Rapid and predictable evolution of admixed populations between two *Drosophila* species pairs

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SUPPLEMENTARY TABLES

TABLE S1. **SRA accession numbers for all the genomes used in this study.**

Genotype	SRA
D. yakuba	SAMN07407328-SAMN07407363
D. santomea	SAMN07407377-SAMN07407393
D. yakuba/ D. santomea hybrid populations	PRJNA588449
D. simulans	PRJNA588407
D. mauritiana	PRJNA158675
D. simulans/ D. mauritiana hybrid populations	PRJNA588449

TABLE S2. Tibial length, a proxy of body size, does not differ between *D. simulans* and *D. mauritiana*. We show the sum of squares (Sum Sq), the mean square difference (Mean Sq), the F value and the P-value of a nested ANOVA (line nested within species), where the tibial length is the response. The mean tibial length in *D. simulans* is 0.448 (SD= 0.022). The mean tibial length for *D. mauritiana* is 0.442 (SD= 0.021).

	Df	Sum Sq	Mean Sq	F value	P
Species	1	1.181×10^{-3}	1.181×10^{-3}	2.579	0.111
Line	4	4.044×10^{-3}	1.011×10^{-3}	2.208	0.073
Residuals	115	0.053	4.579×10^{-4}		

TABLE S3. Mean trait values (SD) and results from the linear models comparing mean trait values among replicates within *D. simulans*, within *D. mauritiana*, and within the hybrid swarms produced with these two species. The F-values show the result of the linear model for each genotype and describe whether there was any phenotypic change in the course of the experiment for a set of bottles (i.e., genotype).

		Sex combs		Face width		Wing area		Genital lobe		Anal plate bristles	
		Mean (SD)	χ^2, df=1	Mean (SD)	$F_{1,798}$	Mean (SD)	$F_{1,798}$	Mean (SD)	$F_{1,798}$	Mean (SD)	χ^2, df=1
A	*D. simulans*	8.993 (0.286)	0.058, P= 0.809	349.650 (2.850)	4.650, P=0.031	789.995 (6.845)	1.671, P=0.197	11.979 (0.194)	0.861 P=0.3537	33.976 (0.778)	1.88×10^{-2}, P=0.891
B	*D. mauritiana*	13.992 (0.363)	0.112, P = 0.738	331.218 (2.100)	0.459, P=0.498	970.340 (11.052)	0.396, P=0.530	2.995 (0.048)	3.661 P=0.05605	48.902, (0.920)	0.387, P= 0.5338
C	*Hybrid swarms*	9.447 (0.240)	69.389, P < 1 × 10^{-10}	350.52, (1.639)	680.38, P < 1 × 10^{-10}	784.582 (7.330)	130.9, P < 1 × 10^{-10}	11.821 (0.614)	922.37, P < 1 × 10^{-10}	33.326 (1.045)	163.82, P < 1 × 10^{-10}

TABLE S4. Tukey HSD tests comparing the mean trait values in *D. simulans*, *D. mauritiana*, and the hybrid swarms across five phenotypic traits.

Pairwise comparison	Sex combs	Face males	Anal plate bristles	Genital lobe area	Area wing
mau-HS	0.385, P < 1 × 10⁻⁴	-33.252, P < 1 × 10⁻⁴	0.38716, P < 1 × 10⁻⁴	-57.501, P < 1 × 10⁻⁴	27.568, P < 1 × 10⁻⁴
Sim-HS	-0.058, P = 0.253	-0.701, P = 0.763	0.02281, P = 0.462	0.792, P = 0.708	0.471, P = 0.885
Sim-mau	-0.443, P < 1 × 10⁻⁴	32.551, P < 1 × 10⁻⁴	-0.36435, P < 1 × 10⁻⁴	58.293, P < 1 × 10⁻⁴	-27.097, P < 1 × 10⁻⁴

Table S5. The hybrid swarms show mating characteristics similar to *D. simulans*. Pairwise comparisons between genotypes in their copulation latency and duration of matings involving males of the three genotypes and *D. simulans* females. Upper half of the triangular matrix shows the result of the t-value for the pairwise comparison in the Tukey HSD test. The lower half of the matric shows the associated p-value.

Latency		Tukey HSD		
	Mean(SD)	*D. simulans* × *D. simulans*	*D. simulans* × *D. mauritiana*	*D. simulans* × HS males
D. simulans × *D. simulans*	8.865 (2.616)	*	-10.621	-2.161
D. simulans × *D. mauritiana*	24.353 (5.694)	$<1 \times 10^{-4}$	*	11.049
D. simulans × HS males	11.328 (6.880)	0.0787	$<1 \times 10^{-4}$	*
Duration		**Tukey HSD**		
	Mean(SD)	*D. simulans* × *D. simulans*	*D. simulans* × *D. mauritiana*	*D. simulans* × HS males
D. simulans × *D. simulans*	30.973 (4.752)	*	10.588	1.672
D. simulans × *D. mauritiana*	9.853 (3.886)	$<1 \times 10^{-4}$	*	-11.482
D. simulans × HS males	28.366 (9.860)	0.214	$<1 \times 10^{-4}$	*

TABLE S6. Mean trait values (SD) and results from the linear models comparing mean trait values among replicates within *D. yakuba*, within *D. santomea*, and within the hybrid swarms produced with these two species. The F-values show the result of the linear model for each genotype and describe whether there was any phenotypic change in the course of the experiment for a set of bottles (i.e., genotype). All F values have 1,798 degrees of freedom.

		Sex comb teeth		Hypandrial bristles		Pigmentation	
		Mean (SD)	$\chi^2_{df=1}$; P	Mean (SD)	$\chi^2_{df=2}$; P	Mean (SD)	$F_{1,798}$
A	*D. yakuba*	7.031 (0.519)	0.014, 0.907	2 (0)	NV	563.125 (59.560)	0.0472, P = 0.828
B	*D. santomea*	8.9 (0.626)	0.194, 0.659	0.013 (0.158)	NV	50.125 (10.093)	18.915, P = 1.544 $\times$ 10^{-5}
C	*Hybrid swarms*	7.306 (1.182)	12.506, P = 4.056 $\times$ 10^{-4}	2 (0)	135.28, P < 1 $\times$ 10^{-10}	516.5 (57.410)	576.07, P < 1 $\times$ 10^{-10}

TABLE S7. Tukey HSD tests comparing the mean trait values in *D. yakuba*, *D. santomea*, and the hybrid swarms across three phenotypic traits.

Pairwise comparison	Sex combs	Hypandrial bristles	Pigmentation
san-HS	0.197, $P < 1 \times 10^{-5}$	NV	86.696, $P < 1 \times 10^{-10}$
yak-HS	-0.038, 0.628	NV	8.667, $P < 1 \times 10^{-10}$
yak-san	-0.236, $P < 1 \times 10^{-5}$	NV	95.364, $P < 1 \times 10^{-10}$

Table S8. The hybrid swarms show mating characteristics similar to *D. yakuba*. Pairwise comparisons between genotypes in their copulation latency and duration of matings involving males of the three genotypes and *D. yakuba* females. Upper half of the triangular matrix shows the result of the t-value for the pairwise comparison in the Tukey HSD test. The lower half of the matric shows the associated p-value.

Latency		Tukey HSD		
	Mean(SD)	*D. yakuba* × *D. yakuba*	*D. yakuba* × *D. santomea*	*D. yakuba* × HS males
D. yakuba × *D. yakuba*	12.243 (5.619)	*	-9.342	-0.566
D. yakuba × *D. santomea*	30.542 (10.815)	$<1 \times 10^{-5}$	*	10.546
D. yakuba × HS males	13.031 (7.193)	0.835	$<1 \times 10^{-5}$	*
Duration		**Tukey HSD**		
	Mean(SD)	*D. yakuba* × *D. yakuba*	*D. yakuba* × *D. santomea*	*D. yakuba* × HS males
D. yakuba × *D. yakuba*	34.568 (9.194)	*	4.080	-0.998
D. yakuba × *D. santomea*	25.000 (11.451)	1.82×10^{-4}	*	-5.650
D. yakuba × HS males	36.231 (8.349)	0.573	$<1 \times 10^{-5}$	*