

Movement and genomic methods reveal mechanisms promoting connectivity in a declining shorebird: the lesser yellowlegs

Supplemental material

Supplemental Table S1. Summary of COLONY v2.0.6.8 analysis results showing familial relationships among samples of lesser yellowlegs. JBER is Joint Base Elmendorf-Richardson.

Individual 1 (Sample location)	Individual 2 (Sample location)	Individual 3 (Sample location)	relationship
ANC31913 (Anchorage)	JBER74413 (JBER)		full-sibling
JBER74413 (Anchorage)	JBER31985 (JBER)		Parent (Ind1)-offspring (Ind2)
JBER74423 (JBER)	JBER74424 (JBER)	ANC33864 (Anchorage)	Parent (Ind1-2)-offspring (Ind3)
MIN82904 (Mingan)	KAN31951 (Kanuti)		Parent (Ind1)-offspring (Ind2)
JB13282m (James Bay)	JB68233m (James Bay)		full-sibling
JB24132 (James Bay)	JB24135 (James Bay)		full-sibling

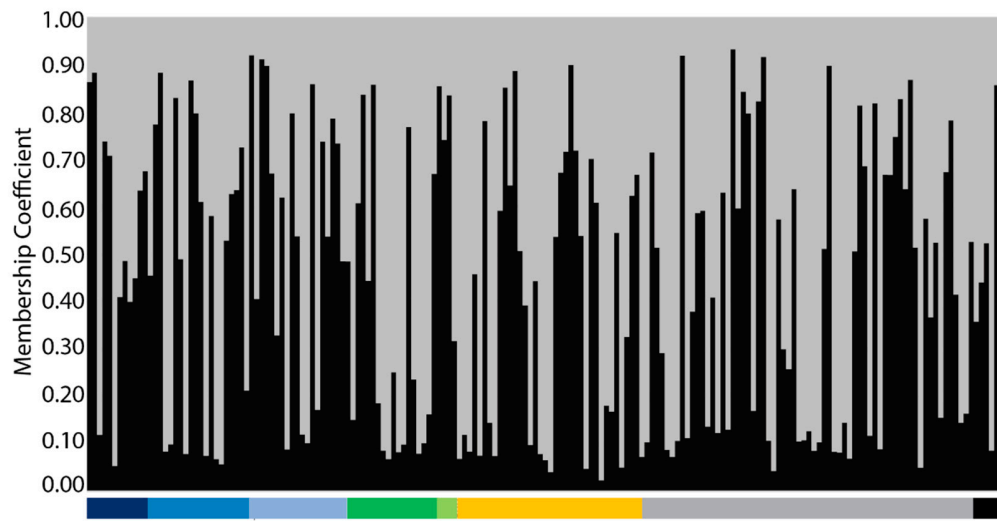
Table S2. Pairwise estimates of population genetic divergence for lesser yellowlegs at mitochondrial DNA (mtDNA) control region: mtDNA F_{ST} is below the diagonal and Φ_{ST} is above. Significant comparisons are in bold text. JBER is Joint Base Elmendorf-Richardson.

Location	Kanuti	Anchorage	JBER	Yellowknife	Alberta	Churchill	James Bay	Mingan
Kanuti	–	0.009	0.013	-0.012	0.049	0.006	0.018	-0.029
Anchorage	0.004	–	0.018	0.000	0.096	0.003	0.004	0.084
JBER	-0.006	0.008	–	0.024	-0.064	0.052	0.065	-0.041
Yellowknife	-0.034	-0.009	0.001	–	0.075	0.002	-0.006	0.000
Alberta	-0.008	0.129	-0.062	0.035	–	0.131	0.127	-0.119
Churchill	0.039	-0.017	-0.049	0.017	0.221	–	-0.003	0.094
James Bay	0.011	-0.013	0.035	-0.006	0.147	-0.007	–	0.066
Mingan	-0.073	0.067	-0.028	-0.038	-0.175	0.131	0.059	–

Table S3. Pairwise estimates of population genetic divergence (Φ_{ST}) for lesser yellowlegs at double digest restriction-site associated DNA (ddRAD) loci: estimates based on Z-linked loci are below the diagonal and autosomal loci are above. JBER is Joint Base Elmendorf-Richardson.

Location	Kanuti	Anchorage	JBER	Yellowknife	Alberta	Churchill	James Bay	Mingan
Kanuti	–	0.003	0.004	0.000	0.006	0.002	0.001	-0.006
Anchorage	0.004	–	0.000	0.002	0.007	0.002	0.002	-0.002
JBER	0.006	-0.007	–	0.003	0.006	0.002	0.003	0.000
Yellowknife	0.005	-0.002	-0.001	–	0.006	0.001	0.000	-0.003
Alberta	-0.008	0.007	0.003	0.005	–	0.007	0.008	0.003
Churchill	0.005	0.003	0.001	0.002	-0.003	–	0.001	-0.002
James Bay	0.004	-0.001	0.000	0.000	0.003	0.001	–	-0.002
Mingan	-0.012	0.000	0.004	-0.009	-0.016	0.005	0.003	–

A.



B.

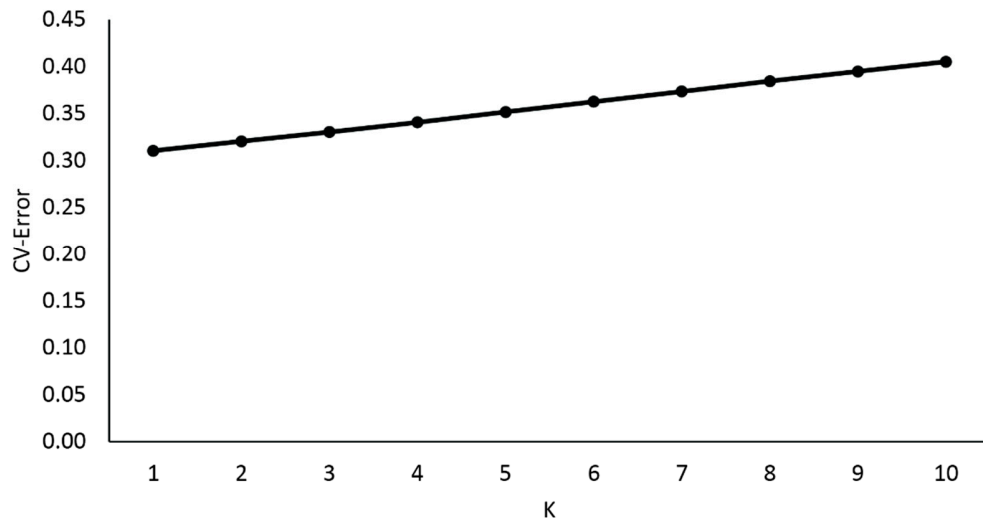


Figure S1. Average membership coefficients of lesser yellowlegs individuals from sampled sites into two clusters inferred from 5,816 autosomal double digest restriction-site associated DNA (ddRAD) loci. A plot of cross-validation (CV) error estimate for each K is shown. Colors correspond to sample locations indicated in Figure 1.

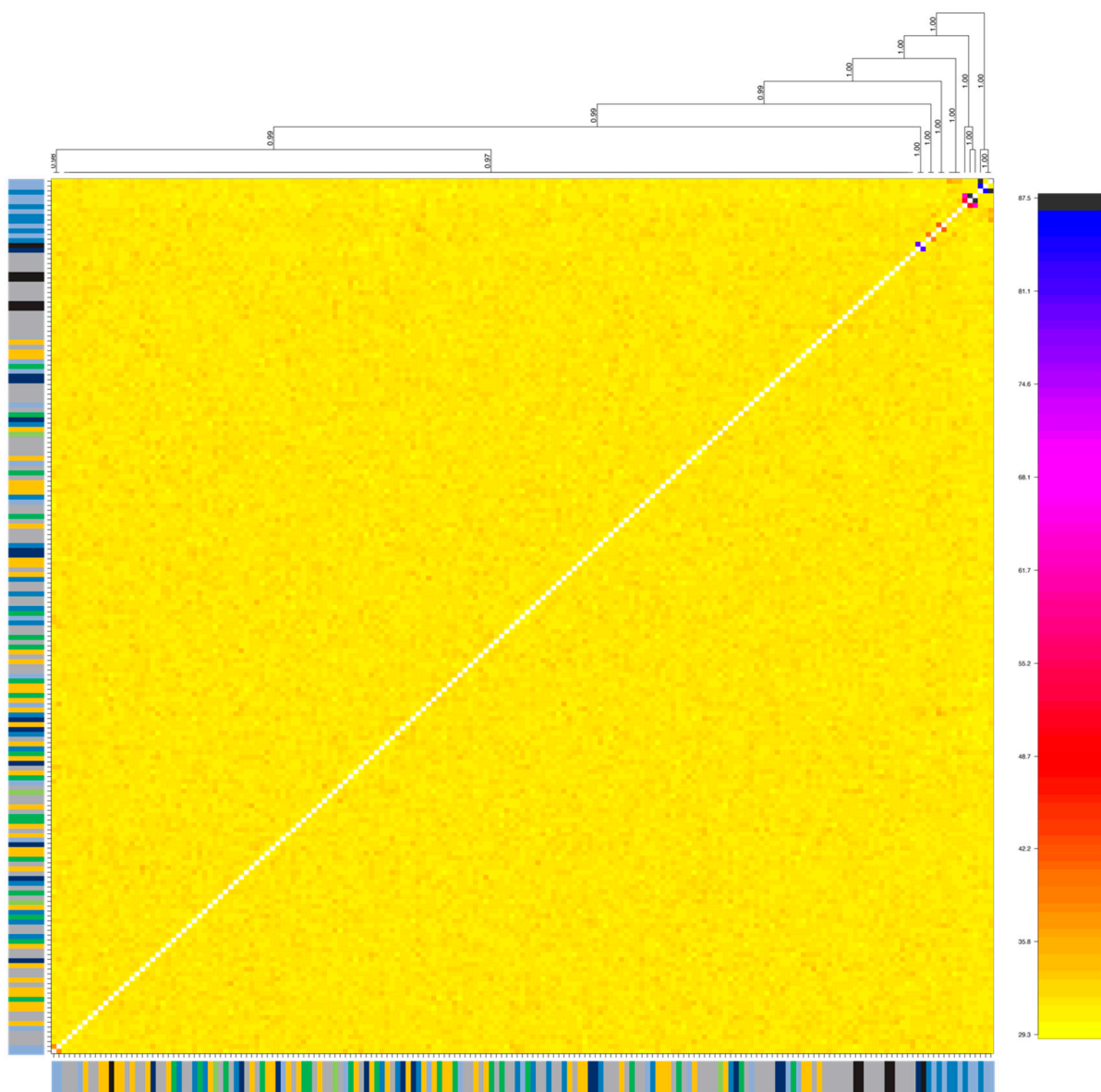


Figure S2. FineRADstructure co-ancestry matrix indicating pairwise genetic similarity between individual lesser yellowlegs. Inferred populations are indicated by clustering in the dendrogram. Colors correspond to sample locations indicated in Figure 1.

A



B

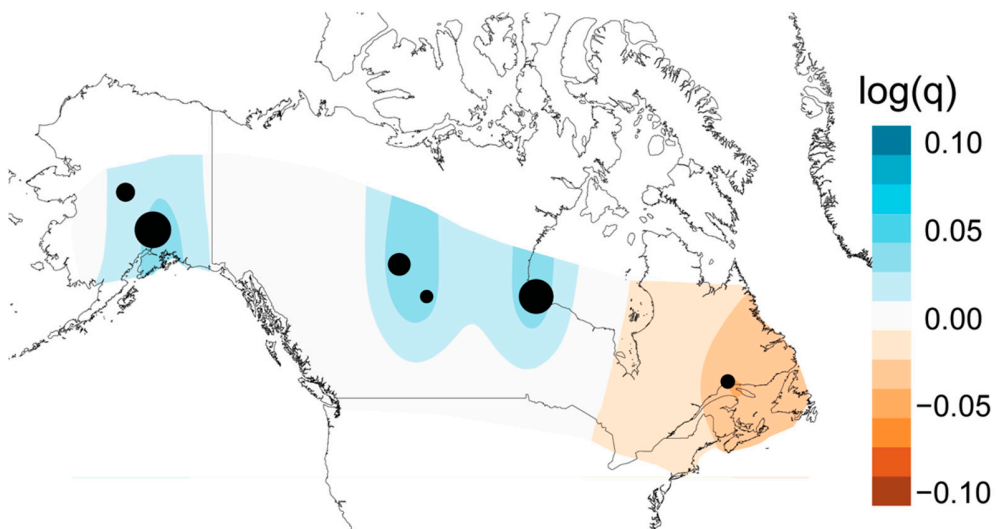


Figure S3. The estimated effective gene flow (A) and genetic diversity (B) surfaces between sites (black circles) sampled for lesser yellowlegs. White areas indicate gene flow rates consistent with isolation by distance expectations whereas shaded areas have dispersal rates that are higher (blue, corridors) or lower (orange, barriers) than expected under isolation-by-distance.