Thirty-three new mutations in *D. simulans*

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About fifty visible markers across the *D. simulans* genome are currently available at the Tucson Drosophila Species Stock Center. We generated six new visible mutations by EMS mutagenesis of the *D. simulans st, e* strain (Tucson Drosophila Species Stock Center strain # 14021-0251.034) and of the *D. simulans* strain collected in Nueva (#14021-0251.006). These new mutations are described in Table 1. The three *white* alleles and the *forked* allele failed to complement the *D. simulans white*^{1} allele and the *D. simulans forked*^{1} allele, respectively. We did not obtain progeny from a cross between our *D. simulans crossveinless*^{2} line and *D. melanogaster crossveinless*^{1} which we performed to test allelism to *D. melanogaster crossveinless*. To our knowledge, the *D. simulans crossveinless*^{1} allele isolated by Sturtevant from a natural population (Sturtevant, 1929) has been lost. Our *crossveinless*^{2} allele is temperature-sensitive: homozygotes display the *crossveinless* phenotype at 17ºC and are wild-type at 25ºC. The new *forked*^{4} allele is strong and resembles the *D. melanogaster forked*^{36a} allele. The *Enhancer of Ubx* allele produces enlarged and flat halteres when transheterozygous with the In(3R)Ubx inversion but it does not give any phenotype in the absence of the In(3R)Ubx inversion.

We also generated 27 homozygous lethal mutations on chromosome three by EMS mutagenesis of the *D. simulans st, e* strain # 14021-0251.034. Mutagenized chromosomes were balanced over the *In(3R)Ubx* inversion (described in Coyne and Sniegowski, 1994) to prevent recombination events in the region covered by the inversion. 222 independent lines carrying a mutagenized chromosome 3 and a chromosome with the *In(3R)Ubx* inversion were generated and screened for recessive lethality, i.e. absence of *ebony* progeny (the *ebony* locus is located in the region covered by the inversion). We obtained 27 lines that produced no *ebony* progeny after at least five generations and we infer that each of these lines carries at least one lethal mutation balanced by *In(3R)Ubx*, which corresponds to regions 81F1-84F and 93F-89E1 in the *D. melanogaster* nomenclature (Coyne and Sniegowski, 1994). Three lines displayed a first-instar larva cuticle phenotype. In line *l(3)106*, anterior and posterior regions are abnormal. This phenotype is not caused by a mutation in the *huckebein* gene because line *l(3)106* complements the *D. melanogaster huckebein*^{2} mutation. Lines *l(3)39* and *l(3)207* failed to complement each other and displayed the same cuticle phenotype, with narrow ventral denticle bands and a malformed head region. This phenotype is characteristic of the *D. melanogaster krotzkopf verkehrt* mutation. Unfortunately we did not obtain progeny from a cross of these *D. simulans* lines with *D. melanogaster krotzkopf verkehrt*^{1} mutants.

All of these stocks, except for w^{3} and w^{4}, are available from the Tucson Drosophila Species Stock Center (http:// stockcenter.arl.arizona.edu).

Table 1. List of the new *D. simulans* mutations.

Allele name	Chromo-some	Strain used for mutagenesis	Phenotypic class	Mutant phenotype
white-apricot2 (*w^{a2}*)	X	14021-0251.006	visible recessive	Eye color: light orange
white-3 (*w^{3}*)	X	14021-0251.006	visible recessive	Eye color: white
white-4 (*w^{4}*)	X	14021-0251.006	visible recessive	Eye color: white
forked-4 (*f^{4}*)	X	14021-0251.034	visible recessive	Macrochaetes and microchaetes shorter and bent
crossveinless-2 (*cv^{2}*)	X	14021-0251.006	visible recessive, temperature-sensitive	Anterior and posterior crossveins missing
Enhancer of Utrabithorax (*E(Ubx)*)	3	14021-0251.034	dominant visible with In(3R)Ubx, homozygote viable	No phenotype on its own. In combination with In(3R)Ubx: enlarged and flat haltere
l(3)39 kkv?	3	14021-0251.034	lethal recessive	Cuticle phenotype: head skeleton malformed, denticle bands narrower
l(3)207 kkv?	3	14021-0251.034	lethal recessive	Cuticle phenotype: head skeleton malformed, denticle bands narrower
l(3)106	3	14021-0251.034	lethal recessive	Cuticle phenotype: anterior and posterior regions abnormal
24 lines named as l(3)* with * being a number between 6 and 209 {*l(3)6, l(3)8, l(3)11, l(3)22, l(3)35, l(3)52, l(3)89, l(3)91, l(3)107, l(3)111, l(3)118, l(3)121, l(3)125, l(3)130, l(3)143, l(3)162, l(3)169, l(3)186, l(3)187, l(3)189, l(3)191, l(3)200, l(3)203, l(3)209*}	3	14021-0251.034	lethal recessive	-

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References: Coyne, J.A. and Sniegowski, P.D. 1994, Dros. Inf. Serv. 75:36—37; Sturtevant, A.H., 1929, Carnegie Inst. Wash. Publ. 399: 1-62.