

In this study, the possibility of using *Ceratitis capitata* (medfly)-derived microsatellites both for developing an SSR-based species-diagnostic PCR assay and studying the genetic structures of a range of congeneric, economically important African fruit fly species has been investigated. The medfly SSR primers used were based on published sequences obtained from the GenBank database. Twenty-four medfly SSR were screened for amplification on the genomic DNA of *C. rosa*, *C. jasciventris* and *C. cosyra*. All primer pairs produced PCR products in at least one of the three species examined. Amplification success ranged from 79.2% (*C. cosyra*) to 91.3% (in both *C. rosa* and *C. jasciventris*). Specifically, a number of loci differentially amplified in the four species examined: of the 24 loci screened, 17 were common to all, five were PCR-negative in *C. cosyra*, two were negative in *C. rosa* and in *C. jasciventris*, while one locus amplified only in *C. capitata*. The majority of the amplicons were similar, if not identical in size to those expected in the medfly. The structures of the repeat motifs and their flanking sequences were examined at a total of repeat units were (CA)_n(TG)_m. Some species-specific nucleotide differences were observed among the four species. Ten of the cross-species SSRs markers were used to survey the levels of genetic variability and analyse the genetic aspects of the population dynamics of *C. rosa*, *C. jasciventris* in Africa, in comparison with variability data from *C. capitata*. The loci proved to be informative. The degree of microsatellite polymorphism in *C. rosa* and *C.*