

**Phylogeographic Patterns of Introduced Populations
of the Coffee Berry Borer *Hypothenemus hampei* (Ferrari)
(Coleoptera: Scolytidae)
Inferred from Mitochondrial DNA Sequences**

**H. BREILID¹, L. O. BRUN², D. ANDREEV¹, R. H. FRENCH-CONSTANT³,
L. R. KIRKENDALL¹**

¹Department of Zoology, University of Bergen, Bergen, Norway

²Institut Français de Recherche Scientifique pour le Développement en Coopération
(ORSTOM), Nouméa, New-Caledonia

³Department of Entomology, University of Wisconsin-Madison, Madison, USA

SUMMARY

The coffee berry borer, *Hypothenemus hampei* (Ferrari), is one of the most serious pests in commercial coffee production. The species is thought to have originated in equatorial Africa but has now spread to most of the major coffee growing regions of the World; it was first recorded from the Far East (Java) in 1909 and the Neotropics (Brazil) in 1924. The genetic variation of 17 widespread populations of *H. hampei*, was assessed by sequencing a 1200 bp regions of the mtDNA genome. A cladistic analysis resolved the haplotype sequences into three main lineages: 1) Mexico, Central America and South America, 2) Central Africa, 3) an unresolved group including the populations from Asia, Ivory Coast, Jamaica and New Caledonia. These results give us an insight into both the genetic relationships among far-flung populations and the main patterns in the dispersal. Three of the populations from New Caledonia are resistant to endosulfan and other cyclodiene-type insecticides. We suggest that this sort of analysis may serve in risk assessment of potential resistance in closely related populations.