As already discussed in part I of this series (Imai, 1969), two major types of origins were showed in Japanese ants based on distribution patterns and karyotype analysis. One is the tropical origin, in which are included species of tropical type I and temperate type I. These species were postulated to have spread to Japan from tropical regions after the latest glacial age of this epoch, and are called "Neo" species. The remaining group of Japanese species is of temperate origin, in which are included species referred to as temperate type II. These species were considered to be presented in Japan before the latest glacial age of the Caenozoic, and are called "Relict" species.

As temperate type I is assumed to have differentiated from tropical type I, *famelica* seems to be closely related to *osimensis*. On the contrary, *smythiesi*, which belongs to temperate type II seems to be rather distant from other two species. Thus, by borrowing the symbols, "→" and "//", which were used for comparing morphological character, the phylogenetic relation could be expressed in the following ways: o→f // s.

Finally, the results of karyotype analysis of these three species are seen to have some phylogenetic utility. The karyotype formula of these three species are expressed as follows:

For *osimensis*, $n=1SM^{2SC}+1ST^{SC}+2M+2SM+10A=16$;
For *famelica*, $n=2T^{SC}+1ST^{SC}+2M+2SM+10A=17$;
For *smythiesi*, $n=1SM+1M+9SM=11$.

The karyotype evolution of these species can be explained by polyploidization and by centric dissociation which are assumed to be characteristic for the alteration of ant's karyotype. It is found that 16 haploid chromosomes of *osimensis* counted 8 pairs of morphologically "homologous" chromosomes as if 16 chromosomes are diploid (Plate 3, figs. 1, 2). The same condition is also found in the karyotype of *famelica* (Plate 3, figs. 3, 4). These evidences strongly suggest that the karyotype of *osimensis* and *famelica* duplicated from the common 8 haploid chromosomes, which could be assumed to be basic number of chromosomes in *Aphaenogaster*. As already mentioned in part I, the mode of basic number of Hymenoptera is $n=7$, 8, and 10 (White, 1954; Nogusa and Kato, 1962, 1963; Nogusa, 1965). Therefore the duplication theory of the *Aphaenogaster* karyotype is not incompatible with the general tendency of the karyotype evolution found in Hymenoptera.

The karyotype of *smythiesi* is much different from those of the other two species (Plate 3, figs. 5, 6). However, there are several common chromosomes, namely, one largest submetacentric, one middle sized submetacentric chromosomes. In order to identify the common ancestral karyotype of these three species, the following three assumptions have to be made. First, the middle sized acrocentric chromosomes of *osimensis* and *famelica* were induced from submetacentrics found in *smythiesi* by inversion. Second, the karyotypes of *osimensis* and *famelica* were brought about by a duplication from the basic karyotype of $n=8$. Third, partial polyploidization of submetacentric chromosomes should occur in the karyotype of *smythiesi*. On these assumptions, the common ancestral karyotype could be deduced as follows: