Supplementary Materials

Table S1 GenBank accession numbers of *COI-COII* and *EF-1α* sequences of *Samia cynthia* subspecies and two outgroup species, *Bombyx mori* and *Antheraea pernyi*, used for the construction of neighbour-joining trees.

Species/subspecies	Accession No.	
	COI-COII	*EF-1α*
Bombyx mori	AY048187	D13338
Antheraea pernyi	AY242996	FJ788508
S. c. ricini	AB558964	AB558961
S. c. walkeri	AB558962	AB558959
S. cynthia subsp. indet.	AB558963	AB558960

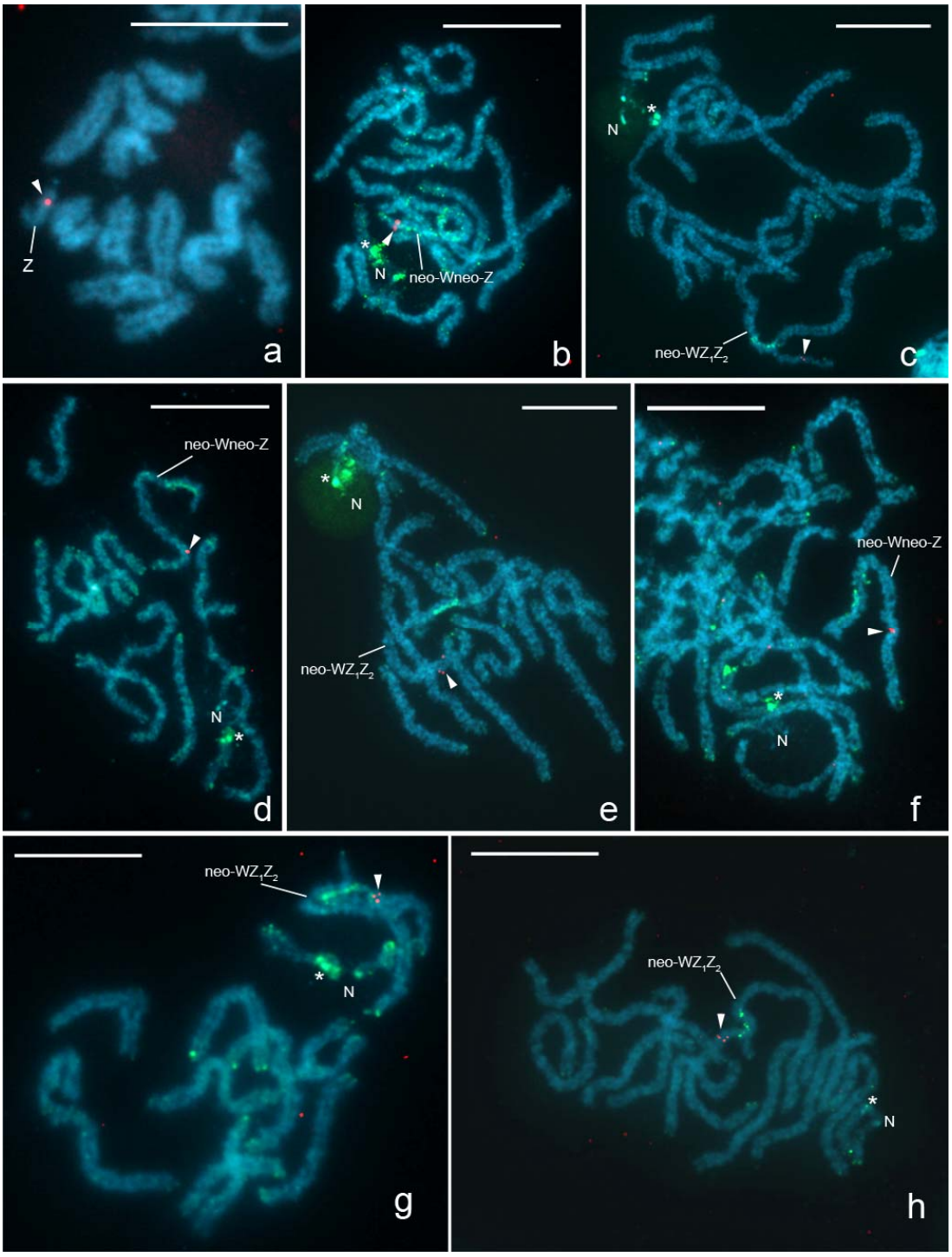

Figure S1 FISH mapping of *S. cynthia* orthologues of *B. mori* genes on female pachytene chromosomes of *S. c. ricini* (a), *S. c. walkeri* (b, d, f), and *S. cynthia* subsp. indet. (c, e, g, h). Images in a-c, d-f, and g-h show the whole oocyte complements from the same FISH experiments as presented in Figure 1f-h, Figure 2b-d, and Figure 3b-c, respectively, showing only sex chromosomes. Red signals (arrowheads) are Cy3-labelled orthologous probes of the *B. mori* genes: *kettin* (a-c), *XDH 1* (d, e), *lysozyme* (f), *Topo II* (g), and *RpL18* (h). Green-labelled female genomic probe (green signals) identified the original W compartment and also highlighted a heterochromatin block on the NOR bivalent (asterisk) in *S. c. walkeri* (b, d, f) and *S. cynthia* subsp. indet. (c, e, g, h). Chromosomes were counterstained with DAPI (light blue). N, nucleous. Bars represent 10 μm.

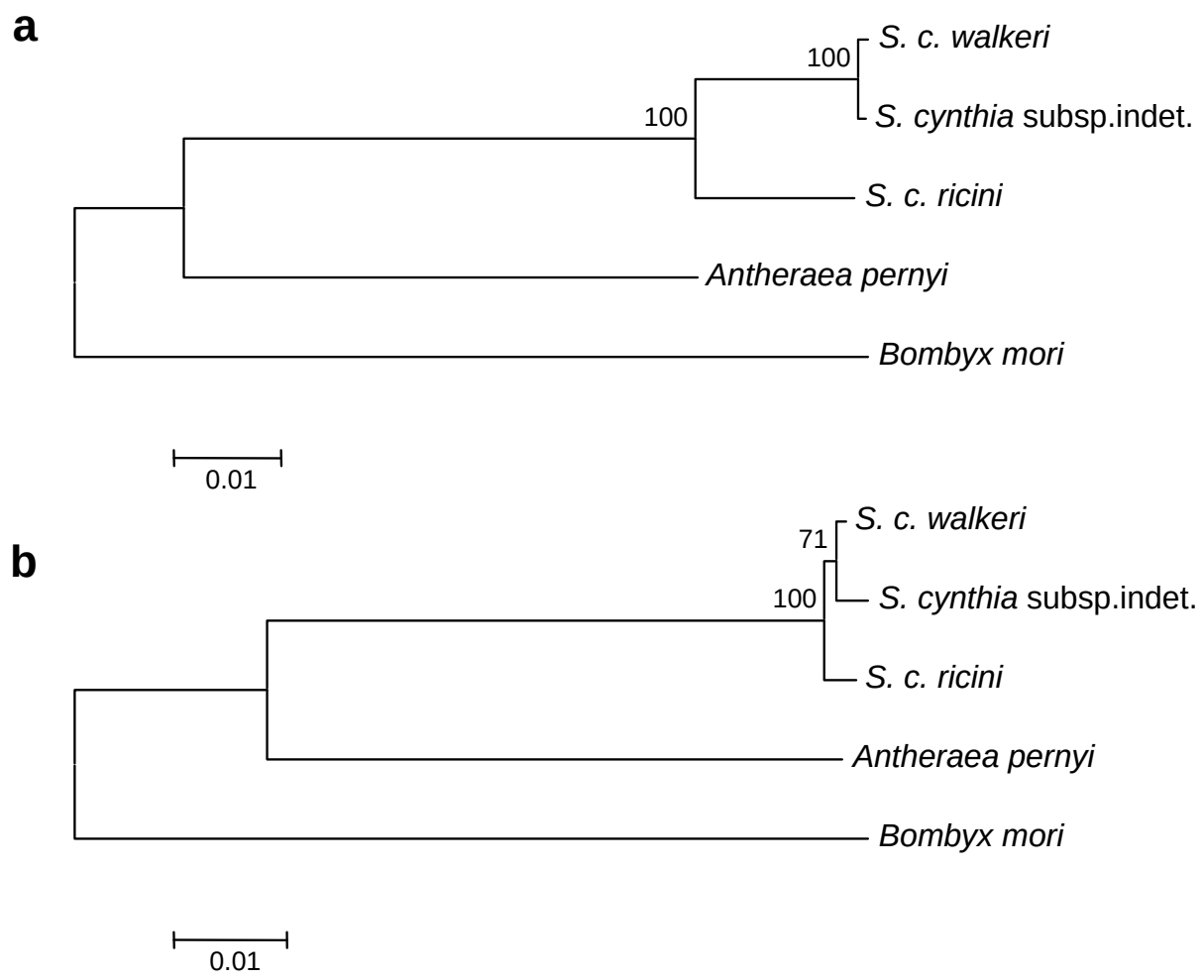

Figure S2 Neighbour-joining trees showing evolutionary relationships of three geographical subspecies of wild silkmoths, *Samia cynthia* ssp. (Saturniidae), constructed with the use of mitochondrial DNA (*COI-COII*) (a) and a nuclear gene (*EF-1α*) (b). The domesticated silkworm, *Bombyx mori* (Bombycidae), and the Chinese oak silkmoth, *Antheraea pernyi* (Saturniidae), were used as outgroups. Scales indicate the number of base substitutions per site, computed with the maximum composite likelihood method. The bootstrap values (1000 replicates) are shown next to the branches.