The spatial genetic differentiation of the legume pod borer, *Maruca vitrata* F. (Lepidoptera: Crambidae) populations in West Africa

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**ABSTRACT**

We applied a set of microsatellite markers to assess the population structure of *Maruca vitrata* collected at five sites from Burkina Faso, Niger and Nigeria. Observed polymorphism ranged from 1 to 8 alleles per locus, and observed heterozygosities were from 0.0 to 0.8. Analysis of molecular variance (AMOVA) indicated that 67.4% of the genetic variation was among populations and among individuals (Table 1). Using a set of microsatellite markers to develop microsatellite markers by enrichment with biotinylated (CA) and (GA) probes followed by cloning and sequencing of individual microsatellite loci. The original *M. vitrata* genomic DNA samples were also genotyped using polymerase chain reaction (PCR) markers that amplified the microsatellite loci. The number of alleles per locus, observed heterozygosities and expected heterozygosities were calculated using AMOVA. 3.3.2.3. The program STRUCTURE 2.3.3 was used to estimate the co-ancestry among *M. vitrata* genotypes and to estimate the number of distinct populations (K) present in the set of samples.

**RESULTS**

The 6 microsatellite loci used to screen *M. vitrata* samples collected at 5 West African sites showed significant deviation from HWE at 13 instances following 30 loci-by-site calculation. The mean number of alleles per locus was similar across all sample sites and the overall observed heterozygosity was less than expected (Table 1). The program STRUCTURE predicted the number of distinct ancestries to be three genetically distinct subpopulations of *M. vitrata* across West Africa. The three genetically distinct ancestries exist across collection sites were represented in Figure 1 as vertical bars with Niger, Nigeria and Fada, Burkina Faso primarily green, Farkoko, Burkina Faso primarily brown, Kamboinse, Burkina Faso primarily green and red and a minor cluster represented by yellow across sites.

**DISCUSSION**

Our study indicated some level of genetic differentiation in *M. vitrata* populations in West Africa and that there may be 3 distinct subpopulations of *M. vitrata* in West Africa. This evidence suggest that although *M. vitrata* has a seasonal north-south migration, there appears to be evidence of reduced gene flow that results in population differentiation. Regression of uncorrected *F* estimates and geographic distance (km) among West African sample sites showed a significant dependence of genetic variation on geographic distance (*R* = 0.6, Mantel *P* = 0.04), and showed the relative genetic similarity (*F* estimates of genotypes at Niger and Nigeria, and at Burkina Faso sample sites (Figure 1). The "real" number of populations (K) estimated from the microsatellite-defined *M. vitrata* genotypes from the ML(K|X|L) statistic calculated from STRUCTURE 2.3.3 output achieved a maximum value of 14.5 at K = 3 and suggested that three genetically-distinct *M. vitrata* ancestries exist in West Africa. The three genetically distinct ancestries are primarily green, brown and red for the different stages of seasonal migration.

Figures and tables are not included in the natural text representation.