Supplementary Materials

Dapper, AL and MJ Wade (2016) The evolution of sperm competition genes: the effect of mating system on levels of genetic variation within and between species.

Supplemental Table 1: The change in frequency of the *A* allele (Δp) when each female mates with exactly two males ($k = 2$) for Case 1 (haploid adults).

♂ **Genotypes**	F_i	p_i	q_i	$\Delta p_i W$	$F_i \Delta p_i$
A X A	p^2	1	0	0	0
A X a	$2pq$	$(1/2)$	$(1/2)$	$s/4$	$spq/2W$
a X a	q^2	0	1	0	0
Total:	**1**				$\boldsymbol{spq/2W}$

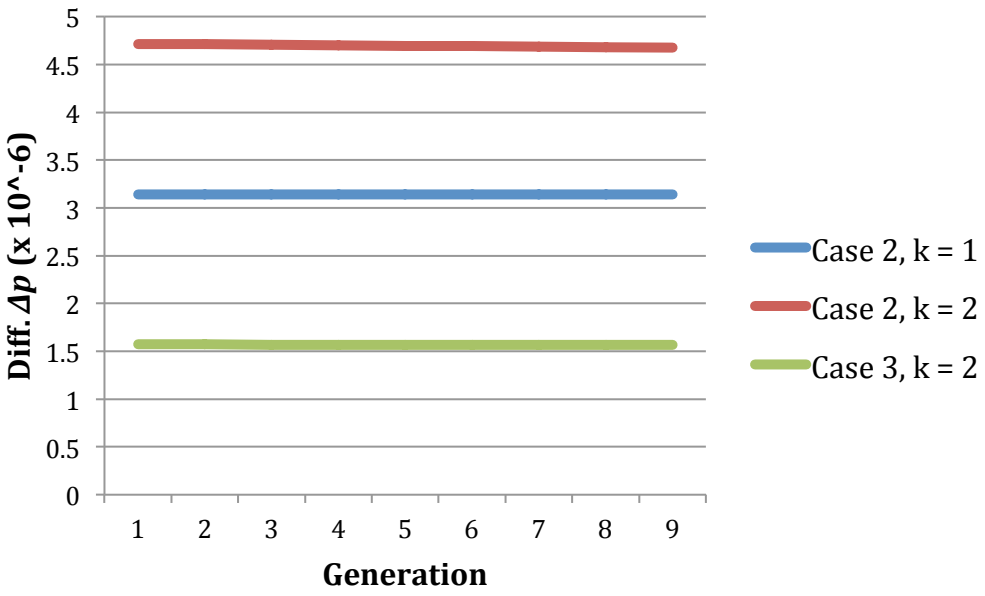
Supplemental Table 2: The change in frequency of the *A* allele (Δp) when each female mates with exactly two males ($k = 2$) for Case 2 (diploid adults, gametic expression of sperm proteins).

♂ **Genotypes**	F_i	p_i	q_i	$\Delta p_i W$	$F_i \Delta p_i$
AA X AA	p^4	1	0	0	0
AA X Aa	$4p^3q$	$(3/4)$	$(1/4)$	$(3/16)s$	$(3/4)sp^3q/W$
AA X aa	$2p^2q^2$	$(1/2)$	$(1/2)$	$(1/4)s$	$(1/2)sp^2q^2/W$
Aa X Aa	$4p^2q^2$	$(1/2)$	$(1/2)$	$(1/4)s$	sp^2q^2/W
Aa X aa	$4pq^3$	$(1/4)$	$(3/4)$	$(3/16)s$	$(3/4)spq^3/W$
aa X aa	q^4	0	1	0	0
Total:	**1**				$\boldsymbol{(3/4)spq/W}$

Supplemental Table 3: The change in frequency of the *A* allele (Δp) for exactly two males ($k = 2$) for Case 3.

♂ **Genotypes**	F_i	G_{ij}		p_{ij}	W_{ij}	$W_{.j}$	$\Delta p_i W$	$F_i \Delta p_i$
AA X AA	p^4	$G_{i,AA}$	1	1	1	1	0	0
		$G_{i,Aa}$	0	-	-	-	-	-
		$G_{i,aa}$	0	-	-	-	-	-
AA X Aa	$4p^3q$	$G_{i,AA}$	(1/2)	1	1	1-(hs/2)	sh/4	shp^3q/W
		$G_{i,Aa}$	(1/2)	(1/2)	1-hs	1-(hs/2)	-sh/8	-shp^3q/2W
		$G_{i,aa}$	0	-	-	-	-	-
AA X aa	$2p^2q^2$	$G_{i,AA}$	(1/2)	1	1	1-(s/2)	s/4	sp^2q^2/2W
		$G_{i,Aa}$	0	-	-	-	-	-
		$G_{i,aa}$	(1/2)	0	-	-	-	-
Aa X Aa	$4p^2q^2$	$G_{i,AA}$	0	-	-	-	-	-
		$G_{i,Aa}$	1	(1/2)	1-hs	1-hs	0	0
		$G_{i,aa}$	0	-	-	-	-	-
Aa X aa	$4pq^3$	$G_{i,AA}$	0	-	-	-	-	-
		$G_{i,Aa}$	(1/2)	(1/2)	1-hs	1-(h+1)(s/2)	(1-h)s/8	(1-h)spq^3/2W
		$G_{i,aa}$	(1/2)	0	-	-	-	-
aa X aa	q^4	$G_{i,AA}$	0	-	-	-	-	-
		$G_{i,Aa}$	0	-	-	-	-	-
		$G_{i,aa}$	1	0	-	-	-	-
Total:	**1**						$spq(ph + q(1-h))/2W$	

Supplemental Figure 1: Difference in the magnitude of Δp x 10^{-6} between the analytical approximation, which assumes a Hardy-Weinberg distribution of offspring genotypes after selection, and the simulation results of the exact equation without that assumption, ($\Delta p_{HW} - \Delta p_{NO\_HW}$). The initial conditions assume a constant selection coefficient, s = 0.01, and frequency of the favored allele, p, of 0.5. For Case 2 (diploid adults, haploid sperm), the difference in Δp is shown for two conditions: (1) each female has 1 mate (blue), and (2) each female has two mates (red). For Case 3 (diploid adults, diploid sperm), only the second condition (k = 2) is shown (green), because there is no sperm competition when k = 1. The largest difference is ~5 x 10^{-6}, which is of order $(s)^3$, demonstrating that analysis facilitated by the Hardy-Weinberg is excellent for the case of weak selection.



Supplementary Figures

Supplementary Figure 2: Change in Frequency of Beneficial Alleles

Beneficial alleles (s = 0.1, h = 0.5) take longer to fix when they occur in sex-specific genes (dashed, black) in comparison to constitutively expressed genes (solid, black). If they occur in sex-specific genes that function primarily in sperm competition, the expected time to fixation increases as the harmonic mean number of mates per female (H) decreases (H=3, blue; H=2, red; H=1.5, yellow). **(A)** Case 1 – haploid males, **(B)** Case 2 – diploid males, gametic expression of reproductive proteins, and **(C)** Case 3 – diploid males, somatic expression of reproductive proteins.

Supplementary Figure 3: Relative Levels of Gene Diversity

Sex-specific genes are expected to exhibit twice as much gene diversity at the mutation selection balance relative to standard constitutively expressed genes (black, dashed line). In Case 1 and 3, sperm competition genes are expected to exhibit even higher levels of gene diversity relative to constitutively expressed genes (grey, dotted line). In contrast, in Case 2 (diploid adults, gametic expression), sperm competition genes are expected to exhibit reduced levels of gene diversity in comparison to sex-specific genes not involved in sperm competition (grey, solid line). The relative increase in gene diversity is a function of the harmonic mean number of mates per female (H) decreases.

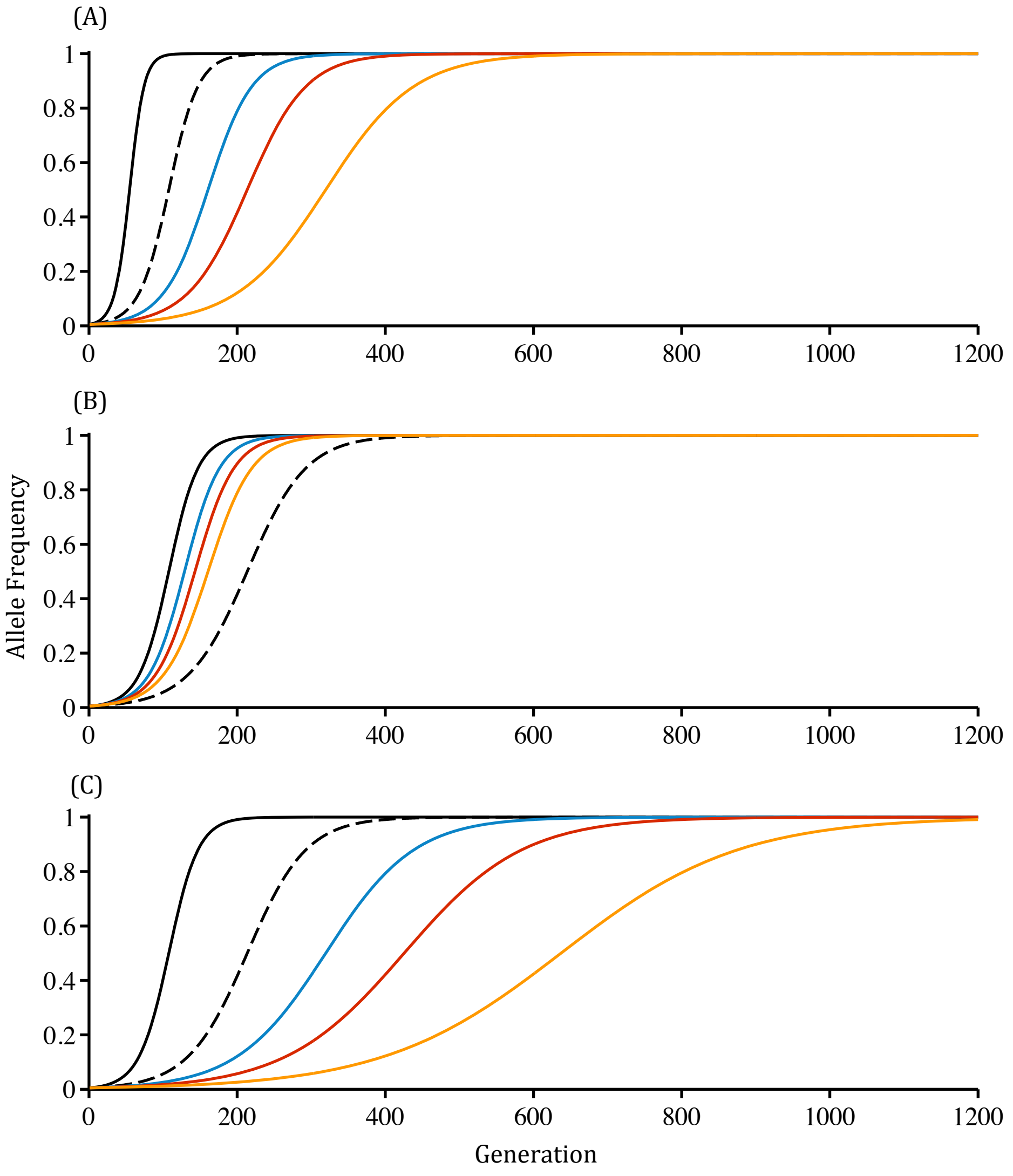
Supplementary Figure 4: Probability of Fixation of a New Mutation

(A, C, E) New deleterious mutations ($s < 0$, $h = 0.5$) have a higher probability of fixing in sex-specific gene relative to standard constitutively expressed genes (black, dashed). **(B, D, F)** Conversely, new beneficial mutations ($s > 0$, $h = 0.5$) have a lower probability of fixing in sex-specific gene relative to standard constitutively expressed genes. These effects are exaggerated in sex-specific genes that function primarily in sperm competition. Among sperm competition genes, the relative probability of fixation is a function of the harmonic mean number of mates per female (H) (H=3, blue; H=2, red; H=1.5, yellow). **(A, B)** Case 1 – haploid males, **(C, D)** Case 2 – diploid males, haploid expression of reproductive proteins, and **(E, F)** Case 3 – diploid males, diploid expression of reproductive proteins.

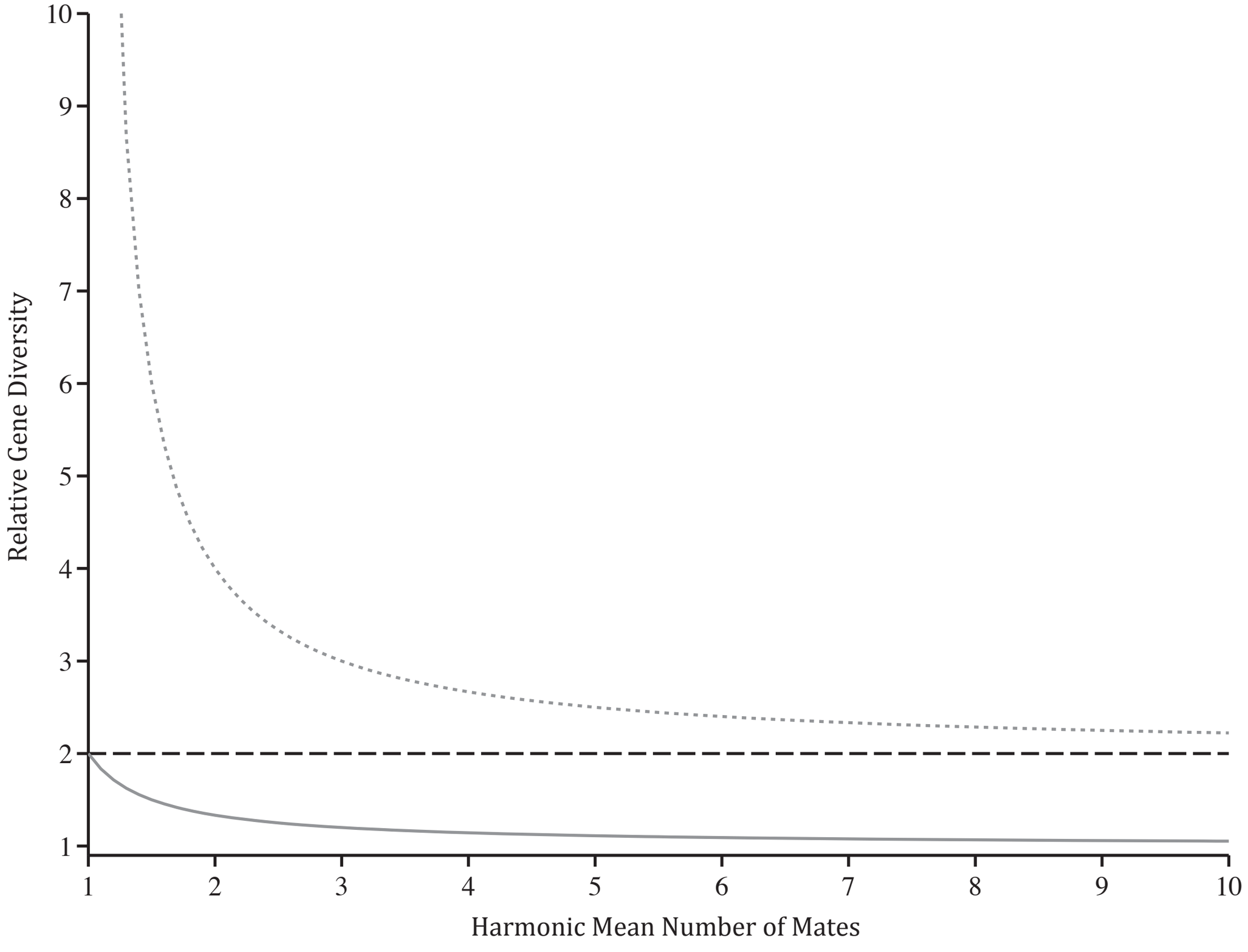
Supplementary Figure 5: Expected Ratio of Non-synonymous to Synonymous Substitutions

Sperm competition (grey, dotted/solid lines) and sex-specific genes (black, dashed line) are expected to exhibit elevated ratios of non-synonymous to synonymous substitutions (*dN/dS*) in comparison with standard, constitutively expressed genes (black, solid), given the same average selective effect of new mutations ($Ns = -1$). While sperm competition increases expected *dN/dS* in Case 1 (haploid adults) and 3 (diploid adults, somatic expression) (grey, dotted line), it decreases expected *dN/dS* in Case 2 (diploid adults, gametic expression) (grey, solid line). Among sperm competition genes, the expected *dN/dS* ratio increases with decreasing harmonic mean number of mates per female (H).

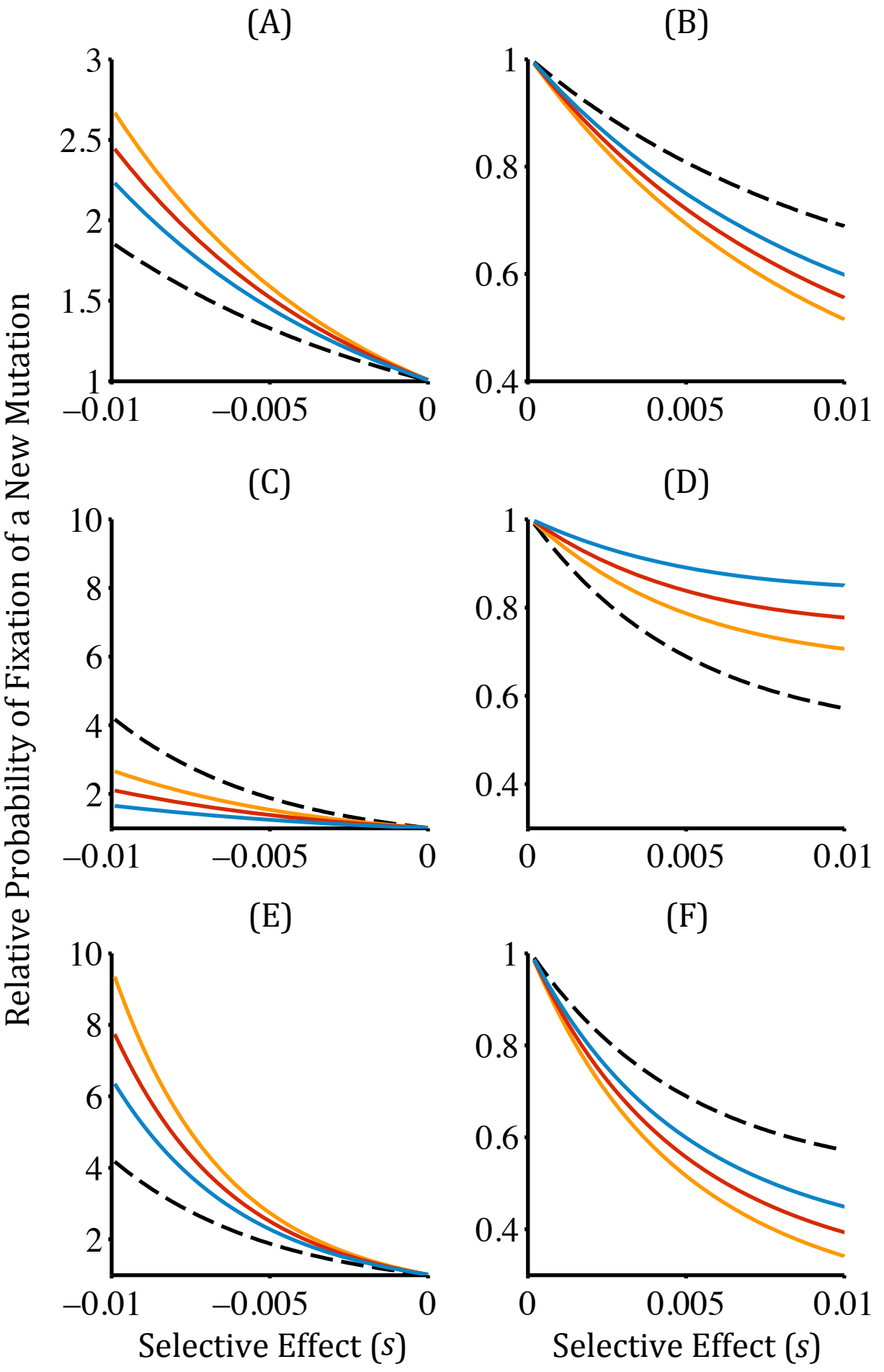
Supplementary Figure 2. Change in frequency of beneficial alleles.



Supplementary Figure 3. Relative Levels of Gene Diversity.



Supplementary Figure 4. Probability of fixation of a new mutation.



Supplementary Figure 5. Expected ratio of non-synonymous to synonymous substitutions.