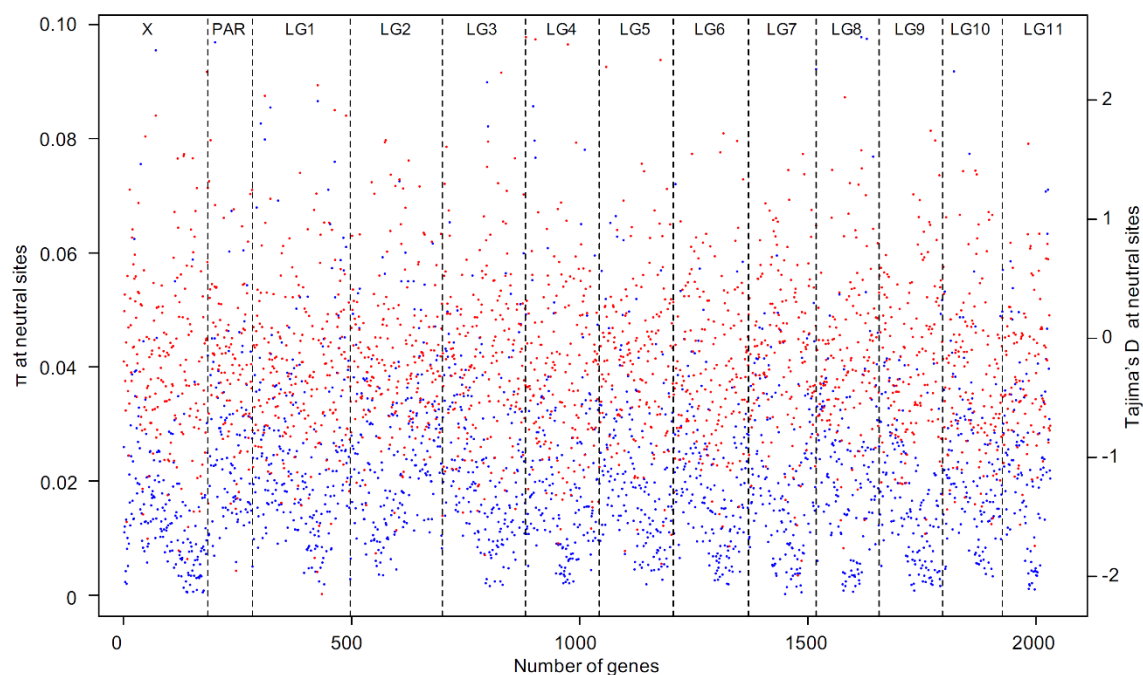


Supplementary Materials:



Supplementary figure S1. Genetic diversity at silent sites of X-linked and autosomal genes mapped in the previous study [21]. The per nucleotide average heterozygosity (π) values are shown in blue; the Tajima's D values are in red.

Supplementary table S1. The numbers of preferred (P) and un-preferred (U) codon changes in *S. latifolia* and *S. vulgaris* lineages from their common ancestor, assuming preferred codon set defined in the previous study [56].

	<i>S. latifolia</i>		<i>S. vulgaris</i>	
	X	A	homologous to X-linked	homologous to autosomal
P=>U	510	1721	575	1748
U=>P	295	870	276	949
total	805	2591	851	2697