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Cytogenetic and Molecular Analysis Aspects on some Local Romanian *Bombyx mori* Races

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SUMMARY

About 3000 distinct genotypes of *Bombyx mori*- an excellent model for Genomics- situates this species on second place after *Drosophila*, as an insect model for studying heredity which started in Japan, at the beginning of XIXth century.

The *appearance* of some local *B. mori* races in Romania imposed the necessity of studying them under cytogenetic and molecular aspects for their precise identification.

The analyses done on six Romanian *B. mori* races employing some classic cytogenetics methods (aceto-carmine, DAPI and Giemsa staining) have demonstrated normal meiotic and mitotic chromosomal complements (n=28; 2n=56) as well as in some cases hypo- and hyper-ploidy. Using TEM (transmission electron microscopy) technique, the synaptonemal complexes in pachytene-diplotene stages were detected. In silk-glands of IVth stage larvae, the polyteny phenomenon was described associated with the ribosomal gene amplification process visualized as a plethora of RNPs (ribonucleoprotein particles) of different sizes and shapes. The chromosomal bivalents in different stages of meiosis, with a typical structure and behavior, were identified.

Optimization and implementation of modern molecular methods, as well as the study of some molecular markers (RAPD-RFLP) allowed us to obtain different electrophoretic patterns valuable for differentiating and identification of the studied races.

All electrophoretic patterns obtained from PCR-RAPD reaction with *OPA4*, *OPA7*, *OPA8*, *P1*, *P4* and *P5* primers followed by RFLP reaction using *HaeIII* enzyme proved to be different, so that each studied race could be discriminated.

Applying molecular methods can be helpful in the breeding process of silkworms assisted by classical and modern molecular genetics approaches.