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 sepia (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'-CTATCACCACTTGCATCTCTGGACC, 5'-GGAACCGGTTATGGACTGCATTTAT, 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'-AGAATGCCCGTCTGCTCGCCACCAAAGAATTCCGTACCAC. 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'-GTGGGTAGAGCCAGGAAACC, 5'-TCTGCTCGCCACCAAAGAAT, 60°C annealing). This allele is likely an amorph 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 P40OD018537) were used in this study.

References: Bridges, C., and T.H. Morgan 1923, *The Third-Chromosome Group of Mutant Characters of* Drosophila melanogaster. Carnegie Inst. Washington, Publ. 327, p. 86; Kim, J., H. Suh, S. Kim, K. Kim, C. Ahn, and J. Kim 2006, Biochem. J. 398: 451-460; St. Pierre, S.E., L. Ponting, R. Stefancsik, P. McQuilton, and the FlyBase Consortium 2014, Nucleic Acids Res. 42: D780-D788.

New mutants of *Drosophila mediopunctata*.

Batista, M.R.D.[a], V.M. Birsenek[1], F. Pradella[2], A.S. Farias[2], and L.B. Klaczko[1].
[1]Laboratório de Biodiversidade Genética e Evolução de *Drosophila*, Departamento de Genética, Evolução e Bioagentes, Instituto de Biologia, Universidade Estadual de Campinas – UNICAMP, Cx. Postal 6109, Campinas, 13083-970 SP, Brazil; [2]Neuroimmunomodulation Group, Departamento de Genética, Evolução e Bioagentes, Instituto de Biologia, Universidade Estadual de Campinas – UNICAMP, Cx. Postal 6109, Campinas, 13083-970 SP, Brazil. E-mail: LBK@unicamp.br

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 (Δ_6 and Δ_7 located in *DA-PA0* chromosome from different X-ray mutated males ITA-24P; Δ_8 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_3) 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.

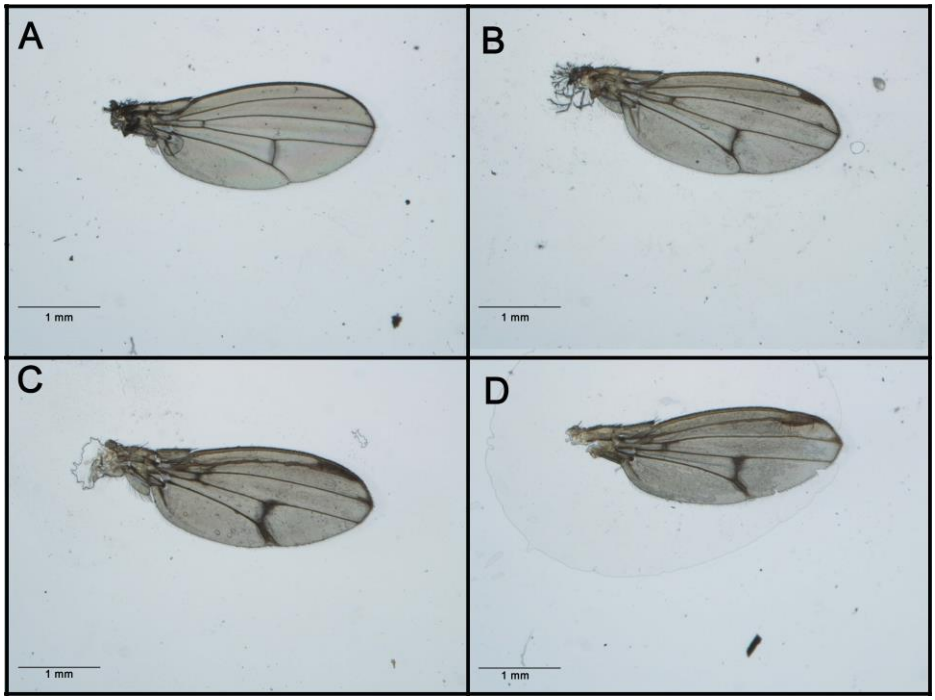

Figure 1. *Drosophila mediopunctata Delta* mutant wings. A) wild type; B) Δ_5; C) Δ_7; D) Δ_8.

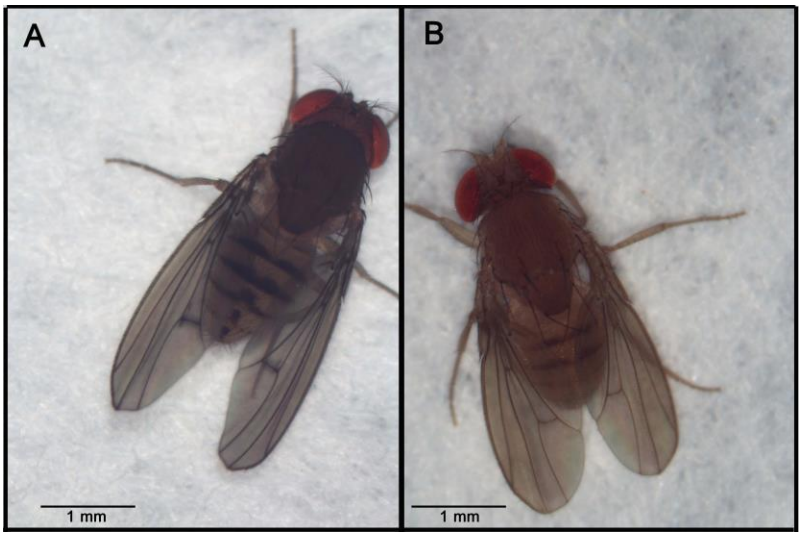

Figure 2. Adult males of *Drosophila mediopunctata*: A) *Drosophila mediopunctata* wild type; B) "*louro*" (*ll)* mutant (yellow body color).

Acknowledgments: We would like to thank Claudete do Couto and Klélia A. de Carvalho for technical help. We also thank Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Coordenação de Aperfeiçoamento de Pessoal de Ensino Superior (CAPES); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP); Fundo de Apoio ao Ensino e à Pesquisa (FAEPEX-UNICAMP) for financial support.

References: Hatadani, L.M., J.C.M. Batista, W.N. Sousa, and L.B. Klaczko 2004, Heredity 93: 525-534; Marques, H.V.S., A.B. Carvalho, C.A. Elias, and L.B. Klaczko 1991, Dros. Inf. Serv. 70: 280; Yotoko, K.S.C., H.F. Medeiros, V.N. Solferini, and L.B. Klaczko 2003, Mol. Phylogenet. Evol. 28: 614-619.