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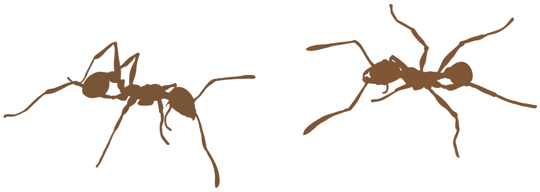

ANTS AND SPECIATION PATTERNS

Himender Bharti

Department of Zoology,
Punjabi University Patiala, India-147002
www.antdiversityindia.com
himenderbharti@antdiversityindia.com/himender_bharti@yahoo.com

The process of speciation has been a debated issue among evolutionary biologists for a long time now. How new species originate in nature and which selective agents force them to do so has been a puzzling question. Various models have been proposed theoretically, but the most accepted model to date is allopatric speciation, i.e. reproductive isolation attained by geographical separation. The late evolutionary biologist Ernst Mayr argued throughout his life in favour of allopatric speciation, but other models gained momentum as well. Guy Bush's findings in 1969 on fruitflies set the tone with the sympatric mode (in which reproductive isolation occurs without geographical separation). Subsequently there was recognition of other modes: peripatric (speciation by modification of peripherally isolated founder populations), parapatric (where populations have contiguous but not overlapping ranges) and stasipatric (speciation by chromosomal rearrangements giving homozygotes which are adaptively superior in part of the original range). Although it is hard to conceive of the forces that can prevent gene exchange in sympatry, scientific evidence has been pouring in consistently (Butlin & Tregenza, 1997; Dieckmann & Doebeli, 1999; Coyne & Orr, 2004; Feder *et al.*, 2005; Balakrishnan & Sorenson, 2006).

Ants could act as model organisms for the study of speciation patterns. Scattered evidence has trickled in from studies conducted on ants, but no serious effort has been made to investigate ants as model organisms. I wish to present here some plausible reasons to do so. They have been haunting my mind for a long time now; it seems timely to share them, as perhaps we will reach a pinnacle of myrmecological work in the coming years, given the efforts being put forth by ANeT and other myrmecologists around the globe.

1. The mode of reproduction in ants is based on the haplodiploidy phenomenon, the males being haploid and the workers and queens being diploid. Males receive only one genetic