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Repetitive DNA Localization in Two Homosequential Species of the Genus *Chironomus* Kieffer (Diptera: Chironomidae) and their Genome Reaction to Anthropogenic Factors

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Abstract: The two homosequential species *Chironomus riparius* Mg. and *Chironomus piger* Strenzke are differentiated at cytological level by the localization of their constitutive heterochromatin. They can also be distinguished by the number and position of the sites of two tandem repeated DNA families (Alu and Hinf) as well as by the number and position of fixed insertion sites of the retrotransposon NLRCth1. The phylogenetically younger species *C. riparius* is much richer in the above-mentioned repetitive DNA clusters than the phylogenetically older species *C. piger*. It is possible that both species have diverged from a common ancestor because of amplification and transposition processes of repetitive DNA elements in the younger species.
In both species the localization of repetitive DNA and breakpoints of chromosome rearrangements were significantly more frequent in the proximal than in the distal regions of chromosomes. *C. riparius* has a high frequency of somatic rearrangements (51.92%) distributed in the whole genome, while *C. piger* has a far lower amount of somatic aberrations (21.31%) concentrated in centromere or pericentromere regions of chromosomes. In both species the chromosome rearrangements are not randomly distributed along the polytene chromosomes. It was discussed that DNA clusters have played an important role in genomic reorganization under stress conditions.

Key words: Homosequential species, repetitive DNA clusters, species-specific markers, somatic rearrangements, NLRCth1 retrotransposon