ABSTRACT

Mitotic metaphase karyotypes and larval salivary gland polytene chromosomes of two major tropical insect pests i.e. the Asian papaya fruit fly, Bactrocera papayae Drew and Hancock and the carambola fruit fly, B. carambolae Drew and Hancock were studied. The initial cultures were obtained from MARDI Serdang, and laboratory populations were established in UKM and maintained at 25±1°C with 70±5% relative humidity and a 10h light-14h dark cycle. Mitotic chromosomes were obtained from the neural ganglia of third-instar larvae using 5% Giemsa and polytene chromosomes were examined from the salivary gland of third-instar larvae using lacto-acetic-orcein method. The karyotypic complements of B. papayae and B. carambolae consist of five autosomal pairs and one pair of sex chromosomes (females XX/males XY). Chromosome morphology was determined from the mean of 30 measured metaphase preparations for each species. The karyotype formulae of both species were 2sm+1m+2a+Xm/Ydot-shape. In all somatic cells of B. papayae and B. carambolae, homologous chromosomes showed tendency to adjoin each other at metaphase. Analysis of polytene chromosomes of B. papayae and B. carambolae showed total number of 10 polytene arms. The X and Y chromosomes, being under replicated (not polytenized), were not visible in the polytene nuclei. Thus the five polytene chromosomes must correspond to the five autosomes of the mitotic nuclei. The identifying tips, characteristic features and the most prominent landmarks of each polytene chromosome were determined based on the standard procedure for the polytene chromosomes of the Mediterranean fruit fly, Ceratitis capitata. Photographic polytene chromosome maps were constructed for B. papayae and chromosomal homology to those of B. carambolae was determined by comparing chromosome banding patterns. The whole polytene genome was divided into 100 sections and each component, irrespective of its size, into 20 sections, and further into subsections considering prominent or distinctive banding features. The chromosomes of B. papayae showed extensive banding pattern similarities to the chromosomes of B. carambolae. In particular, the banding patterns homology of chromosomes 2 (right arm), 3, 4 and 5 (right arm) of both species were very remarkable. The homology of the left arm of chromosome 2 extends over sections 1-2 and 9, and for the right arm, in sections 12-13 and 17-20. The banding homology of chromosome 3 extends over the full length. The tips of chromosome 3 of B. papayae can be correlated with the respective tips of chromosome 3 of B. carambolae. The homology of chromosome 4 was clearly observable in sections 41, 45-49, 57-60 in terms of corresponding telomere regions, band structure and presence of puffs along the chromosome length. The homology of chromosome 5 was supported by identical banding pattern similarities between the right arms of both species whereas the left arm had limited similarity, restricted to the tip and section 66. Chromosome 6 of both the species was somewhat difficult for observing details of banding homology due to their twisting and folding nature. However, similarities were noticed for the telomere regions of both arms, conspicuous puffs in sections 82 and 98, and a particular banding morphology of sections 88-89. These findings indicate that karyotypic information and salivary gland polytene chromosomes of these two species would be of significant importance to gain insight into the structure, organization and evolution of the B. papayae and B. carambolae genomes and in improving control interventions.

Publications

