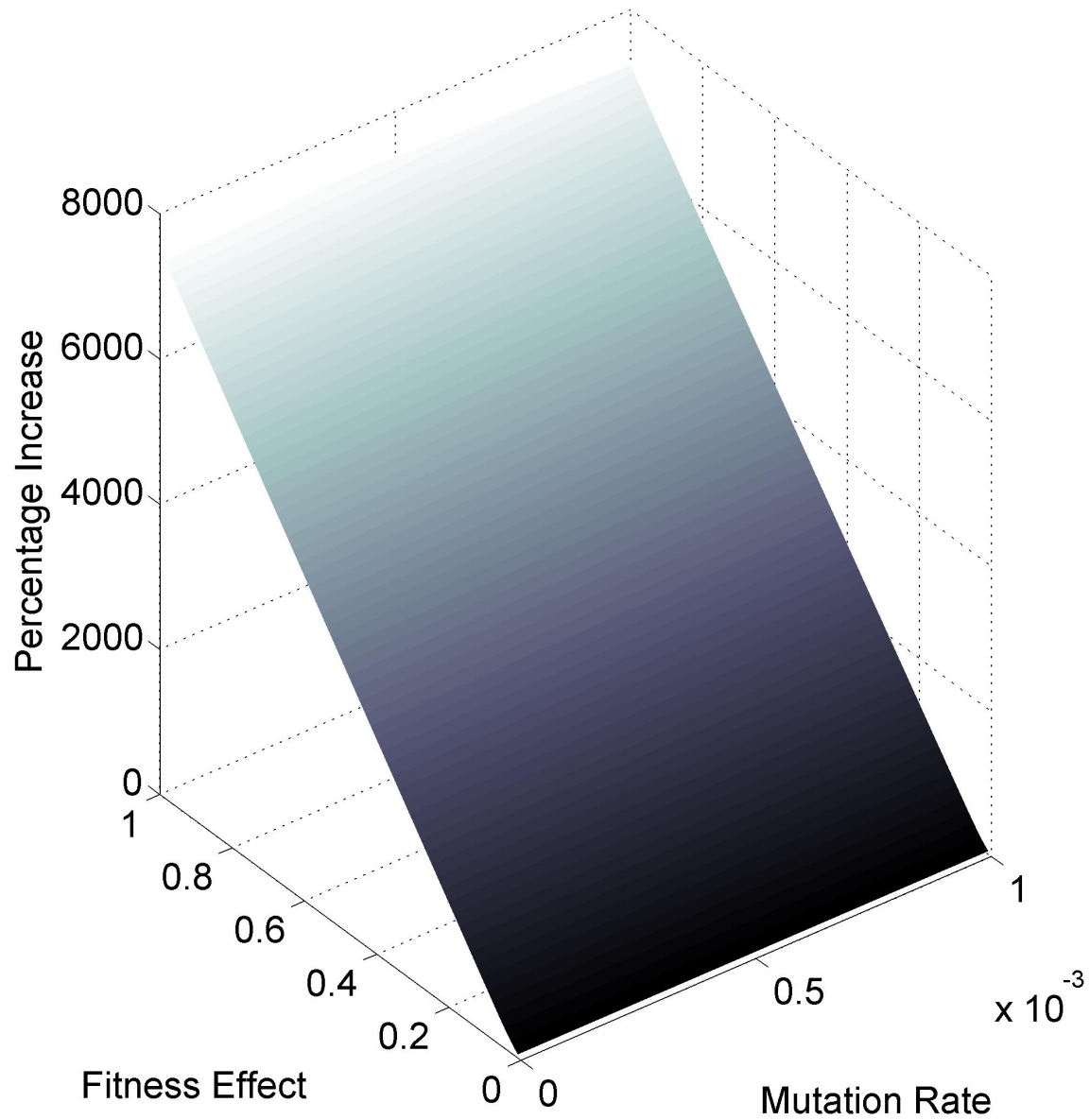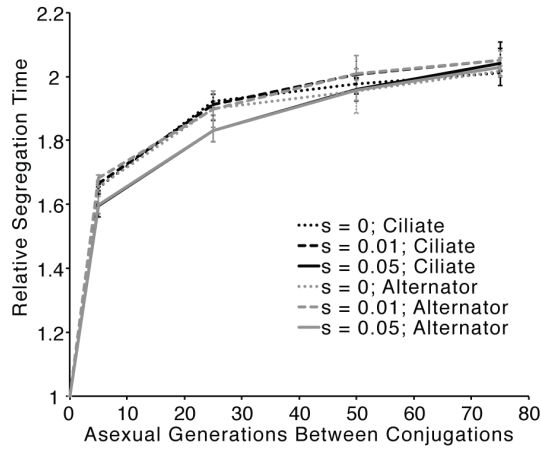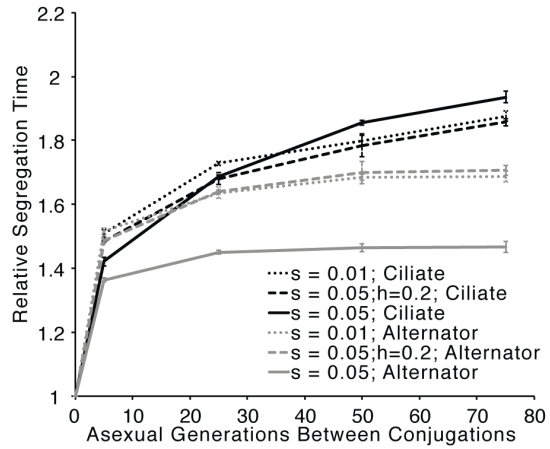**Contents:**

Figure 1S. Percentage increase in the equilibrium frequency of a dominant deleterious mutation in ciliate populations over sexual populations for different mutation rates and fitness effects (in this figure the number of asexual generations between conjugations, *n*, is equal to 75 in the ciliate populations).
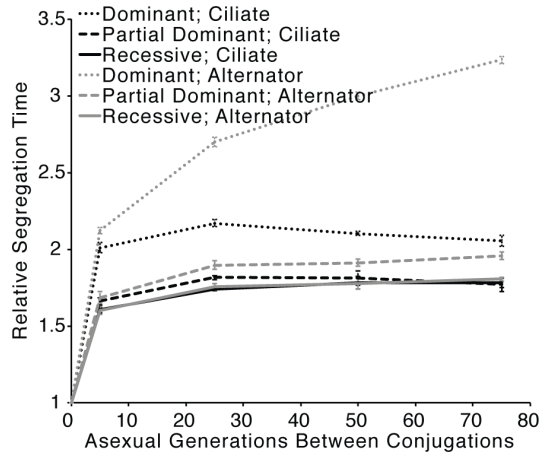
Figure 2s. Results of selection-drift and mutation-selection-drift simulations (population size = 100). Panels a, b and c show the ratio of the segregation times for different alleles in ciliate and alternator populations versus sexual populations for various *n* (number of asexual generations between sexual conjugations). n=0 corresponds to sexual organisms. The average of 100,000 simulations is reported. The simulation was performed in triplicate and the error bars represent the standard deviation of the average. **A.** Neutral allele (s=0) and recessive deleterious alleles (s=0.01 and s=0.05). **B.** Dominant (s=0.01 and s=0.05) and partial dominant (s=0.05; h=0.2) deleterious alleles. **C.** Recessive (s=0.05), dominant (s=0.05) and partial dominant (s=0.05; h=0.2) beneficial alleles. **D.** Ratio of the average allelic frequency for ciliates or alternators versus sexual populations for various n, under mutation-selection-drift (population size=100). Values generated via finite population simulations with both forward (10-4) and back mutation (10-5). The simulation is run for 100,000 generations, and the average allele frequency is calculated for the last 90,000 generations. This was repeated 32 times to estimate the variance. Error bars represent a single standard deviation as calculated from the 32 averages. Note that the error bars go above and below the graph area and were cropped for clarity.
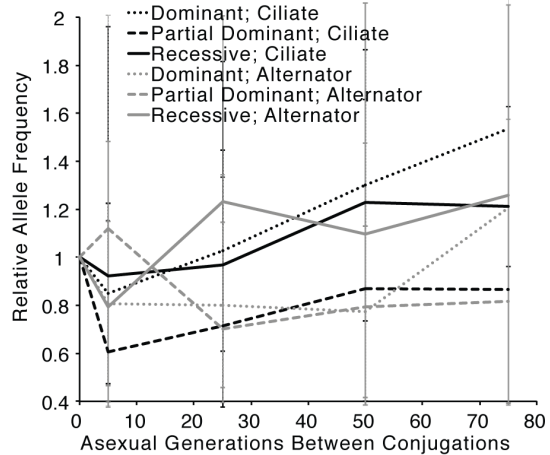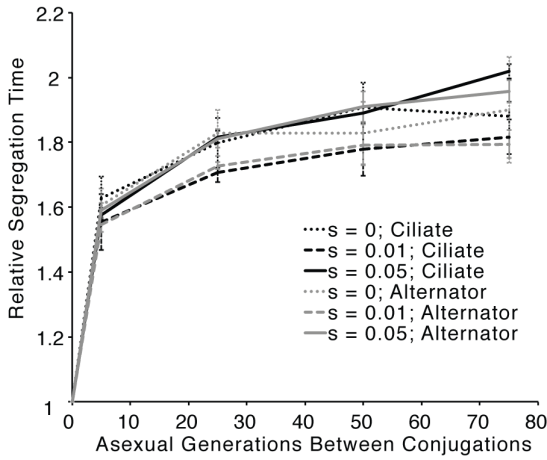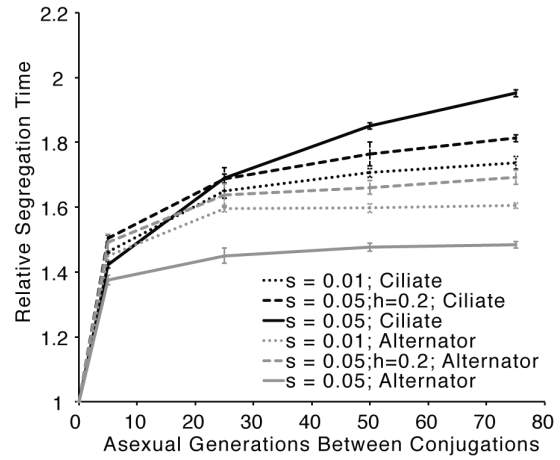
Figure 3s. Results of selection-drift and mutation-selection-drift simulations (population size = 500). Panels a, b and c show the ratio of the segregation times for different alleles in ciliate and alternator populations versus sexual populations for various *n* (number of asexual generations between sexual conjugations). *n*=0 corresponds to sexual organisms. The average of 100,000 simulations is reported. The simulation was performed in triplicate and the error bars represent the standard deviation of the average. **A.** Neutral allele (s=0) and recessive deleterious alleles (s=0.01 and s=0.05). **B.** Dominant (s=0.01 and s=0.05) and partial dominant (s=0.05; h=0.2) deleterious alleles. **C.** Recessive (s=0.05), dominant (s=0.05) and partial dominant (s=0.05; h=0.2) beneficial alleles. **D.** Ratio of the average allelic frequency for ciliates or alternators versus sexual populations for various n, under mutation-selection-drift (population size=500). Values generated via finite population simulations with both forward (10-4) and back mutation (10-5). The simulation is run for 100,000 generations, and the average allele frequency is calculated for the last 90,000 generations. This was repeated 32 times to estimate the variance. Error bars represent a single standard deviation as calculated from the 32 averages.

A) Selection Drift: Neutral and Recessive Alleles

Relative Segregation Time vs Asexual Generations Between Conjugations

- ⋯⋯ s = 0; Ciliate
- ▬ ▬ s = 0.01; Ciliate
- ▬▬ s = 0.05; Ciliate
- ⋯⋯ s = 0; Alternators
- ▬ ▬ s = 0.01; Alternator
- ▬▬ s = 0.05; Alternator

B) Selection Drift: Dominant and Partial Dominant Alleles

Relative Segregation Time vs Asexual Generations Between Conjugations

- ⋯⋯ s = 0.01; Ciliate
- ▬ ▬ s = 0.05;h=0.2; Ciliate
- ▬▬ s = 0.05; Ciliate
- ⋯⋯ s = 0.01; Alternator
- ▬ ▬ s = 0.05;h=0.2; Alternator
- ▬▬ s = 0.05; Alternator

C) Selection Drift: Beneficial Alleles

Relative Segregation Time vs Asexual Generations Between Conjugations

- ⋯⋯ Dominant; Ciliate
- ▬ ▬ Partial Dominant; Ciliate
- ▬▬ Recessive; Ciliate
- ⋯⋯ Dominant; Alternator
- ▬ ▬ Partial Dominant; Alternator
- ▬▬ Recessive; Alternator

D) Mutation Selection Drift

Relative Segregation Time vs Asexual Generations Between Conjugations

- ⋯⋯ Dominant; Ciliate
- ▬ ▬ Partial Dominant; Ciliate
- ▬▬ Recessive; Ciliate
- ⋯⋯ Dominant; Alternator
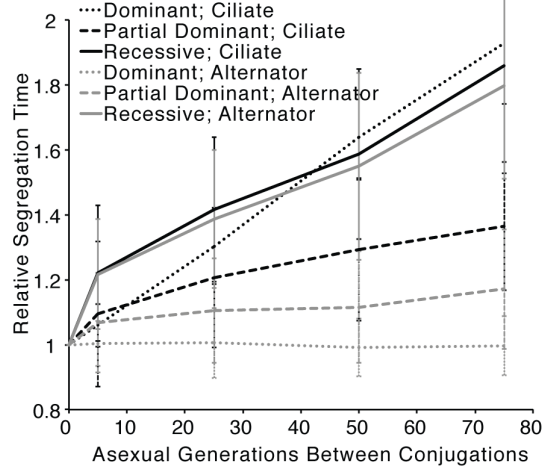- ▬ ▬ Partial Dominant; Alternator
- ▬▬ Recessive; Alternator

Figure 4s. Results of selection-drift and mutation-selection-drift simulations (population size = 1,000). Panels a, b and c show the ratio of the segregation times for different alleles in ciliate and alternator populations versus sexual populations for various *n* (number of asexual generations between sexual conjugations). *n*=0 corresponds to sexual organisms. The average of 100,000 simulations is reported. The simulation was performed in triplicate and the error bars represent the standard deviation of the average. **A.** Neutral allele (s=0) and recessive deleterious alleles (s=0.01 and s=0.05). **B.** Dominant (s=0.01 and s=0.05) and partial dominant (s=0.05; h=0.2) deleterious alleles. **C.** Recessive (s=0.05), dominant (s=0.05) and partial dominant (s=0.05; h=0.2) beneficial alleles. **D.** Ratio of the average allelic frequency for ciliates or alternators versus sexual populations for various n, under mutation-selection-drift (population size=1,000). Values generated via finite population simulations with both forward (10-4) and back mutation (10-5). The simulation is run for 100,000 generations, and the average allele frequency is calculated for the last 90,000 generations. This was repeated 32 times to estimate the variance. Error bars represent a single standard deviation as calculated from the 32 averages.
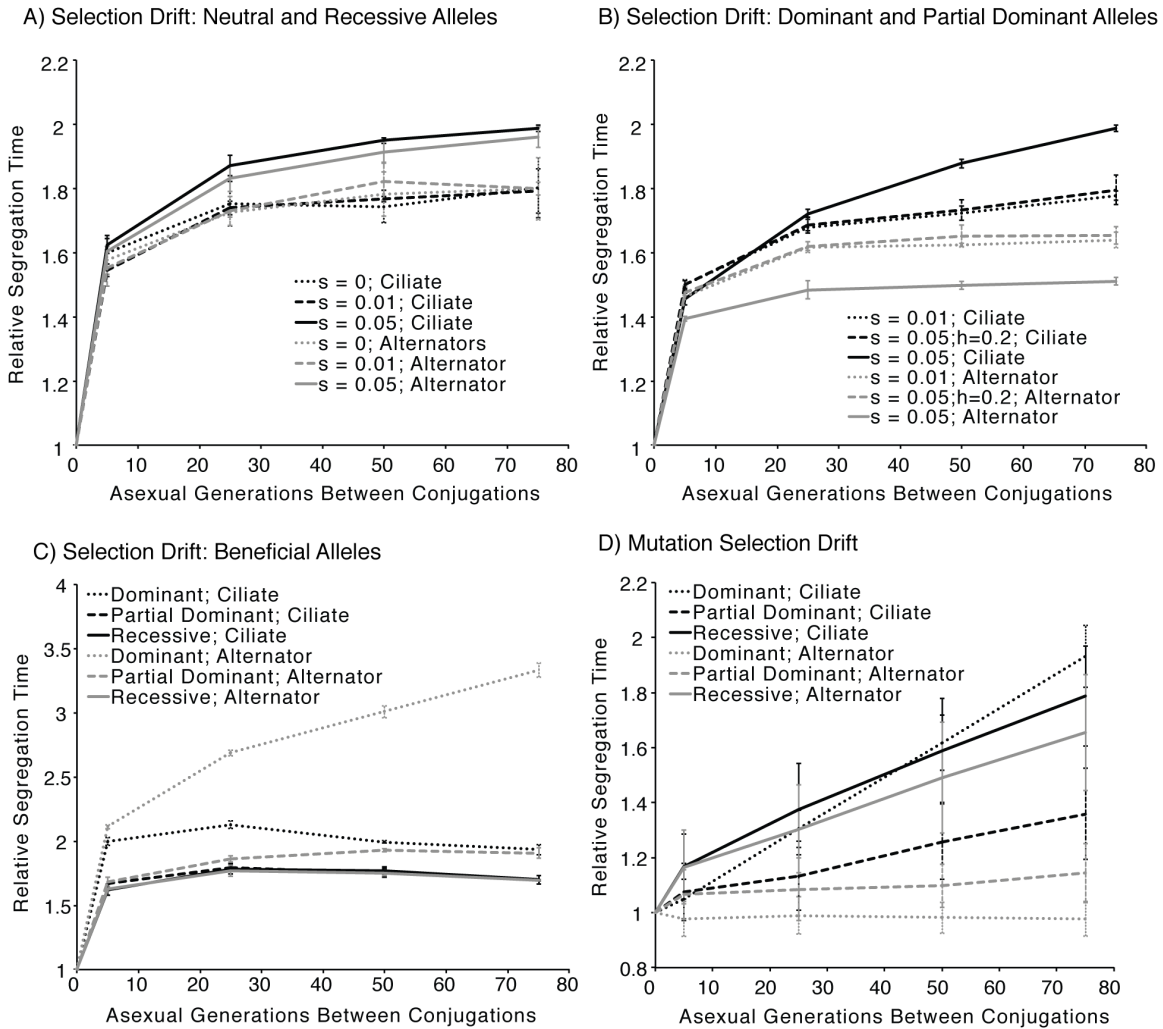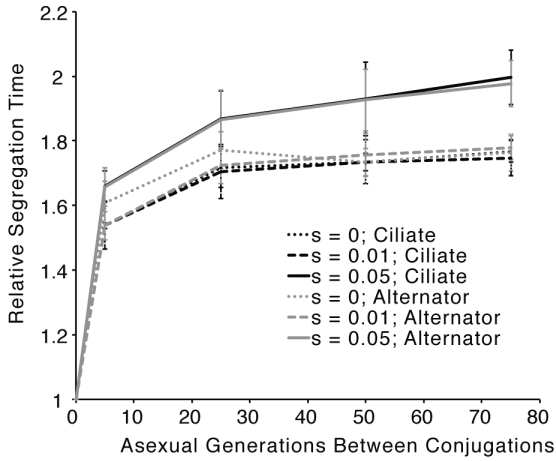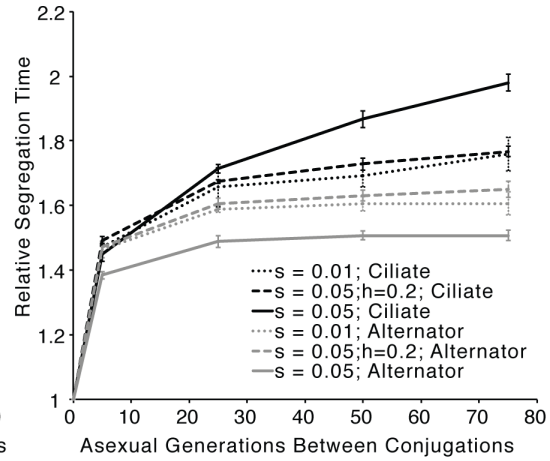
Figure 5s. Results of selection-drift and mutation-selection-drift simulations (population size = 3,000). Panels a, b and c show the ratio of the segregation times for different alleles in ciliate and alternator populations versus sexual populations for various *n* (number of asexual generations between sexual conjugations). *n*=0 corresponds to sexual organisms. The average of 100,000 simulations is reported. The simulation was performed in triplicate and the error bars represent the standard deviation of the average. **A.** Neutral allele (s=0) and recessive deleterious alleles (s=0.01 and s=0.05). **B.** Dominant (s=0.01 and s=0.05) and partial dominant (s=0.05; h=0.2) deleterious alleles. **C.** Recessive (s=0.05), dominant (s=0.05) and partial dominant (s=0.05; h=0.2) beneficial alleles. **D.** Ratio of the average allelic frequency for ciliates or alternators versus sexual populations for various *n*, under mutation-selection-drift (population size=3,000). Values generated via finite population simulations with both forward (10-4) and back mutation (10-5). The simulation is run for 100,000 generations, and the average allele frequency is calculated for the last 90,000 generations. This was repeated 32 times to estimate the variance. Error bars represent a single standard deviation as calculated from the 32 averages.
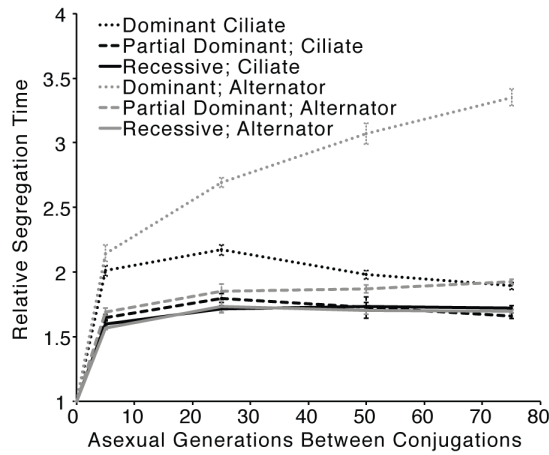
Table 1S: Segregation times for neutral and recessive alleles in sexual populations, and in ciliate and alternator populations with different values of n.*

Selection Coefficient	Population	Sexual Population	Ciliate Population				Alternator Population			
			n=5	n=25	n=50	n=75	n=5	n=25	n=50	n=75
s = 0	100	11.85	19.59	22.79	23.42	23.85	19.60	22.51	23.17	23.89
		(0.06)	(0.21)	(0.29)	(0.10)	(0.21)	(0.11)	(0.25)	(0.82)	(0.15)
	500	15.12	24.57	27.15	28.80	28.43	24.27	27.62	27.61	28.67
		(0.66)	(0.34)	(0.14)	(0.35)	(0.58)	(0.57)	(0.16)	(0.72)	(1.71)
	1000	16.10	25.74	28.18	28.05	28.97	25.35	27.76	28.66	28.92
		(0.55)	(0.37)	(0.47)	(0.85)	(0.49)	(0.25)	(0.70)	(0.52)	(0.57)
	3000	15.97	24.55	27.40	27.69	28.22	25.68	28.28	27.67	28.15
		(0.17)	(0.39)	(0.82)	(0.88)	(0.70)	(0.77)	(0.86)	(0.64)	(0.85)
	10000	15.57	24.48	27.18	27.50	27.43	25.02	27.25	28.32	27.81
		(0.43)	(0.35)	(0.64)	(0.48)	(0.64)	(0.86)	(0.55)	(0.13)	(0.07)
s = 0.01	100	11.70	19.48	22.37	23.47	24.00	19.70	22.21	23.49	24.00
		(0.24)	(0.29)	(0.22)	(0.36)	(0.35)	(0.32)	(0.21)	(0.21)	(0.29)
	500	14.20	22.05	24.26	25.25	25.80	21.94	24.55	25.44	25.49
		(0.40)	(0.69)	(0.27)	(0.48)	(0.25)	(0.36)	(0.65)	(0.23)	(0.46)
	1000	14.33	22.15	24.92	25.32	25.67	22.23	24.78	26.09	25.79
		(0.14)	(0.47)	(0.22)	(0.36)	(0.81)	(0.59)	(0.40)	(0.78)	(0.20)
	3000	15.21	23.37	25.93	26.37	26.55	23.37	26.20	26.69	27.05
		(0.50)	(0.34)	(1.17)	(0.51)	(0.44)	(0.50)	(0.17)	(0.18)	(0.34)
	10000	15.26	24.03	27.19	27.77	27.05	23.69	27.01	27.22	26.96
		(0.09)	(0.12)	(0.89)	(0.62)	(0.27)	(0.47)	(0.36)	(0.45)	(0.74)
s = 0.05	100	10.60	16.91	19.39	20.76	21.61	16.93	19.40	20.74	21.50
		(0.18)	(0.08)	(0.09)	(0.16)	(0.41)	(0.03)	(0.03)	(0.11)	(0.12)
	500	11.61	18.29	21.10	21.94	23.44	18.47	21.04	22.19	22.72
		(0.09)	(0.26)	(0.09)	(0.22)	(0.07)	(0.10)	(0.47)	(0.38)	(0.33)
	1000	12.13	19.72	22.71	23.66	24.12	19.48	22.21	23.23	23.78
		(0.07)	(0.35)	(0.36)	(0.25)	(0.26)	(0.06)	(0.34)	(0.26)	(0.37)
	3000	12.89	21.39	24.06	24.83	25.71	21.35	24.03	24.80	25.46
		(0.51)	(0.24)	(0.29)	(0.69)	(0.35)	(0.07)	(0.32)	(0.28)	(0.11)
	10000	14.44	23.07	25.44	26.39	26.44	23.31	25.06	26.56	26.48
		(0.50)	(0.28)	(0.35)	(0.71)	(0.48)	(0.33)	(0.70)	(0.70)	(1.29)

* These results are based on 3 sets of simulations. Each set consisted of 100,000 replicates. The average segregation time was calculated for the replicates. To estimate the precision of the average segregation times, we repeated each set of simulation 3 times and calculated the average and standard deviation (given in parentheses). Values in bold in the ciliate and alternator columns correspond to values that are significantly larger than: the sexual populations (for n = 5) or the previous value of n (all other n).

Table 2S: Segregation times for beneficial alleles in sexual populations, and in ciliate and alternator populations with different values of *n*.*

Selection Coefficient	Population	Sexual Population	Ciliate Population				Alternator Population			
			n=5	n=25	n=50	n=75	n=5	n=25	n=50	n=75
Recessive Beneficial Alleles										
s = 0.05	100	10.99	17.63	19.13	19.58	19.57	17.58	19.29	19.53	19.84
		(0.1)	(0.22)	(0.06)	(0.28)	(0.18)	(0.14)	(0.06)	(0.24)	(0.19)
	500	12.5	19.56	21.41	21.5	21.41	19.87	21.4	21.45	21.22
		(0.34)	(0.24)	(0.45)	(0.43)	(0.26)	(0.42)	(0.25)	(0.2)	(0.1)
	1000	12.8	20.74	22.81	22.61	21.76	20.83	22.64	22.43	21.73
		(0.11)	(0.36)	(0.44)	(0.25)	(0.4)	(0.34)	(0.49)	(0.12)	(0.22)
	3000	13.84	22.15	23.71	24.02	23.85	21.71	23.98	23.55	23.49
		(0.05)	(0.3)	(0.44)	(0.49)	(0.28)	(0.27)	(0.68)	(0.45)	(0.23)
	10000	14.75	23.69	25.56	25.76	25.1	23.22	25.58	25.54	25.32
		(0.3)	(0.46)	(0.97)	(0.16)	(0.35)	(0.53)	(0.19)	(0.48)	(0.7)
Partial Dominant Beneficial Alleles										
s = 0.01/0.05	100	12.49	20.73	22.67	22.63	22.11	21.02	23.68	23.86	24.46
		(0.19)	(0.17)	(0.17)	(0.34)	(0.4)	(0.25)	(0.21)	(0.06)	(0.14)
	500	15.49	26.11	28.08	27.56	26.86	26.75	29.17	30	29.6
		(0.16)	(0.17)	(0.67)	(0.04)	(0.11)	(0.44)	(0.34)	(0.4)	(0.27)
	1000	17.2	28.69	30.86	30.15	29.19	28.92	32.02	33.14	32.79
		(0.21)	(0.58)	(0.06)	(0.29)	(0.45)	(0.28)	(0.03)	(0.5)	(0.37)
	3000	19.83	32.69	35.64	34.2	32.94	33.57	36.65	37.06	38.15
		(0.22)	(0.41)	(0.39)	(1.36)	(0.07)	(0.25)	(0.74)	(0.8)	(0.8)
	10000	22.69	37.91	40.59	39.33	36.97	38.57	42.86	43.1	42.86
		(0.28)	(0.84)	(0.33)	(0.3)	(1.18)	(1)	(0.54)	(1.06)	(1.11)
Dominant Beneficial Alleles										
s = 0.05	100	22.61	45.47	49.07	47.56	46.50	48.00	61.04	67.84	73.13
		(0.15)	(0.49)	(0.4)	(0.39)	(0.7)	(0.46)	(0.62)	(0.35)	(0.52)
	500	45.00	87.29	92.01	87.79	83.32	92.93	116.5	129.4	142.2
		(0.42)	(0.6)	(0.79)	(1.92)	(0.83)	(1.43)	(1.62)	(0.19)	(0.84)
	1000	57.67	115.1	122.7	115.0	111.6	121.8	154.9	173.4	192.1
		(0.46)	(0.9)	(0.81)	(0.58)	(1.47)	(1)	(0.78)	(1.74)	(3.63)
	3000	89.43	179.7	194.1	176.9	169.2	191.7	240.7	274.3	299.6
		(2.09)	(1.51)	(1.51)	(2.21)	(4.75)	(1.42)	(2.46)	(1.15)	(1.87)
	10000	143.0	286.4	291.3	266.5	242.9	303.1	372.2	405.5	427.8
		(0.06)	(3.26)	(3.79)	(2.21)	(2.13)	(3.23)	(2.15)	(1.71)	(7.09)

* These results are based on 3 sets of simulations. Each set consisted of 100,000 replicates. The average segregation time was calculated for the replicates. To estimate the precision of the average segregation times, we repeated each set of simulation 3 times and calculated the average and standard deviation (given in parentheses). Values in bold in the ciliate and alternator columns correspond to values that are significantly larger than: the sexual populations (for n = 5) or the previous value of n (all other n).

Table 3: Average frequency of deleterious alleles in mutation-selection-drift simulations in sexual populations, and in ciliate and alternator populations with different values of *n*.*

Selection Coefficient	Population	Sexual Population	Ciliate Population				Alternator Population			
			n=5	n=25	n=50	n=75	n=5	n=25	n=50	n=75
Dominant Beneficial Alleles										
s = 0.05	100	0.095 (0.2822)	0.005 (0.0008)	0.006 (0.001)	0.007 (0.0009)	0.027 (0.1044)	0.005 (0.0006)	0.005 (0.0007)	0.004 (0.0007)	0.007 (0.0129)
	500	0.004 (0.0003)	0.004 (0.0002)	0.005 (0.0002)	0.007 (0.0002)	0.008 (0.0004)	0.004 (0.0002)	0.004 (0.0002)	0.004 (0.0003)	0.004 (0.0002)
	1000	0.004 (0.0002)	0.004 (0.0002)	0.005 (0.0002)	0.006 (0.0002)	0.008 (0.0002)	0.004 (0.0002)	0.004 (0.0001)	0.004 (0.0001)	0.004 (0.0001)
	3000	0.004 (0.0001)	0.004 (0.0001)	0.005 (0.0001)	0.006 (0.0001)	0.008 (0.0001)	0.004 (0.0001)	0.004 (0.0001)	0.004 (0.0001)	0.004 (0.0001)
	10000	0.004 (0.0001)	0.004 (0.0001)	0.005 (0.0001)	0.006 (0.0001)	0.008 (0.0001)	0.004 (0.0001)	0.004 (0.0001)	0.004 (0.0001)	0.004 (0.0001)
Partial Dominant Beneficial Alleles										
s = 0.05; h=0.2	100	0.135 (0.1741)	0.016 (0.0031)	0.02 (0.0086)	0.023 (0.0034)	0.023 (0.0045)	0.026 (0.0426)	0.018 (0.0038)	0.023 (0.0186)	0.021 (0.0042)
	500	0.017 (0.002)	0.018 (0.0023)	0.02 (0.002)	0.022 (0.0022)	0.023 (0.0022)	0.018 (0.0015)	0.019 (0.0019)	0.019 (0.0017)	0.02 (0.0023)
	1000	0.017 (0.0012)	0.019 (0.0013)	0.02 (0.0016)	0.022 (0.0014)	0.023 (0.0021)	0.018 (0.0012)	0.019 (0.0013)	0.019 (0.0013)	0.02 (0.0016)
	3000	0.019 (0.0011)	0.019 (0.0006)	0.02 (0.001)	0.022 (0.0008)	0.023 (0.0008)	0.019 (0.0007)	0.019 (0.0007)	0.019 (0.0008)	0.019 (0.0008)
	10000	0.019 (0.0005)	0.019 (0.0004)	0.02 (0.0004)	0.022 (0.0004)	0.023 (0.0005)	0.019 (0.0005)	0.019 (0.0004)	0.019 (0.0005)	0.019 (0.0004)
Recessive Beneficial Alleles										
s = 0.05	100	0.097 (0.1359)	0.032 (0.0299)	0.033 (0.0062)	0.039 (0.0173)	0.045 (0.0107)	0.027 (0.0087)	0.036 (0.0194)	0.037 (0.0081)	0.043 (0.007)
	500	0.036 (0.0046)	0.043 (0.0048)	0.05 (0.0055)	0.056 (0.0059)	0.066 (0.0077)	0.043 (0.0035)	0.049 (0.0052)	0.054 (0.0063)	0.063 (0.0066)
	1000	0.043 (0.0038)	0.05 (0.0036)	0.059 (0.0044)	0.068 (0.0056)	0.077 (0.0059)	0.05 (0.0034)	0.056 (0.0047)	0.064 (0.0055)	0.071 (0.0062)
	3000	0.054 (0.0032)	0.058 (0.0021)	0.068 (0.0029)	0.076 (0.0035)	0.087 (0.004)	0.058 (0.0025)	0.067 (0.0025)	0.074 (0.0034)	0.08 (0.0029)
	10000	0.06 (0.002)	0.063 (0.0015)	0.071 (0.0015)	0.081 (0.0026)	0.09 (0.0024)	0.062 (0.0012)	0.07 (0.0018)	0.078 (0.0021)	0.085 (0.0024)

* Values generated via finite population simulations with both forward (10^{-4}) and back mutation (10^{-5}). The simulation is run for 100,000 generations, and the average allele frequency is calculated for the last 90,000 generations. This was repeated 32 times to estimate the standard deviation of the average values. Standard deviations smaller than 0.0001, were rounded up to 0.0001 for clarity of presentation.