D-11: Organisation of a cloned repetitive DNA sequence in the genomes of mosquitoes (Diptera: Culicidae)

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A repetitive DNA fragment (Rp217) of size 120bp, isolated from the sibling species B of the *Anopheles culicifacies* complex and which had been

previously characterized by DNA sequencing, was examined for its organisation in the nosquito genomes. Dot-blot and Southern hybridization assays revealed that the sequences homologous to Rp217 were present in 9 species of mosquitoes examined, belonging to the sub-families Culicinae and Anophelinae. A higher copy number of this sequence was found in the genomes of species B and C of *Anopheles culicifacies* than in the genomes of other anophelines as well as Culex and Aedes mosquitoes. Surprisingly, Rp217 sequence was hardly detectable in the sibling species of A of *An. culicifacies* which may suggest that it is mutated in the genome of this species. Thus, Rp217 was a repetitive sequence common to the mosquito family Culicidae and may have evolved independently to maximize the divergence of *An. culicifacies* species A from B and C species.