## Supplementary Information

Table S1: Linear regression equations for scaled root mean square error (SRMSE) for each parameter in which breaking lineages into low-divergence and high-divergence groups improved the regression model, summarizing how accuracy declines with diminished sample sizes. Parameters are effective population size (*ν1* and *ν2*), time since divergence (*T*), and *Θ* (defined as 4*Nrefμ*, where *Nref* is ancestral population size and *μ* is mutation rate per generation). Note that these are based on SMRSE values (to enable among-lineage comparisons; Table 3). Thus, *y* in the regression equation *y = mx + b* is SMRSE for that particular demographic variable (*m* is slope, *x* is *N*, and *b* is the *y* intercept).

|  |  |  |  |
| --- | --- | --- | --- |
| **SMRSE for variable** | **Regression equation (y = mx + b)** | **r2** | ***P*** |
| *ν1* (low-div group) | y = -0.04467 \* *N* + 0.40622 | 0.304 | 0.0052 |
| *ν1* (high-div group) | y = -0.30251 \* *N* + 1.68585 | 0.189 | 0.0299 |
| *ν2* (low-div group) | y = -0.10533 \* *N* + 0.69169 | 0.355 | 0.0021 |
| *ν2* (high-div group) | y = -0.21646 \* *N* + 1.25166 | 0.352 | 0.0018 |
| *T* (low-div group) | y = -0.04739 \* *N* + 0.40888 | 0.395 | 0.0010 |
| *T* (high-div group) | y = -0.15276 \* *N* + 0.99239 | 0.328 | 0.0028 |
| *Θ* (low-div group) | y = -0.02843 \* *N* + 0.26395 | 0.202 | 0.0275 |
| *Θ* (high-div group) | y = -0.04878 \* *N* + 0.43241 | 0.303 | 0.0043 |

Table S2. Genomes used for calculation of substitution rates and time since most recent common ancestor (TMRCA, from Claramunt & Cracraft, 2015), substitution rate, and generation time for each lineage in which demographic parameters are translated into biologically meaningful values in this paper.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Genome | GenBank accession number | TMRCA (my) | Substitution rate (subs/site/gen) | Generation time (yrs) | Sources |
|  |  |  |  |  |  |  |
| ***Tringa brevipes /T. incana***  | *Charadrius vociferus* | GCA\_000708025.2 | 53.5153 | 2.453 x 10-9 | 4.88 | [(Gill, McCaffery, & Tomkovich, 2002)](https://paperpile.com/c/lPzM9a/2zsk) |
|  |  |  |  |  |  |  |
| ***Pinicola enucleator* subspp.** | *Zonotrichia albicollis* | GCA\_000385455.1 | 21.7098 | 1.577 x 10-9 | 2 | [(Adkisson, 1999)](https://paperpile.com/c/lPzM9a/d0Fd) |
| ***Pica pica/Pica hudsonia*** | *Taeniopygia guttata* | GCA\_000151805.2 | 41.5132 | 1.304 x 10-9 | 2.5 | [(Trost, 1999)](https://paperpile.com/c/lPzM9a/McqJ) |

## Supplementary Information figures



Figure S1: Estimates of *ν1* (effective size of population 1) at varying sample sizes in eight lineages (vertical axis is *ν1*, and horizontal axis is sample size as number of individuals). Parameters are raw, unconverted values directly from δaδi analyses.



Figure S2**:** Estimates of *ν2* (effective size of population 2) at varying sample sizes in eight lineages (vertical axis is *ν2*, and horizontal axis is sample size as number of individuals). Parameters are raw, unconverted values directly from δaδi analyses.



Figure S3:Estimates of *m* (migration or gene flow)at varying sample sizes in eight lineages (vertical axis is *m*, and horizontal axis is sample size as number of individuals). Parameters are raw, unconverted values directly from δaδi analyses.



Figure S4: Estimates of *T* (time since divergence) at varying sample sizes in eight lineages (vertical axis is *T*, and horizontal axis is sample size as number of individuals). Parameters are raw, unconverted values directly from δaδi analyses.



Figure S5: Estimates of *Θ* (4*Nrefμ*) at varying sample sizes in eight lineages (vertical axis is *Θ*, and horizontal axis is sample size as number of individuals)**.** Parameters are raw, unconverted values directly from δaδi analyses.

**Figure S6.** Parameter-specific scaled root mean square error (SRMSE) values plotted against sample size (*N*). Note that vertical scales vary in each panel.

 **Low-divergence lineages High-divergence lineages**

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**Figure S6, continued.** Parameter-specific scaled root mean square error (SRMSE) values plotted against sample size (*N*). Note that vertical scales vary in each panel.

**Low-divergence lineages High-divergence lineages**

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