

$$n=1SM+1SM+1M+5SM=8.$$

Starting from this formula, evolutionary changes in the karyotype of these three species can be hypothesized. The karyotype of *smythiesi* can easily be derived by a partial polyploidy of three medium sized SM chromosomes, possibly through a series of nondisjunctions. Thus the chromosome number increases and the karyotype would be:

$$n=1SM+1SM+1M+1SM+2(3SM)+1SM=11$$

The karyotype of *osimensis* might develop through three hypothetical steps. The first step would be the occurrence of pericentric inversions, which produce two types of chromosomes, namely,  $1SM^{2sc}$  from the largest SM and 4A from 4SM chromosomes, respectively. The karyotype can be expressed in the following formula:

$$n=1SM^{2sc}+1SM+1M+5A=8.$$

The second step would be the genome duplication. The chromosome number is doubled to  $n=16$ . The chromosome configuration is then:

$$n=2(1SM^{2sc}+1SM+1M+5A)=16.$$

The third step would be a chromosome breakage at the secondary constriction of the short arm of one of the large  $SM^{2sc}$  chromosomes. This gives rise to a small sized submetacentric chromosome from the large original one having one secondary constriction on its long arm. The haploid set could be shown by the following configuration:

$$n=1SM^{2sc}+1ST^{sc}+2(1SM+1M+5A)=16.$$

This corresponds to the karyotype formula of the present *osimensis*.

The karyotype of *famelica* could be derived from the karyotype of *osimensis* by centric dissociation of the remaining one large submetacentric chromosome having two secondary constrictions ( $SM^{2sc}$ ), giving rise to two telocentric chromosomes having one secondary constriction in their long arms. Therefore, the chromosomes would increase to  $n=17$  as shown in the following formula:

$$n=2T^{sc}+1ST^{sc}+2(1SM+1M+5A)=17.$$

These relations are shown schematically in Fig. 3.

The phylogenetic relation of the three Japanese *Aphaenogaster* were morphologically showed  $o \rightarrow f \rightarrow s$  relation mainly owed to increased rugosity, but the results of both distribution and karyotype comparisons showed another relation  $o \rightarrow f // s$ . So far described, an intimate phylogenetic relation could be concluded between *osimensis* and *famelica* from three lines of evidences, morphological, distributional, and karyotypic, but the phylogenetic position of *smythiesi* deduced from morphology alone does not agree with the other results. As the distribution pattern of *osimensis* conforms to tropical type I and that of *famelica* to temperate type I, then both *osimensis* and *famelica* are considered to belong to "Neo" species. Moreover, based on the karyotype analysis, it was showed that the karyotype of *famelica* was derived from the centric dissociation of the largest submetacentric chromosomes of *osimensis*. On the other hand, the distribution pattern of *smythiesi* conforms to temperate type II, which was found in "Relict" species. The karyotype is characterized by low chromosome number and primitiveness. Although there is a intimate relation on morphology between