Genetica
DOI 10.1007/s10709-011-9601-1

Structure and population dynamics of the major satellite DNA in the red flour beetle *Tribolium castaneum*

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Received: 5 May 2011 / Accepted: 1 August 2011

Abstract In the beetle genus *Tribolium*, satellite DNAs comprise a significant amount of pericentromeric heterochromatin and are characterized by rapid turnover resulting in species specific profiles. In the present work we characterize the major pericentromeric satellite DNA TCAST of the beetle *T. castaneum* and analyse its population dynamics. Using direct sequencing of genomic PCR products we show that the TCAST satellite exists in the form of two related subfamilies: Tcast1a and Tcast1b that make up 20 and 15% of the genome, respectively. Tcast1a and Tcast1b have consensus sequences of 377 and 362 bp respectively, share an average similarity of 79% and are characterized by a divergent, subfamily specific region of approximately 100 bp. The two subfamilies are prevalently organized in the interspersed form, although a portion exists in the form of homogenous tandem arrays composed of only Tcast1a or Tcast1b. The pattern of restriction enzyme digestion indicates that Tcast1a and Tcast1b are organized in composite higher order repeats. Comparison of sequence variability of Tcast1a and Tcast1b among ten strains reveals a difference in the frequency of particular mutations present at some positions. However, no difference in the organization and in the amount of subfamilies was detected among strains. The results show that direct genomic sequencing can be a useful method for the detection of population specific features of satellite DNA. In the case of TCAST satellite DNA, changes in the mutational profiles seem to represent the first step in the genesis of a population specific satellite profile.

Keywords Satellite DNA · Heterochromatin · Concerted evolution · *Tribolium castaneum*

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Introduction

Satellite DNAs are tandemly repeated sequences that are present as long uninterrupted arrays in heterochromatic regions of most eukaryotes (Charlesworth et al. 1994; Ugarković and Plohl 2002). In the insect genus *Tribolium* (Tenebrionidae, Coleoptera) cytogenetic studies of eight species revealed a conserved karyotype of 20 or 18 chromosomes characterized by the presence of large blocks of pericentromeric heterochromatin (Juan and Petitpierre 1991). Molecular analyses suggested that these blocks are composed almost exclusively of satellite DNAs that comprise up to 40% of the whole genome and encompass the regions of functional centromeres (Ugarković et al. 1996; Durajlija Žinić et al. 2000). *Tribolium* species have sequence specific satellite DNA profiles: in each species a single highly represented satellite is detected and the satellites exhibit no significant sequence similarity except common structural features in the form of stable dyad structures and A + T rich blocks (Plohl et al. 1993; Ugarković et al. 1996; Mravinac et al. 2004). Due to the high turnover of *Tribolium* satellite DNAs it may be expected that the divergence of their profiles precedes the speciation process and could be detected even at the population level.

In the red flour beetle *T. castaneum*, TCAST satellite DNA has been previously characterized as the major

Published online: 12 August 2011