A natural mutation of *sepia* was identified among the descendants of *Drosophila* collected in Kiel, Germany in 2009. The flies were inbred for six generations with a chain of repeatedly isolated single sib-pair matings. The phenotype was recognized as consistent with classical *se* (CG6781; Bridges and Morgan, 1923) and the location was confirmed by a complementation test with *se*1. Part of the PDA synthase gene region was amplified and sequenced with a set of primers (5'-CTATCACACTTGCATCTTGGACC, 5'-GGAACCGTTATGGACTGCAATT, 56°C annealing, Kim et al., 2006) and the nature of the mutation was found to be a 40 base pair frameshift deletion in the second exon from position 3L:8521107..8521146 [+] (bases 461-500 of the CDS), which creates a premature stop codon at codon position 157 (the *sepia* gene product is normally 243 amino acids long). The deleted sequence is 5'-AGAATGCCGTCTGCTGACCCACAAATCCTACCAC. A set of diagnostic primers was designed with one primer within the deleted region that can test for the presence of the allele in heterozygotes by PCR (5'-GTGGGTAGAGCCAGGAAAACC, 5'-TCTGCTGGACCACAAAGAT, 60°C annealing). This allele is likely an amphor and is only the second molecularly characterized mutation of *sepia*. The allele, *se*Kiel, has been deposited at the Bloomington Drosophila Stock Center (Bloomington, IN 47405) as stock 55131 and is listed in FlyBase (St. Pierre et al., 2014) as http://flybase.org/reports/FBal0294757.html. Stocks obtained from the Bloomington Drosophila Stock Center (NIH P400D018537) were used in this study.


### New mutants of *Drosophila mediopunctata*.


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For almost three decades we have been working with *Drosophila mediopunctata*, a species of the *tripunctata* group (Yotoko et al., 2003), studying various aspects of its biology. In this note we describe new X-ray induced mutations in this species. We exposed three hundred males from two homokaryotypic strains ([150 males ITA-24P, phenotype: wild; chromosome karyotypes: II: DA-PA0/DA-PA0; III: St/St; IV: St/St; V: St/St; X: St/Y]; [150 males ITC-229ET, phenotype: wild; chromosome karyotypes: II: DI-PB0/DI-PB0; III: St/St; IV: St/St; V: St/St; X: St/Y]) to three X-ray doses (2200 rad; 4400 rad; and 6600 rad; equivalent to the absorbed dosage suggested by Marques et al., 1991). After one day of recovery, irradiated males were individually crossed with virgin females from the same strain or from a strain (CR-27A or CR-32C) with four visible mutations marking each major autosome (as described by Hatadani et al., 2004). In the first generation, we selected dominant visible mutations and those inherited in sexual chromosomes. Then, the F1 progeny were allowed to mate (brother-sister mating) to select recessive mutants in the F2 using the marked chromosomes.

We obtained three new *Delta* (Δ) alleles (Δ6 and Δ7 located in DA-PA0 chromosome from different X-ray mutated males ITA-24P; Δ8 located in DI-PB0 from an X-ray mutated male from ITC-229ET). *Delta* is a dominant mutation that produces deltas at junctions of wing veins, or wing veins with margins (Figure 1). We also found flies with yellow body color, named “louro” (ll) mutation from irradiated strain ITC-229ET flies (Figure 2). This mutation is recessive and linked to the X chromosome. It is probably homologous to *D. melanogaster yellow* gene. Our perspective is to develop new mutations and balanced strains with visible and cytological markers in all chromosomes in this species.
Figure 1. *Drosophila mediopunctata* Delta mutant wings. A) wild type; B) Δ5; C) Δ7; D) Δ8.

Figure 2. Adult males of *Drosophila mediopunctata*: A) *Drosophila mediopunctata* wild type; B) “louro” (ll) mutant (yellow body color).

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