ANT CHROMOSOMES

II. KARYOTYPES OF WESTERN PALEARCTIC SPECIES *

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SUMMARY

The chromosome numbers of 40 ant species are reported. For 22 species the karyotypes as well as the chromosome numbers are presented. The chromosome numbers range between n = 8 and n = 26. Remarkable karyotypes are those of the genus *Lasius* in exhibiting mainly acrocentric chromosomes. In all other karyotypes the majority of chromosomes show medio- or submediocentric centromere position.

Differences in chromosome numbers in the genus *Camponotus* reflect the grouping in subgenera with the exception of *Tanæmyrmex*. This pattern is not true for the genera *Aphænogaster* and *Leptothorax*, where a variety of chromosome numbers were found in the different subgenera.

ZUSAMMENFASSUNG

Ameisenchromosomen. - II. Karyotypen westpaläarktischer Arten

Die Chromosomenzahlen von 40 Ameisenarten werden mitgeteilt. Für 22 Arten wird zusätzlich der Karyotyp vorgelegt. Die haploiden Chromosomenzahlen bewegen sich zwischen n = 8 und n = 26. Bemerkenswert sind die Karyotypen der Gattung *Lasius*. Diese Karyotypen besitzen, abgesehen von einem oder zwei mediozentrischen Paaren, ausschliesslich acrozentrische Chromosomen. Alle übrigen Karyotypen bestehen überwiegend aus medio- bzw. submediozentrischen Chromosomen.

In der Gattung *Camponotus* entspricht die Gruppierung in Untergattungen auch einer Gruppierung von unterschiedlichen Chromosomenzahlen. Für die Gattungen *Aphæno-gaster* und *Leptothorax* gilt diese Entsprechung nicht.

INTRODUCTION

The origin of the Formicidæ is in the Mesozoic era (WILSON *et al.*, 1967), so the morphological and behavioural characteristics as well as the chromosome sets could develop over a long time span. In fact, the haploid chromosome numbers of Formicidæ cover the range between 4 (HAUSCHTECK, 1962 ; IMAI and KUBOTA, 1972) and 42 (IMAI *et al.*, 1977), eventually even more than 45 (TAYLOR, 1978). The chromosome diversification arose independently in different subfamilies. Mechanisms of karyotype evolution, such as centric fission and fusion, chromosome polymorphism, B chromosomes, translocations, pericentric and paracentric inversions and DNA amplification have been discussed by CROZIER (1975) and IMAI *et al.* (1977).

Besides insights into general mechanisms of karyotype evolution, which are summarized for instance by JOHN and LEWIS (1968) or WHITE (1973), the karyotype analysis should clarify taxonomy. The karyotypical variability in some genera, e.g. *Camponotus* or *Aphænogaster*, can be quite large. Of course, morphological or ecological variability of a taxon does not have to be paralleled by karyological variability.

CROZIER (1975) summarized all chromosomal data on ants up to 1975. Since then, additional results were presented on the genus *Formica* (HAUSCHTECK-JUNGEN and JUNGEN, 1976) on Australian species (IMAI *et al.*, 1977). In spite of a relatively large number of species investigated up to now, cytotaxonomic information on the western palearctic ant species is still fragmentary. With two exceptions, this paper presents karyotypes of European and North African species of Formicidæ. Most of the chromosome numbers are already previously mentioned in CROZIER (1975).

MATERIAL AND METHOD

As in other insects, the suitable material to find mitosis are the cerebral ganglia of prepupæ. Dissected ganglia from all castes available were kept in sterile ringer solution to which Colcemid was added to a final concentration of 0,004 %. After one to three hours incubation the organs were transferred to a 1 % sodium citrate solution for 20 to 40 min. They were then fixed in 50 % acetic acid and stained in acetic orcein. The cells were squashed under a siliconized coverslip, which was removed after being frozen on dry ice. Permanent preparations were made by mounting in Euparal. For determination of the chromosome number ten mitoses with the same maximal chromosome number were thought to be enough to determine the diploid or haploid chromosome number of the species.

RESULTS AND DISCUSSION

Bothriomyrmex : The karyotype of *B. gibbus* (not figured, *table I*) is characterized by one long subtelocentric chromosome, twice as long as the

next one, which is submediocentric. Pair three is mediocentric, pairs five and six are submediocentric. The smaller chromosomes are acrocentric.

Tapinoma (fig. 1 a, 1 b, table I) : The karyotype of *T. erraticum* looks similar to one of the karyotypes known from the American *T. sessile*. CROZIER (1970 b) describes for this species a chromosomal polymorphism, the karyotypes differing by pericentric inversions. One of the karyotypes
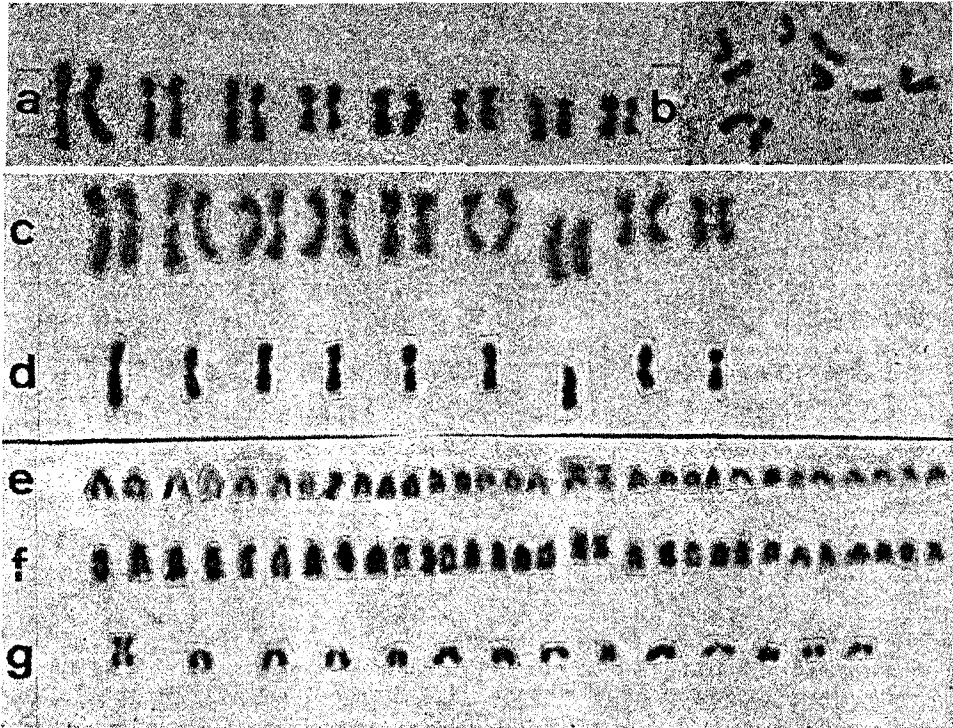

Fig. 1. — Karyotypes and metaphase plate. 2 000 ×.
  a) *Tapinoma erraticum*, diploid set, 2 n = 16.
  b) *T. nigerrimum*, haploid metaphase, n = 9.
  c) *Plagiolepis pygmaea*, diploid set, 2 n = 18.
  d) *P. barbara*, haploid set, n = 9.
  e) *Lasius (Lasius) alienus*, diploid set, 2 n = 30.
  f) *L. (Cautolasius) flavus*, diploid set, 2 n = 30.
  g) *L. (Dendrolasius) fuliginosus*, haploid set, n = 14.

Abb. 1. — Karyotypen und Metaphaseplatten. 2 000 ×.
  a) *Tapinoma erraticum*, diploider Satz, 2 n = 16.
  b) *T. nigerrimum*, haploide Metaphase, n = 9.
  c) *Plagiolepis pygmaea*, diploider Satz, n = 18.
  d) *P. barbara*, haploider Satz, n = 9.
  e) *Lasius (Lasius) alienus*, diploider Satz, 2 n = 30.
  f) *L. (Cautolasius) flavus*, diploider Satz, 2 n = 30.
  g) *L. (Dendrolasius) fuliginosus*, haploider Satz, n = 14.

Table I. — Haploid chromosome numbers of European and North African ant species. Metaphases from queens and workers were diploid, those from males haploid. At least one nest from each collection site was analysed. Nests with chromosomal aberrations are omitted here.
CH : Switzerland, D : Federal Republic of Germany, E : Spain, F : France, GR : Greece, I : Italy, TN : Tunisia, USA : United States of America, YU : Yugoslavia. n : haploid chromosome number.

Tabelle I. — Haploide Chromosomenzahlen europäischer und nordafrikanischer Ameisen-arten. Metaphasen von Königinnen und Arbeiterinnen waren diploid, solche von Männchen haploid. Von jedem Fundort wurde mindestens ein Nest untersucht. Nester, in denen Tiere mit chromosomaler Aberration gefunden wurden, sind hier nicht aufgeführt.
CH : Schweiz, D : Bundesrepublik Deutschland, E : Spanien, F : Frankreich, GR : Griechenland, I : Italien, TN : Tunesien, USA : Vereinigte Staaten von Amerika, YU : Jugoslawien.
n : haploide Chromosomenzahl.

Species	Collection site	n	Caste analysed	Number of nuclei analysed
Dolichoderinæ				
Tapinomini				
Bothriomyrmex gibbus	Genova (I)	11	☿	> 10
Tapinoma erraticum	Pfinwald (CH) Dielsdorf (CH) Boppelsen (CH) Prèles (CH) Locarno (CH)	8	♀ ☿ ♂	> 10
T. nigerrimum	Tunis (TN) Tabarka (TN)	9	♂	> 10
T. simrothi	Tunis (TN) Jefna (TN) Malaga (E)	9	♀ ☿	> 10
Formicinæ				
Plagiolepidini				
Plagiolepis barbara	Tunis (TN)	9	☿ ♂	> 10
P. pygmaea	Torremolinos (E) Malaga (E) Loja (E) Tessin (CH) Wallis (CH) Podgara (YU)	9	♀ ☿ ♂	> 10
Formicini				
Lasius (Cautolasius) flavus	Zürich (CH)	15	♀ ☿	> 10
L. (Dendrolasius) fuliginosus	Zürich (CH) Pavia (I)	14	☿	> 10
L. (Lasius) alienus	Kaiserstuhl (D) Sur En (CH) Celoni Gerona (E) Fürstenau (CH)	15	♀ ☿	> 10
Camponotini				
Camponotus (Camponotus) ligniperda	Wallis (CH)	14	♀ ☿	> 10
Camponotus (Myrmosericus) cruentatus	Diezma (E)	18	♀	7

Species	Collection site	n	Caste analysed	Number of nuclei analysed
C. (M.) rufoglaucus	Sedjenane (TN) Tabarka (TN) Granada (E)	18	☿ ♂	> 10
Camponotus (Tanæmyrmex) œthiops	St-Giles (F) Yugoslavia	21	♀ ☿	> 10
C. (T.) alii	Alcoy (E)	21	☿	6
C. (T.) compressus	Tabarka (TN) Tunis (TN)	20	☿ ♂	> 10
C. (T.) foreli	Malaga (E)	17	♀ ☿ ♂	> 10
C. (T.) pilicornis	Ordal (E)	25	☿	6
C. (T.) sylvaticus	Rhodos (GR) Hospitalet (E) Ordal (E)	20	☿ ♂	> 10
Cataglyphis albicans	Hospitalet (TN)	26	♂	> 10
C. bicolor	Israel Tabarka (TN)	26	♀ ♂	> 10

Ponerinæ

Ponerini

    Ponera pennsylvanica USA 6 ♀ ☿ > 10

Myrmicinæ

Myrmicini (broad sense)

Aphœnogaster (Aphœnogaster) depilis	Tunis (TN) Sedjenane (TN)	17	☿	2
A. (A.) sardoa	Sedjenane (TN)	17	☿	2
A. (A.) testaceopilosa	Malaga (E) Tunis (TN) Sibenik (YU)	17	☿ ♂	> 10
Aphœnogaster (Attomyrma) subterranea	Pfinwald (CH) Tessin (CH) Prèles (CH) Kaiserstuhl (D)	11	♀ ☿.	> 10
Harpagoxenus sublœvis	Nürenberg (CH)	20	☿ ♂	> 10
Leptothorax (Leptothorax) acervorum	Bonn (D) Sur En (CH) Wallis (CH) Malix (CH)	13	☿ ♂	> 10
Leptothorax (Myrafant) interruptus	Würzburg (D)	12	☿	> 10
L. (M.) nylanderi	Boppelsen (CH)	11	☿ ♂	3
L. (M.) schaumi	Ithaka (USA)	9	♂	2
L. (M.) tuberum	Graubünden (CH) Wallis (CH) Braunwald (CH) Sur En (CH)	9	♀ ☿ ♂	> 10

Species	Collection site	n Caste analysed	Number of nuclei analysed
L. (M.) unifasciatus	Bonn (D) Prèles (CH) Dielsdorf (CH) Graubünden (CH)	9 ☿	> 10
Manica rubida	Bürglen (CH)	22 ☿	> 10
Myrmica lævinodis	Greifensee (CH) Zürich (CH)	24 ♀ ☿	> 10
M. ruginodis	Fürstenau (CH)	24 ♂	> 10
M. sabuleti	Rodels (CH)	23 ♀	> 10
M. schencki	Switzerland	23 ☿	> 10
M. sulcinodis	Povil Muogl (CH)	24 ☿ ♂	> 10
Pheidole pallidula	Tessin (CH) Gordemo (CH) Malaga (E) Rhodos (GR) Gabès (TN)	10 ♀ ☿ ♂	> 10

has a single acrocentric chromosome pair like *T. erraticum*. *T. melano-cephalum* differs from all other species in having only n = 5 chromosomes (CROZIER, 1970 b).

Plagiolepis: The karyotypes of *P. pygmœa* and *P. barbara* look very similar *(fig. 1 c, 1 d, and table I)*.

Lasius: Chromosome numbers of *L. alienus*, *L. flavus* and *L. fuliginosus* were already reported by HAUSCHTECK (1962) *(table I)*. In this work the karyotypes of these species are shown *(fig. 1 e-g)*. Our results are confirmed for *L. alienus* from England (PEARSON, pers. comm.). However, in the drawing of HAUSCHTECK (1962) the diploid metaphase plate displays only 28 chromosomes instead of 30 as in this paper. In the case of the n = 14 chromosomes one large submediocentric chromosome was found which is absent in all n = 15 *Lasius* karyotypes.

Other species with n = 14 chromosones are *L. pallitarsis* from the USA, reported by HUNG (1969), and *L. fuliginosus (fig. 1 g, table I)*. The karyotype of this latter species includes two mediocentric chromosomes in contrast to the n = 15 species which exhibit only one.

For *L. niger* we confirm the karyotype as published by IMAI (1969) and IMAI and KUBOTA (1972) from Japan. It resembles those of the *Lasius* species with 15 chromosones, as for instance *L. alienus*, *L. flavus* or *L. nearcticus* (CROZIER, 1970 a).

Judging from the representation of the *Lasius* phylogeny given by WILSON (1955), one may assume that n = 15 was the basic number of the genus.
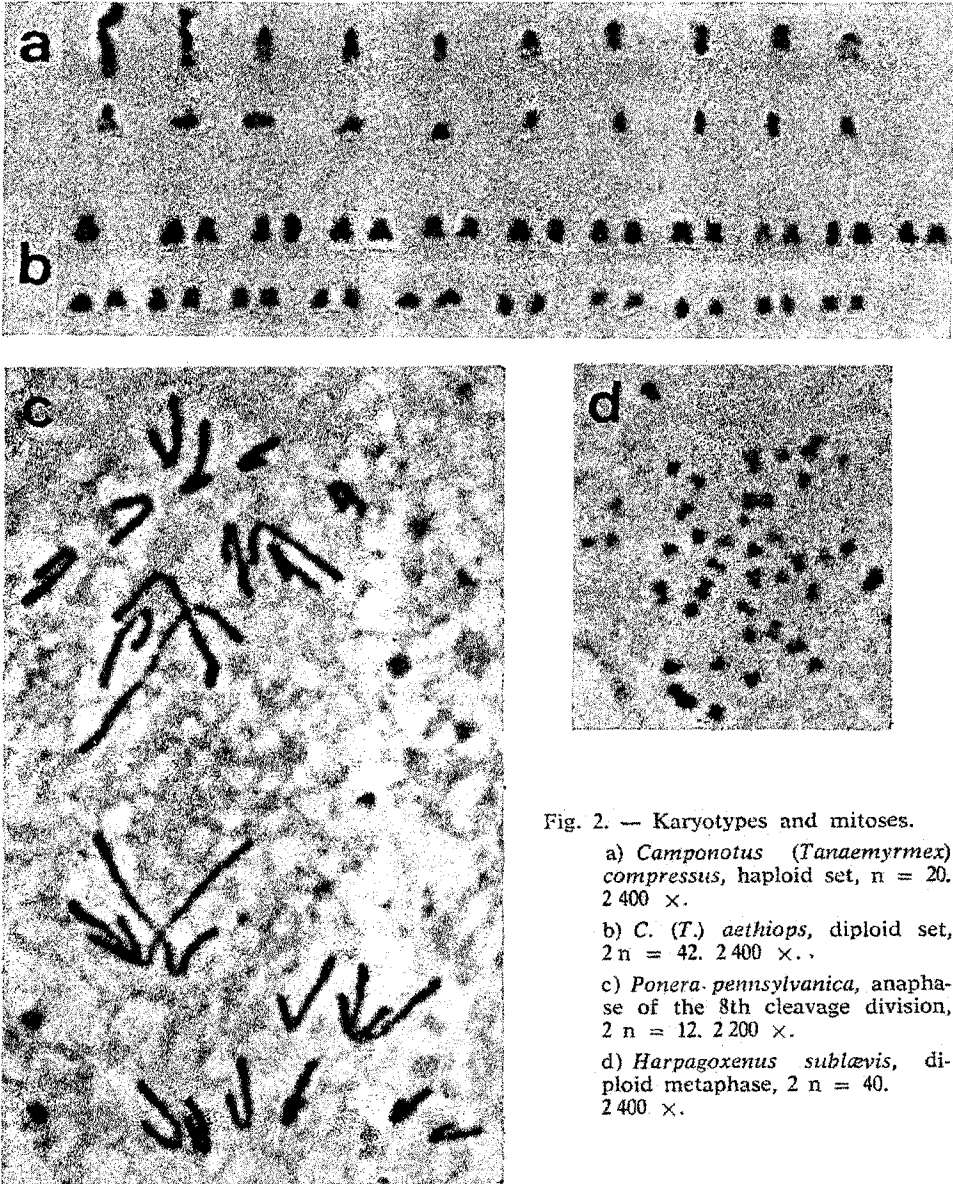
Fig. 2. — Karyotypes and mitoses.

a) *Camponotus (Tanaemyrmex) compressus*, haploid set, n = 20. 2 400 ×.

b) *C. (T.) aethiops*, diploid set, 2 n = 42. 2 400 ×.

c) *Ponera pennsylvanica*, anaphase of the 8th cleavage division, 2 n = 12. 2 200 ×.

d) *Harpagoxenus sublævis*, diploid metaphase, 2 n = 40. 2 400 ×.

Abb. 2. — Karyotypen und Mitosen.

a) *Camponotus (Tanaemyrmex) compressus*, haploider Satz, n = 20. 2 400 ×.

b) *C. (T) aethiops*, diploider Satz, 2 n = 42. 2 400 ×.

c) *Ponera pennsylvanica*, Anaphase der achten Furchungsteilung, 2 n = 12. 2 200 ×.

d) *Harpagoxenus sublaevis*, diploide Metaphase, 2 n = 40. 2 400 ×.

Table II. — Haploid chromosome numbers in the subgenera of Camponotus. Compiled data.

Tabelle II. — Haploide Chromosomenzahlen in den Untergattungen von Camponotus. Zusammenstellung der bis jetzt bekannten Zahlen.

Subgenus	Species group	Species	Haploid chromosome number	Geograph. origin	Source
Camponotus		japonicus	13, 14	Japan	IMAI, KUBOTA (1972)
		ligniperda	14	Switzerland	HAUSCHTECK (1961)
		obscuripes	14	Japan	IMAI (1969)
		vagus	14	Switzerland	HAUSCHTECK (1962)
Colobopsis	impressus	sp.	26	USA	CROZIER (1970)
Myrmamblis		tokioensis	9	Japan	IMAI, KUBOTA (1972)
		sp.	9	Japan	" "
Myrmentoma	lateralis	lateralis	14	Switzerland	HAUSCHTECK (1962)
Myrmosericus		cruentatus	18	Spain	HAUSCHTECK-JUNGEN, JUNGEN (this work)
		rufoglaucus	18	Spain, Tunisia	" " "
Myrmothrix		rufipes	20	Uruguay	Goñi (pers. comm.)
Paramyrmamblis		kiusiuensis	14	Japan	IMAI (1966)
Tanaemyrmex	aethiops	ethiops	21	France, Yugoslavia	HAUSCHTECK-JUNGEN, JUNGEN (this work)
	aethiops	foreli	17	Spain	" " "
	compressus-sylvaticus	compressus	10	India	KUMBKARNI (1965)
	compressus-sylvaticus	compressus	20	Tunisia	
	compressus-sylvaticus	pilicornis	25	Spain	} HAUSCHTECK-JUNGEN, JUNGEN (this work)
	compressus-sylvaticus	sylvaticus	20	Spain, Greece	
	irritans-thraso	alii	21	Spain	
	picipes-fumidus	bonariensis	20	Uruguay	Goñi (pers. comm.)

Camponotus : Karyotypes are presented from *C. (Tanœmyrmex) œthiops* and *C. (T.) compressus (fig. 2 a, 2 b).*

This genus includes as many as 1 500 species, subspecies, and varieties, now subdivided into about 45 subgenera. In this group, chromosome numbers (from n = 9 to n = 25) and morphology of chromosomes are highly variable (IMAI, 1966 and 1969 ; IMAI and KUBOTA, 1972 ; CROZIER, 1970 ; KUMBKARNI, 1965 ; IMAI *et al.,* 1977). Therefore it seems attractive to look at the chromosome numbers in the subgenera *(table II).* In spite of the fact that taxonomists as for instance EMERY (1925) were aware that some groups are rather artificially defined, the different subgenera seem to be characterized by different chromosome numbers. The uniform look of taxa like *Myrmamblis* or *Myrmosericus* may partially be induced by the small numbers of species investigated. So, *Camponotus s. str.* seems to be characterized by n = 14, *Myrmamblis* by n = 9, *Myrmosericus* by n = 18. In *Tanœmyrmex,* species are assembled with rather high chromosome numbers. The only exception here would be *C. compressus,* described by KUMBKARNI (1965), from India. Unfortunately, in his paper convincing photographs are missing. However, our Tunisian specimens fit well the general trend. No correlation is visible as yet between the species groups and chromosome numbers within *Tanœmyrmex.*

Cataglyphis : In *C. albicans* and *C. bicolor* (not figured, *table I),* the three largest chromosomes are submediocentric. The smallest chromosomes are at the limit of being recognized by the light microscope and may be of the smallest ones found in ants.

Ponera : Figure 2 c shows an anaphase from an egg. All chromosomes are obviously long which on one hand is due to the early stage of development from which the nucleus was taken. On the other hand species with low chromosome numbers as also known from *P. scabra* (n = 7) (IMAI and KUBOTA, 1972) and *Stenamma brevicorne* (n = 4) (HAUSCHTECK, 1962) have larger chromosomes than species with high chromosome numbers.

Aphaenogaster : In our material we found two groups of karyotypes, one with n = 11 and the other with n = 17. *A. subterranea·(fig. 3 a)* belongs to the first group and all of its chromosomes are longer than those of the n = 17 karyotypes. With the exception of one acrocentric chromosome all are mediocentric. From the n = 17 group the karyotype of *A. testaceopilosa (fig. 3 b)* was compared to *A. subterranea.* In the first group of six chromosomes all are submedio- or mediocentric, the remaining chromosomes are submedio- or acrocentric.

A. subterranea inhabits central and southern Europe, spreading to the Caucasus. In contrast, the three remaining species with higher chromosome numbers are restricted to the Mediterranean area. This situation — different climatic regions inhabited by species with different chromosome numbers — is paralleled in Japan where *A. smythiesi (table III)* is of temperate origin
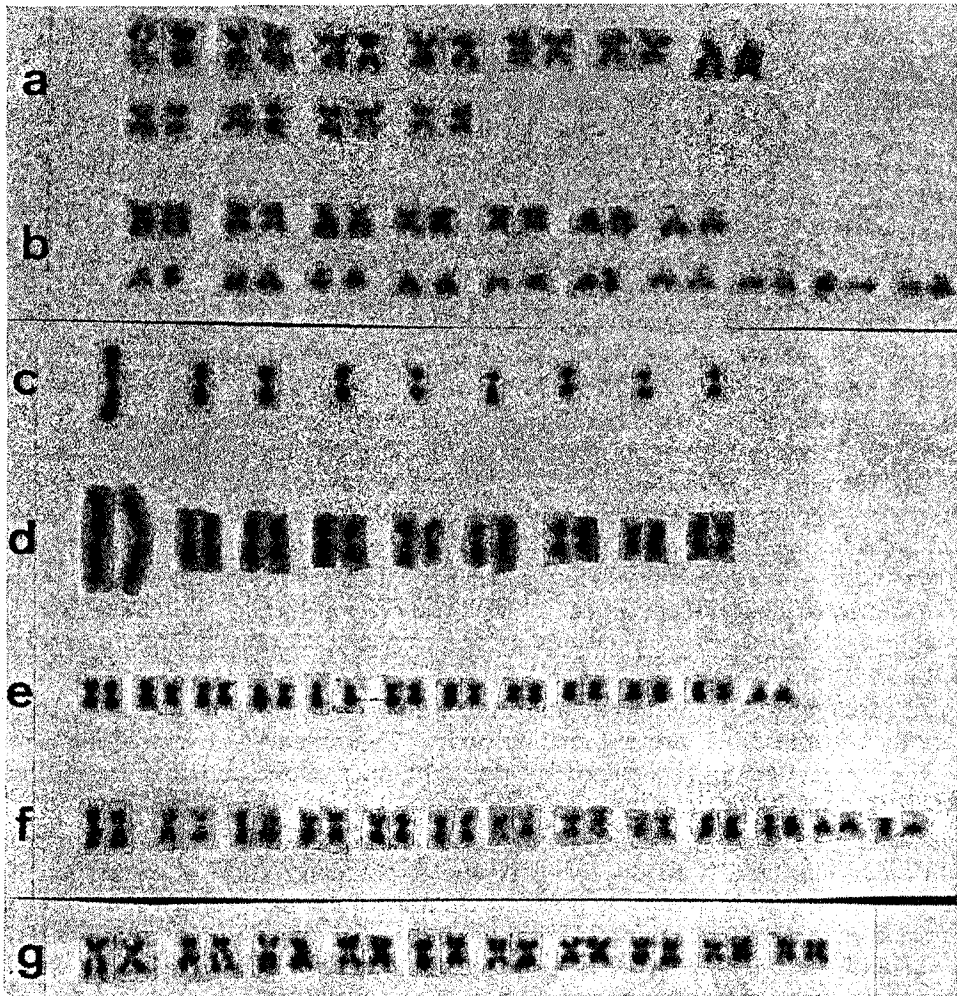
Fig. 3. — Karyotypes. 2 000 ×.
    a) *Aphænogaster subterranea*, diploid set, 2 n = 22.
    b) *A. testaceopilosa*, diploid set, 2 n = 34.
    c) *Leptothorax (Myrafant) tuberum* haploid set, n = 9.
    d) *L. (M.) unifasciatus*, diploid set, 2 n = 18.
    e) *L. (M.) interruptus*, diploid set, 2 n = 24.
    f) *L. (M.) acervorum*, diploid set, 2 n = 26.
    g) *Pheidole pallidula*, diploid set, 2 n = 20.

Abb. 3. — Karyotypen. 2 000 ×.
    a) *Aphænogaster subterranea*, diploider Satz, 2 n = 22.
    b) *A. testaceopilosa*, diploider Satz, 2 n = 34.
    c) *Leptothorax (Myrafant) tuberum*, haploider Satz, n = 9
    d) *L. (M.) unifasciatus*, diploider Satz, 2 n = 18.
    e) *L. (M.) interruptus*, diploider Satz, 2 n = 24.
    f) *L. (M.) acervorum*, diploider Satz, 2 n = 26.
    g) *Pheidole pallidula*, diploider Satz, 2 n = 20.

Table III. — Haploid chromosome numbers of *Aphaenogaster* species, subdivided into subgenera according to EMERY (1922). Compiled data.

Tabelle III. — Haploide Chromosomenzahlen, die in *Aphaenogaster*-Arten vorkommen. Die Gattung wurde nach EMERY (1922) in Untergattungen eingeteilt. Zusammenstellung der bis jetzt bekannten Zahlen.

Subgenus	Species	Haploid chromosome number	Geographic origin	Source
Aphaenogaster	*depilis*	17	Mediterranean	⎫
	sardoa	17	Mediterranean	⎬ HAUSCHTECK-JUNGEN, JUNGEN (this work)
	testaceopilosa	17	Mediterranean	⎭
Attomyrma palearctic spec.	*famelica*	17	Japan	IMAI (1966, 1971)
	gibbosa	11	Switzerland	HAUSCHTECK-JUNGEN, JUNGEN (this work)
	osimensis	16	Japan	IMAI (1971)
	smythiesi	11	Japan	IMAI (1969, 1971)
	subterranea	11	Switzerland	HAUSCHTECK (1962), HAUSCHTECK-JUNGEN, JUNGEN (this work)
nearctic spec.	*fulva*	18	USA	⎫
	lamellidens	19	USA	⎪
	miamiana	18	USA	⎪
	" rudis "	18	USA	⎬ CROZIER (1977)
	" rudis "	20	USA	⎪
	" rudis "	21	USA	⎪
	" rudis "	22	USA	⎪
	treatae	21	USA	⎭
Nystalomyrma	*longiceps*	23, 22	Australia	IMAI et al. (1977)

whereas *A. osimensis* and *A. famelica* with higher chromosome numbers are assumed to be of tropical origin (IMAI, 1971). However, a detailed analysis of European and Japanese species with the same chromosome numbers reveals many differences in chromosome sizes and centromere positions. So one has to conclude that either the same chromosome numbers are derived independently or, if *A. subterranea* and *A. smythiesi* are close relatives, the karyotypes, although from a common ancestor, have differentiated themselves by pericentric inversions and translocations. Evidence that pericentric inversions have played a role in the evolution of *Aphænogaster* may be drawn from karyotypes with even higher chromosome numbers but only a few acrocentric chromosomes, as for instance in the Australian species *A. longiceps* with n = 23 (IMAI *et al.*, 1977) or some American species (CROZIER, 1977). In *A. rudis* karyotypes with n = 21 chromosomes two or three additional acrocentrics were found but those are much smaller and perhaps relicts of centric fission. It is tempting to assume that such medium sized acrocentric chromosomes are protected from being changed by pericentric inversions.

Table III gives the subdivision of the investigated species into subgenera. In *Aphænogaster* s. str. there are only species with n = 17. They are probably closely related to each other. The palearctic species group of *Attomyrma* is marked by the occurrence of n = 11 karyotypes, whereas the American species show higher chromosome numbers from n = 17 to n = 22. We guess that a number like n = 17 or near was present in the common ancestor of *Aphænogaster* s. str. and *Attomyrma*. However, IMAI (1971) proposed a hypothetical basic karyotype with n = 8 chromosomes, all medio- or submediocentric, for the Japanese *Aphænogaster* species.

Harpagoxenus (fig. 2 d, table I) : *H. sublævis* is a dulotic species and a parasite mainly of *Leptothorax acervorum*. Both genera are commonly regarded as closely related. BUSCHINGER (1971) stated that *H. sublævis* together with other parasitic species are closer to the *Leptothorax* subgenus *Mychothorax* than to *Leptothorax* s. str. KUTTER (1977) calls *Harpagoxenus* like some other social parasitic genera a " satellite genus " of *Leptothorax* in the sense that these social parasites are all derived from *Leptothorax* species and are still parasiting on their ancestral forms or at least on a related species. However, the karyotype of *H. sublævis* differs remarkably from that of *L. acervorum* as well as from the karyotypes of other *Leptothorax* species. So we think that *H. sublævis* is rather distant from the genus *Leptothorax*.

Leptothorax (fig. 3 c-f, table I) : The karyotypes of *L. (M.) interruptus* and *L. (L.) acervorum* resemble each other in spite of the species belong to different subgenera, and there is no evidence for a close relationship.

IMAI and KUBOTA (1972) described the karyotype of the Japanese species *L. congruus* with n = 9 chromosomes which seems to be identical with the n = 9 karyotypes given in this paper, because the submediocentric chromo-
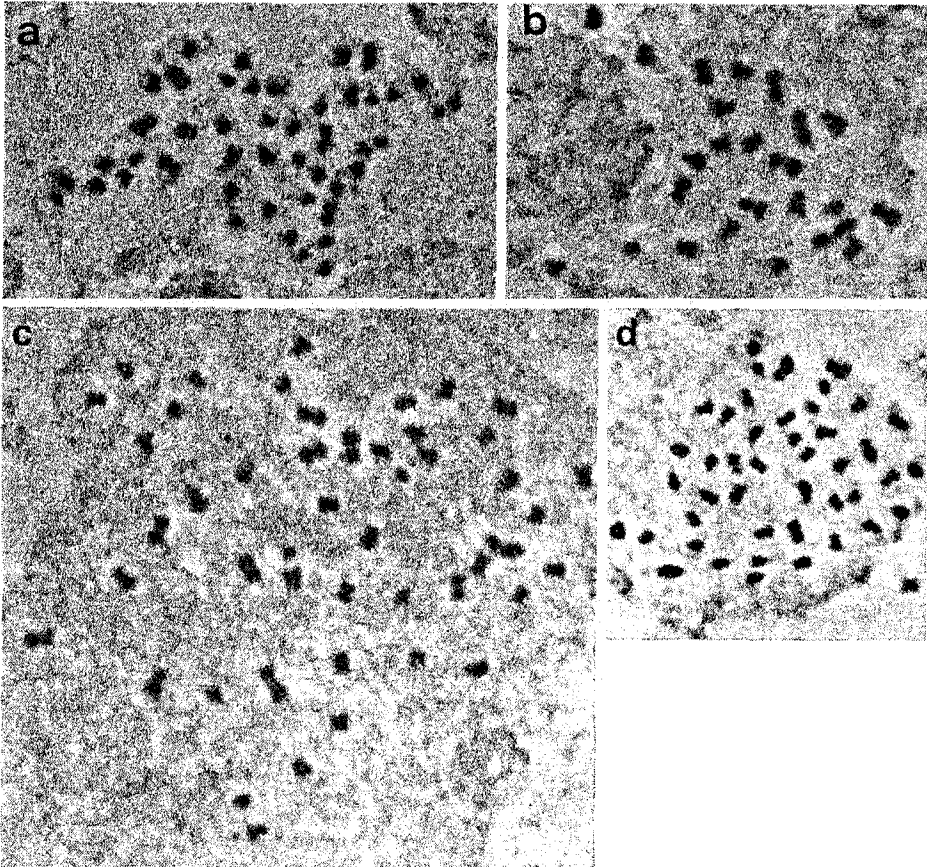
Fig. 4. — Metaphase plates. 2 000 ×.
  a) *Myrmica schencki,* diploid metaphase, 2 n = 46.
  b) *M. ruginodis, haploid metaphase,* n = 24.
  c) *M. laevinodis,* diploid metaphase, 2 n = 48.
  d) *Manica rubida, diploid metaphase,* 2 n = 44.

Abb. 4. — Metaphasenplatten. 2 000 ×.
  a) *Myrmica schencki,* diploide Metaphase, 2 n = 46.
  b) *M. ruginodis,* haploide Metaphase, n = 24.
  c) *M. laevinodis,* diploide Metaphase, 2 n = 48.
  d) *Manica rubida,* diploide Metaphase, 2 n = 44.

some may be placed at the fifth position as well as at the sixth. But also the morphological similarity of the n = 12 karyotypes seems quite high. So *L. spinosior* from Japan (IMAI, 1966), *L. longispinosus* from the USA as well

as *L. interruptus* from Switzerland seem to contain one subtelocentric chromosome besides medio- and submediocentric elements.

Manica : Manica rubida (fig. 4 d, table I).

Myrmica : (fig. 4 a-c, table I).

BERNARD (1968) divided the European *Myrmica* species into two groups. The *scabrinodis* group shares a short scapus in the male and a preference for warm and dry habitats whereas the *rubra* group assembles species with a long scapus in the males and a preference for cooler and moister nesting sites. Of our investigated species, *M. sabuleti* and *M. schencki* belong to the first group, *M. lævinodis*, *M. ruginodis*, and *M. sulcinodis* to the second. Moreover, *M. lobicornis* which shows n = 24 chromosomes (unpublished) belongs also to the second group. So it seems that, in addition to morphological characters, the *scabrinodis* group is characterised by n = 23 chromosomes and the *rubra* group by n = 24. IMAI (1969) listed *M. rubra*, which may be *M. ruginodis* or *M. lævinodis*, with n = 23.

Pheidole (fig. 3, table I): HAUSCHTECK (1961) drew from *P. pallidula* a set of 2 n = 24 instead of 2 n = 20 chromosomes with at least one chromosome pair obviously smaller than the others, thus differing from the karyotype in this paper. A reinspection of the slides confirmed the number. So this species is probably polymorphic for the chromosome number. *P. pallidula* is not the only polymorphic species of this genus. IMAI and KUBOTA (1972, 1975) observed a series of different chromosome numbers in *P. nodus*, a Japanese species, which polymorphism is brought about by Robertsonian rearrangements. In three American species the karyotypes are similar as in *P. pallidula*, also with n = 10 chromosomes (CROZIER, 1970 a).

CONCLUDING REMARKS

The chromosome numbers presented in this paper fit the range of those already known and reviewed by CROZIER (1975). B-chromosomes as occurring in Japanese ants (IMAI, 1974) were not observed.

The cytotaxonomic results in the family Formicidæ are, in spite of the investigation of a large number of species, rather poor what concerns insights into phylogenic relationships among the subfamilies. The main reason may be the remarkable karyotype evolution in the different taxa. This fact is not surprising if one considers that the evolution of the Formicidæ must have begun not later than during the cretaceous period or 100 million years ago. In the Baltic ambers we find many still existing genera, or at least near relatives. So it would be unwise to speculate about phylogeny on the level of subfamilies, on the contrary, we think that the study of ant cytotaxonomy may be promising between the level of tribes and the level of

species groups and in some cases even on the level of species. In general, we obtained satisfying concordance between the karyological findings and groupings established by taxonomists on morphological traits.

The genera *Tapinoma, Plagiolepis, Lasius,* and *Myrmica* exhibit more or less stable chromosome numbers. A stable karyotype can consist of acrocentric chromosomes as in *Lasius* s. str. No pericentric inversion has changed the centromeric position in any of these species. But stable karyotypes may also carry mainly medio- and submediocentric chromosomes, as in *Myrmica* or *Formica* (HAUSCHTECK-JUNGEN and JUNGEN, 1976). It seems that in all of these cases speciation is not obviously correlated with karyotype evolution. On the other hand species within the genera *Camponotus, Aphœnogaster* and *Leptothorax* differ greatly in their chromosome numbers.

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