**Tables and Figures for:**

Comparative Urban Evolution in Two Closely Related Desert Songbirds, Northern Cardinals and Pyrrhuloxia

**Authors**

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**Tables and Figures**

**Figure 1:** A. Sampling locations across the state of Arizona, with northern cardinals in purple and pyrrhuloxia in green. The sample that was ( B. PCA of all genomes retained after filtering for potential close relatives (Northern cardinals: urban N=6, rural N=6; Pyrrhuloxia: urban N=6; rural N=5). C. Admixture plot ordered by species and then by ecoregion.

A close-up of a map

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**Figure 2:** PCoA dissimilarity plots of semantic similarity for FDR-corrected overrepresented GO terms in northern cardinals for A. the full list of candidate genes identified by either FST or RAiSD analyses, B. only genes identified by FST, and C. only genes identified by RAiSD. Terms in these plots cluster by meaning, but the units of the axes are meaningless and are therefore not included.

A diagram of a cell organ

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**Figure 3:** PCoA dissimilarity plots of semantic similarity for FDR-corrected overrepresented GO terms in pyrrhuloxia for A. genes identified by FST and B. genes identified by RAiSD. Analyses of the full list of candidate genes identified by either FST or RAiSD analyses revealed no significantly overrepresented GO terms. Terms in these plots cluster by meaning, but the units of the axes are meaningless and are therefore not included.

A diagram of a diagram

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**Figure 4.** Evidence of parallel evolution across cardinals. A. Venn diagrams of genes identified in either cardinal species by FST or RAiSD analyses. B. Signal of selection of the same region on chromosome 2 in pyrrhuloxia (top) and northern cardinals (bottom). In these plots, only signals from urban samples in the absence of a signal from rural samples were considered significant. To visualize this, the rural statistics are plotted over top of the urban statistics, and only regions where the urban datapoints are visible were significant. Horizontal lines show the 1% cutoff of significance. The full genome plot can be found in Figure S3. C. FST plots comparing urban and rural samples in pyrrhuloxia (top) and northern cardinals (bottom). The annotated genes were the 9 genes identified in both cardinal species that also were associated with a significant GO term in both species (Table S1).

**A diagram of different types of numbers

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A graph of different colored lines

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A close-up of a graph

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**Figure 5.** Evidence of parallel evolution across cardinals and other avian taxa. B. Venn diagrams of genes identified in northern cardinals, pyrrhuloxia, burrowing owls, and great tits, and C. PCoA dissimilarity plots of semantic similarity for FDR-corrected overrepresented GO terms of the list of genes found to be present in one of either cardinal species and at least one of the other two species (burrowing owls or great tits). **A diagram of the number of birds

AI-generated content may be incorrect.**Terms in this plot cluster by meaning, but the units of the axes are meaningless and are therefore not included.

**Tables**

Table 1: Sample Information.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample** | **Species** | **Population** | **Source** |
| NOCA\_003 | Northern cardinal | Urban | Field |
| NOCA\_004 | Northern cardinal | Urban | Field |
| NOCA\_006 | Northern cardinal | Urban | Field |
| NOCA\_008 | Northern cardinal | Urban | Field |
| NOCA\_012 | Northern cardinal | Urban | Field |
| NOCA\_013 | Northern cardinal | Urban | Field |
| PYRR\_003 | Pyrrhuloxia | Urban | Field |
| PYRR\_004 | Pyrrhuloxia | Urban | Field |
| PYRR\_006 | Pyrrhuloxia | Urban | Field |
| PYRR\_007 | Pyrrhuloxia | Urban | Field |
| PYRR\_009 | Pyrrhuloxia | Urban | Field |
| PYRR\_012 | Pyrrhuloxia | Urban | Field |
| UWBM\_100619 | Northern cardinal | Rural | University of Washington Burke Museum |
| UWBM\_100620 | Northern cardinal | Rural | University of Washington Burke Museum |
| UWBM\_100621 | Northern cardinal | Rural | University of Washington Burke Museum |
| UWBM\_103345 | Northern cardinal | Rural | University of Washington Burke Museum |
| UWBM\_103346 | Pyrrhuloxia | Rural | University of Washington Burke Museum |
| UWBM\_77548 | Pyrrhuloxia | Rural | University of Washington Burke Museum |
| UWBM\_77718 | Pyrrhuloxia | Rural | University of Washington Burke Museum |
| UWBM\_77780 | Pyrrhuloxia | Rural | University of Washington Burke Museum |
| UWBM\_77781 | Pyrrhuloxia | Rural | University of Washington Burke Museum |
| UWBM\_77856 | Northern cardinal | Rural | University of Washington Burke Museum |
| UWBM\_77978 | Northern cardinal | Rural | University of Washington Burke Museum |
| MSB\_25201 | Pyrrhuloxia | Rural | Museum of Southwestern Biology |

**Supplementary Tables and Figures**

**Figure S1:** Population genomics of all samples. ADMIXTURE plot (left) and PCA (right) show unusual patterns of clustering between UWBM77548 and UWBM77718 that are consistent with these two individuals being close relatives. They were both sampled from the same location.

A screen shot of a graph

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**Figure S2:** Comparison of log2 fold change in representation of genes between species in overrepresented GO terms across all analyses in both species.



**Figure S3.** Signals of selection from RAiSD in pyrrhuloxia (top, green) and northern cardinals (bottom, purple). In these plots, only signals from urban samples in the absence of a signal from rural samples were considered significant. To visualize this, the rural statistics are plotted over top of the urban statistics, and only regions where the urban datapoints are visible were significant. Horizontal lines show the 1% cutoff of significance.

PyrrhuloxiaA green graph with black text

AI-generated content may be incorrect.Northern cardinals

A graph of a number of chromatography

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**Table S1**: Candidate genes associated with significantly overrepresented GO terms in either northern cardinals or pyrrhuloxia.

**Table S2**: All candidate genes.