**Supplemental Figures**

Figure S1: Maximum likelihood ddRAD phylogenies using alignments with varying proportions of missing data for range-wide *R. clamitans* samples and all members of the *Aquarana* clade. Branch lengths are proportional to expected substitutions per site. Nodes with less than 50% bootstrap support are collapsed.

Figure S2: ddRAD species tree estimated using Tetrad. Branch lengths are arbitrary. Nodes with less than 50% bootstrap support are collapsed.

Figure S3: Maximum likelihood mtDNA phylogeny. Branch lengths are proportional to expected substitutions per site. Nodes with less than 50% bootstrap support are collapsed.

Figure S4. LEA and tess3R cross-entropy scores for different numbers of ancestral populations across different datasets. Red point indicates K=3 for *R. clamitans* + *R. okaloosae* or K=2 for *R. clamitans* alone.

Figure S5. LEA and tess3R ancestry coefficient bar plots for different numbers of genetic clusters (K) with different filtering thresholds for missing data when analyzing only *Rana clamitans*.

Figure S6. LEA and tess3R ancestry coefficient bar plots for different numbers of genetic clusters (K) with different filtering thresholds for missing data when analyzing *Rana clamitans* and *R. okaloosae.*

Figure S7. LEA sensitivity analyses with different snmf regularization parameter (alpha) values. Top row shows cross-entropy scores for different numbers of ancestral populations (K), bottom row shows ancestry coefficient bar plots for different values of K. Dataset analyzed contained *Rana clamitans* and *R. okaloosae* samples with <50% missing genotypes per SNP.

Figure S8. A) Ancestry coefficients from ddRAD genomic data using LEA and tess3R suggest the highest support for K=3 clusters when *Rana okaloosae* and *R. clamitans* are included in the analyses. Results are generally concordant between LEA and tess3R. However, LEA identifies an admixed, putative hybrid *R. okaloosae* sample (RokaC\_FL). B) Interpolated ancestry coefficients for *R. clamitans* and *R. okaloosae*. *Rana okaloosae* is identified as a distinct genetic cluster (pink). Within *R. clamitans,* ancestry appears clinal from southwest (orange) to northeast (green).

Figure S9. TreeMix results for three datasets: *Aquarana*, *R. okaloosae* plus four *R. clamitans* clades, and *R. okaloosae* plus four *R. clamitans* genetic clusters (see Table S3 for sampling details). Within each column, rows represent separate sets of analyses using 100 random, unlinked SNP subsets with a different maximum allowed number of migration edges. Phylogenies match the ML ddRAD topology, with admixture edges represented by colored lines. Note that colors are only consistent within columns. Bar plots show the proportion of random SNP subsets that support each migration edge. Boxplots show the distribution of inferred migration weights for each migration edge. Only migration edges that were supported by >10% of random SNP subsets are displayed.