New Source of Genetic Polymorphisms in Lepidoptera?

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The variability level of the ISSR (inter-simple sequences repeat) primer $(GACA)_4$ was examined in the three Lepidoptera families Pyralidae, Sphingidae and Pieridae. Our study shows that the tetra-repeat $(GACA)_n$ is evidently present in sufficient numbers in these butterflies to provide informative DNA fingerprints. The variability is mostly rather high, but within a comparable range to other ISSR studies. Although less polymorphisms may be encountered in some butterfly families, this study indicates that high variability of this marker may be a common characteristic of Lepidoptera genomes. An appeal for a minimal level of standardization of ISSR-PCR data analysis is formulated to enable an exact comparison between the groups of organisms studied with this fingerprint technique.

Key words: GACA-ISSR-PCR, Standardization, Lepidoptera