

**S2 Table. Values to estimate speciation among parthenogenetic lineages (Birky's 4x rule) for the five genetic lineages of *Parisotoma notabilis* sampled in Europe.** Lineages correspond to nodes connecting clades in Figure 2B, Lineages 1.1 and 1.2 are the two sister clades of Lineage 1 with 26 (L1.1) and 19 (L1.2) individuals. Nucleotide diversity ( $\pi$ ), pairwise difference between sequences (d), number of individuals (n), sequence length (L) and nucleotide diversity estimator ( $\theta$ ). Calculations are based on genetic distances and the phylogeny generated with 120 individuals and a 709 bp fragment of COI. The estimator of nucleotide diversity  $\theta$  was calculated as  $\pi/(1-4\pi/3)$ .

	$\pi$	$\theta$	d	n	L
<b>Lineage 0</b>	0.00	0.00	0.00	12	709
<b>Lineage 1.1</b>	2.35	-0.84	2.26	26	709
<b>Lineage 1.2</b>	0.37	-2.32	0.35	19	709
<b>Lineage 2</b>	3.51	-0.81	3.44	53	709
<b>Lineage 3</b>	3.00	-0.82	2.40	5	709
<b>Lineage 4</b>	2.5	-0.83	2.00	5	709
<b>Lineage1</b>	4.78	-0.75	4.67	45	709
<b>Lineage 0-1</b>	41.52	-0.75	40.79	57	709
<b>Lineage 0-2</b>	69.75	-0.75	69.12	110	709
<b>Lineage 3-4</b>	71.58	-0.75	64.42	10	709