Article

Experimental population genetics in insects: inheritance of ISSR-PCR bands in an artificial population

ANNA K. HUNDSDOERFER [1,2] & MICHAEL WINK [1]

[1] *Institut für Pharmazie und Molekulare Biotechnologie, Abt. Biologie, Im Neuenheimer Feld 364, D-69120 Heidelberg, Germany. Tel. +49 6221 54 48 80 and Fax. +49 6221 54 48 84. E-mail: wink@uni-hd.de*

[2] *Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde, Königsbrücker Landstr. 159, D-01109 Dresden, Germany. Tel. +49 351 89 26 301 and Fax. +49 351 89 26 327. E-mail: anna.hundsdoerfer@senckenberg.de*

Abstract

Inter-simple sequence repeat (ISSR)-PCR fingerprints are being increasingly used to establish relationships between closely related animals, although their inheritance patterns have not been examined closely as yet. To better understand the genetics of this relatively novel genomic fingerprint technique and to assess the tokogenetic information content of the data for the *Hyles euphorbiae* (Linnaeus, 1758) complex (HEC; Lepidoptera: Sphingidae) precisely, we examined five separated pairs of moths of *Hyles euphorbiae* from Spain (10 moths) and their offspring as an artificial population. ISSR-PCR fingerprints were obtained with four primers and the 0/1 matrix analysed. The cluster algorithm Neighbour Joining was successful in reconstructing the families as monophyletic, although intra-familial cluster formation cannot be represented by a dichotomous branching pattern. In contrast, the band sharing index did not detect significant differences in variability between siblings and individuals of *H. euphorbiae* from different localities compared at random. Rather high levels of recombination were detected, which surprisingly did not appear to obscure the tokogenetic signal to a significant degree. Thus ISSR-PCR fingerprints appear to be appropriate markers to study relationships between HEC individuals of two consecutive generations, while being too variable for higher levels.

Key words: genomic fingerprint, tokogeny, signal, recombination, siblings

Introduction

Analyses of differences in genetic characteristics as molecular markers for population structure have also become important in taxonomy and systematics. The genetics of many fingerprint markers is, however, not yet fully understood. Inheritance patterns of inter-simple sequence repeat (ISSR)-PCR fingerprints (Gupta *et al.* 1994, Zietkiewicz *et al.* 1994) have been examined; studies of the segregation of ISSR-PCR bands have corroborated the expected Mendelian inheritance pattern in plants (e.g., Fang & Roose, 1999) and animals (e.g., Nagaraju *et al.* 2002). The technique is being used to rapidly differentiate closely related individuals (e.g., Pradeep *et al.* 2005), examine genetic diversity (e.g., Kol & Lazebny, 2006) and establish relationships between closely related organisms (e.g., Hundsdoerfer *et al.* 2005b, Perteguer *et al.* 2008). Unlike nucleotide sequences, ISSR markers describe DNA characteristics at several, mostly nuclear, chromosomal loci and thus avoid the use of gene trees as surrogates of species trees (Martin & Salamini 2000). Bornet and Branchard (2001) provide a more detailed description of the method and Hundsdoerfer *et al.* (2005b) and Hundsdoerfer and Wink (2005) review the use of this technique in (zoological) genetic studies of natural populations (particularly Lepidoptera).

In a previous study (Hundsdoerfer *et al.* 2005b) we have used ISSR-PCR bands in an attempt to produce a more detailed and informative evolutionary history of the *Hyles euphorbiae*-complex (henceforth the HEC; Lepidoptera: Sphingidae) without prior knowledge of their patterns of inheritance in these organisms. The