CARYOLOGIA Vol. 43, n. 3-4: 321-334, 1990

VARIATIONS AND TAXONOMIC SIGNIFICANCE OF THE CHROMOSOME NUMBERS IN THE NEARCTIC SPECIES OF THE GENUS *LEPTOTHORAX* (S.S.) (FORMICIDAE: HYMENOPTERA)

ROBERT LOISELLE, ANDRÉ FRANCOEUR, KARL FISCHER * and ALFRED BUSCHINGER *

Université du Québec à Chicoutimi, Chicoutimi (Québec), Canada G7H 2B1; and * Institut für Zoologie, Fachbereich Biologie, der Technischen Hochschule Darmstadt, D-6100 Darmstadt, FR Germany.

SUMMARY — The taxonomic situation of the genus *Leptothorax* (sensu stricto = subgenus *Leptothorax* sensu Smith 1950) appears particularly puzzling in North America when using morphological characters alone. This paper analyses the taxonomic impact of the complex variations observed in the chromosome numbers of the presently recognized species. The method of Imai modified for some details was applied to specimens obtained from colonies reared in laboratory. These were collected between 1978 and 1984, in different regions of Québec and in Alberta for Canada, in New Hampshire and Utah for USA. Over 250 slides of testes (male pupae) or brain (female prepupae) were prepared. Results for the nearctic species are compared to European data. For the traditional *muscorum* taxon as applied in North America the haploid numbers varied from 15 to 23 including supernumerary chromosomes. At least four distinct species can be extracted from these results. Male diploidy is documented. Different tendencies are stressed between the actual subgenera *Leptothorax* and *Myrafant.*

INTRODUCTION

In our revision of the northern genera of the tribe Leptothoracini (see FRANCOEUR *et al.* 1985), we have undertaken the study of the ant genus *Leptothorax* (sensu stricto = subgenus *Leptothorax* sensu Smith 1950). The taxonomic situation of this genus appears particularly puzzling in North America when using morphological characters alone. The karyotypes of the constituent species (old and new) were examined in the hope to untangle this situation. Special attention was paid to *L. muscorum* which shows some more or less typical phenotypes in different regions of its large geographical distribution. Do the observed phenotypes correspond to variations in chromosome numbers? If so, is it possible to match different chromosome numbers to