



GENETIC STUDIES OF MEAT ANTS

(*IRIDOMYRMEX PURPUREUS*).

by

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SUMMARY

Meat ants (*Iridomyrmex purpureus* Smith) occur in a number of forms or varieties (approximately eight), which differ in colour and nest structure. However, the absence of clear morphological differences between them has resulted in uncertainty about their taxonomic status and evolutionary relationships. Examination of their ranges throughout Australia shows that they fit into an overall distribution pattern which suggests some degree of ecological differentiation. This is also indicated by detailed examination of areas where two or more colour forms are sympatric. One of the major aims of this project was to determine whether any genetic evidence existed which could be used to clarify the relationships between these forms.

One approach to this problem involves the use of allozyme loci detected by gel electrophoresis. Several polymorphic loci have been identified which show substantial differences in frequency, or an almost complete lack of shared alleles, between some combinations of colour forms. In various areas, it is possible to distinguish almost every colour form, on the basis of its allele frequencies at one or more of these loci. This indicates that they are not interbreeding, and that the meat ant group comprises a complex of sibling species.

Some alleles also show considerable geographic variation in frequency within colour forms, in a way which does not appear to be related to any obvious environmental variables. Factors contributing to this variation could include geographic subdivision of the range of some colour forms, and the fact that breeding only occurs in very specific weather conditions, which may only occur over a small area at any one time. Gene flow between geographically distant populations may therefore be restricted. However, it is not certain whether their gene

frequencies have diverged as a result of differing local selection, or by a combination of founder effects and drift.

Estimating gene frequencies in meat ants is more complicated than in other organisms, since the sterile worker caste is usually all that can be collected. For a locus with co-dominant alleles (e.g., *Amylase*), the genotypes of the sexual portion of the population can be inferred from the genotypes of the workers in each nest. For a locus with dominance this is not possible since heterozygotes cannot be recognized. A maximum likelihood procedure has therefore been used to estimate the gene frequencies of recessive alleles, especially in the case of a null allele at the locus *Esterase-1*.

Several polymorphic marker loci have also provided valuable insights into some aspects of meat ants' social behaviour. In particular, genetic differentiation on a very small scale has been detected, apparently caused by the presence of queens of differing genotypes in colonies which are adjacent, but which do not exchange workers across territorial boundaries.

A total of 15 loci were surveyed in four populations to determine the level of genetic variation present. The average heterozygosity per locus was 3.8% which is much lower than the values for *Drosophila*, other insects, and other invertebrates, but comparable to the results commonly found in vertebrates. It is also very similar to the levels observed in a variety of other species of Hymenoptera which have been surveyed. These species are very diverse in habitat, degree of social behaviour, niche width, and life style. A single explanation for their low levels of heterozygosity in terms of environmental heterogeneity or other parameters is therefore unlikely to be found. Haplodiploidy

itself seems to be the only factor which these species have in common, and both "selectionist" and "neutralist" points of view can provide reasons why this might produce low levels of genetic variability.

This multi-locus survey was also used to derive genetic distances between populations, and a dendrogram was constructed showing the relationships of nine populations, including five colour forms. This did not provide a clear indication of their phylogenetic relationships however, since the extent of geographic variation within colour forms was sometimes greater than the differences between them.

Attempts to establish the relationships among the colour forms using karyotypes and morphological data were also made. These did not provide conclusive results, but when added to the ecological, genetic, taxonomic and behavioural information which is now available they contribute further to increasing our understanding of many aspects of the biology of this group of species.