

**Table S1. Influence of effective population size ( $N_e$ ) on species identification success per method compared**

| <b>Data set</b>              | <b>NJ (liberal)</b> | <b>NJ (strict)</b> | <b>PAR (liberal)</b> | <b>PAR (strict)</b> | <b>NN</b> | <b>BLAST</b> | <b>DNA-BAR</b> | <b>BLOG</b> |
|------------------------------|---------------------|--------------------|----------------------|---------------------|-----------|--------------|----------------|-------------|
| <i>N<sub>e</sub></i> = 1000  | 90.4                | 90.4               | 82.7                 | 82.7                | 92.1      | 92.1         | <b>92.1</b>    | 91.9        |
| <i>N<sub>e</sub></i> = 10000 | 88.9                | 88.2               | 82.8                 | 82.2                | 89.8      | 89.8         | 90.1           | <b>90.2</b> |
| <i>N<sub>e</sub></i> = 50000 | 84.2                | 79.0               | 78.5                 | 73.7                | 85.7      | 85.4         | <b>85.8</b>    | 78.1        |

Species identification success scores (% , N=100) of six methods applied to query data sets simulated under three different effective population sizes ( $N_e$ ). NJ = neighbor joining, PAR = parsimony, NN = nearest neighbor.