative evolutionary history of urban and montane parasites.

Methods

Sample Collection:
- Whole blood samples were collected from juncos across southern California.
- DNA was extracted from the whole blood samples using the Wizard® SV Genomic DNA Purification System.

Parasite Detection and Sequencing
- Haemoproteus and Plasmodium spp. were detected using a nested PCR targeting the mitochondrial cytochrome b gene.
- Sequences were determined using Sanger sequencing and compared against the NCBI database to determine the lineage of each parasite and other susceptible avian species. These lineages have been found to infect avian species and their evolution is based on the mitochondrial cytochrome b gene. Infection prevalence was calculated as the number of individuals infected divided by the total sample size.

Results

Figure 1: Map of collection sites. Red pins are residential sites (University of California campuses). Blue pin is a migratory site (Angeles National Forest). Map of collection sites. Red pins are residential sites (University of California campuses). Blue pin is a migratory site (Angeles National Forest).

Phylogeny
- Parasite Phylogeny: Cladogram was constructed in MrBayes version 3.7.2 using parameters determined by MrModeltest2. Phylogenies were generated using 1 cold chain and 3 heated chains and sampled every 100 generations over 5 million generations. The initial 25% of phylogenies were discarded as burn-in. Remaining trees were used to construct a majority consensus tree. Posterior probabilities (p.p.) were calculated, representing the conditional probability of each branch occurring.
- Avian Phylogeny: The list of susceptible avian species the parasites have been found to infect was used to generate an avian phylogenetic tree via BirdTree.org.
- Tanglegram: Constructed using both the parasite and avian phylogenetic tree. Associations were drawn between the two trees where each line represents an infection of an avian species by a parasitic lineage.

Figure 2: Infection prevalence of Plasmodium and Haemoproteus at urban and montane sites. Haemosporidian, and more specifically, Haemoproteus, infection prevalence was significantly higher in migratory populations than in residential populations (p < .001).

Figure 3: Tanglegram of relative evolutionary relationship between parasites found in juncos and other susceptible avian hosts.

Figure 4: Cladogram of relative evolutionary history of haemosporidians found in juncos. Urban lineages are in blue text. Montane lineages are in red text. Lineages found at both sites are in purple text. Reference sequences are in italicized black text.

Conclusions

Urbanization alters existing environmental conditions, resulting in a difference in parasite distribution. The results from the tanglegram show that the lineages Haemoproteus sp. H.AKO8, JUNHYE004, and JUNHYE12 have only been reported in the family Passerellidae, suggesting a coevolutionary history in this host-parasite relationship (Figure 3).

Movement of juncos into urban areas may have had subsequent effect on the parasites infecting them, resulting in urban lineages of parasites branching off from montane ones. The parasite cladogram shows support for resident-specific lineages of Plasmodium sp. JUNHYE003 and relictum MDG-P11 (p.p. 96%) that are diversifying from migratory lineages.

Urbanization has an impact on parasite distribution and diversification.

Acknowledgements: Thank you to the Yeh Lab for their contributions to this project.

References