

Population genetic structure of the migratory rice leaf roller, *Cnaphalocrocis medinalis* (Lepidoptera: Pyralidae), inferred from the mitochondrial A+T-rich region and nuclear ITS2 sequences

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Genet. Mol. Res. 10 (1): 273-294 (2011)

Received September 9, 2010

Accepted November 10, 2010

Published February 22, 2011

DOI 10.4238/vol10-1gmr1005

ABSTRACT. The population genetics of the migratory rice leaf roller, *Cnaphalocrocis medinalis* (Lepidoptera: Pyralidae), was characterized using the maternally inherited mitochondrial A+T-rich region and bi-parentally inherited nuclear internal transcribed spacer 2 (ITS2). One hundred and eighty-seven specimens of the rice leaf roller collected from 13 Korean and Chinese localities revealed 94 A+T-rich region haplotypes, ranging in sequence length from 339 to 348 bp and 129 ITS2 sequence types, ranging from 444 to 450 bp, with maximum sequence divergences of 4.55 and 4.43%, respectively. The finding of almost no significant F_{ST} even among Chinese and Korean localities, except for one

Chinese island population (ITS2 only), and the finding of genetic variance principally at the within-population level indicate the genetic structure characteristics of a migratory insect that is well connected among populations due to high gene flow. Detection of significant F_{ST} estimates of one offshore island population in China (Haikou) compared to most others only by ITS2 rather than by the mitochondrial A+T-rich region, as well as the somewhat higher degree of genetic differentiation seen on ITS2, suggest the importance of female dispersal. Structural analysis of the A+T-rich region revealed a poly-T stretch (10-16 bp), a microsatellite-like AT repeat (10-14 repeats), and a 5-bp long-motif "ATTTA". The typical 5-bp long conserved motif sequence (ATAGA) previously detected in other lepidopterans was found to be ATAG in the *C. medinalis* A+T-rich region.

Key words: *Cnaphalocrocis medinalis*; A+T-rich region; ITS2; Population genetics; Genetic diversity; Gene flow