

TABLE S1**Additive interactions between sex-antagonistic loci**

fitness estimate	loci linked to the ancestral sex-determination system				loci linked to the novel sex-determination system			all loci
	<i>a</i>	<i>b</i>	<i>c</i>	<i>a, b and c</i>	<i>d</i>	<i>e</i>	<i>d and e</i>	
exact	$-1.09 \cdot 10^{-4}$	$-3.04 \cdot 10^{-5}$	$-5.69 \cdot 10^{-5}$		$1.38 \cdot 10^{-4}$	$1.32 \cdot 10^{-4}$		
population genetic recursions	sum (<i>a</i> + <i>b</i> + <i>c</i>) = $-1.96 \cdot 10^{-4}$				$-1.97 \cdot 10^{-4}$	sum (<i>d</i> + <i>e</i>) = $2.69 \cdot 10^{-4}$		$2.69 \cdot 10^{-4}$
analytical – loose linkage	$-1.11 \cdot 10^{-4}$	$-2.95 \cdot 10^{-5}$	$-1.35 \cdot 10^{-4}$		$1.42 \cdot 10^{-4}$	$1.44 \cdot 10^{-4}$		sum = $1.08 \cdot 10^{-5}$
analytical – tight linkage	$-1.08 \cdot 10^{-4}$	$-3.00 \cdot 10^{-5}$	$-5.75 \cdot 10^{-5}$		$1.37 \cdot 10^{-4}$	$1.31 \cdot 10^{-4}$		sum = $7.29 \cdot 10^{-5}$

We ran a simulation of our model with five sex-antagonistic loci (parameters listed in Table S2). Three loci were linked to the ancestral sex-determination locus (loci *a*, *b* and *c*), the other two were autosomal and linked to the novel sex-determination locus (loci *d* and *e*). The numerical estimate of the invasion fitness based on the exact population genetic recursions for the full model (column ‘all loci’) was then compared with the results of additional simulations where we calculated the contributions of single loci in isolation (column *a*, *b*, ... *e*), or the combined fitness effects of all loci on a single linkage group (columns ‘*a*, *b* and *c*’ and ‘*d* and *e*’). The results in the first row show that the fitness contributions from different sex-antagonistic loci are additive between and within linkage groups (even if linkage between sex-antagonistic loci is tight, e.g., recombination between locus *a* and *b* was 1%), allowing us to consider individual sex-antagonistic loci in isolation in our analytical treatment. The analytical estimates for the fitness contributions of individual loci are shown in the second and third row of the Table. The loose linkage result is reasonably accurate except for locus *c*, which is very tightly linked to the ancestral sex determining gene.