Phthitia spinosa (Collin). These cases belong to three types of w.p.: (1) species having 2 separate forms, i.e. macropterous (f.macr.) and brachypterous (f.brach.) or micropterous; the type is probably genetically based on oligogenes – *Crumomyia pedestris*, *Pullimosina meijerei*, *Pteremis fenestralis*, (2) species exhibiting continual series of transient forms between f.macr. and f.brach.; this type is probably controlled by polygenes or by several complementarily operating oligogenes – *Puncticorpus cribratum*, *Spelobia pseudonivalis*, *Terrilimosina sudetica*, (3) species having, besides f.macr. and f.submacr., f.brach. with only weakly reduced wings; this type might be genetically similar to the type 2 but it seems to represent an initial stage of w.p. – *Phthitia spinosa*, *Spelobia manicata*. Variability in venation of wing polymorphic and brachypterous W. Palaearctic species of Sphaeroceridae was studied and general trends in the reduction of venation during the evolution are established. The reduction of veins differs in the Copromyzinae (*Crumomyia pedestris*) from that in the Limosininae where 5-6 successive stages are recognized. Causes of the origin and evolution of w.p. in European species of Sphaeroceridae are discussed. Except for *Crumomyia pedestris*, all the other cases evolved in consequence of colonizing terricolous habitat-niches, especially deeper layers of forest litter. Obligatory microptery of *Crumomyia pedestris* is due to its adaptation to extremely moist boggy habitats. Dependence of the wing length upon geographical and climatic conditions is demonstrated in 2 wing polymorphic species, *Pteremis fenestralis* and *Puncticorpus cribratum*. Wing polymorphism is considered a transient and temporary stage in the evolution of brachypterous and apterous species.

Key words: Sphaeroceridae, wing polymorphism, evolution, venation.

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Adaptative and evolutionary radiations in Syrphidae – evidence from larval stages.

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Branch points within a cladogram developed for Palaearctic Syrphidae are characterised by varying levels of speciation. Putative adaptative radiations and falsifiable hypotheses to test them, can only be developed within a phylogenetic framework. To determine whether branch points within the syrphid cladogram represent adaptative, as opposed to evolutionary radiations, a protocol is applied that tested which branch points contained significantly more species than sister groups and whether such species richness is apomorphic. Three branch points, comprising species with larvae that live in wet fungal decay, decaying heartwood and predators, met these conditions.

The next step in recognising adaptative radiations, involves a search for apomorphic characters present in species-rich groups that could enhance the potential for adaptively driven modes of speciation to occur. These characters are found by analysing functional morphology in relation to sister groups and looking for performance advantages. At all three branch points characters associated with locomotion, and in one case, feeding, could have resulted in adaptively driven modes of speciation.

Finally, these three branch points are examined to see if adaptively-driven speciation modes could have actually occurred. At only one branch point is this supported. Evidence from larval stages suggests that, in syrphids, an adaptative radiation only occurred at one branch point, the predators.

Key words: adaptative radiation, syrphid, larvae, speciation.

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Syrphid larvae as sources of phylogenetic information.

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The external morphology of larvae belonging to five Aschiza families, Lonchopteridae, Platypezidae, Phoridae, Pipunculidae and Syrphidae, is analysed. When larvae are studied sclerotised structures like the cephalopharyngeal skeleton and respiratory organs receive most attention. However, we use integumental characters extensively, finding them a rich source of new information. To establish a sequence for outgroups, we first attempted to resolve phylogenetic relationships within Aschiza. We chose to examine more than one outgroup because understanding their morphological trends should help clarify those of the syrphid ingroup. The resulting cladogram supports each family and shows that Lonchopteridae and Platypezidae are plesiomorphic and Syrphidae is the most derived. Pipunculidae is the sister group to the Syrphidae. *Eumerus* is the most plesiomorphic syrphid taxon. Morphological transitions among outgroup families explain much of the characteristic morphology of the *Eumerus* larva.

Relationships between 49 Palaearctic syrphid genera (65% of the fauna), represented by 128 species, were then analysed from a set of 136 larval characters and rooted on *Eumerus*. The result, obtained by successive weighting, supports most genera previously defined on only adult characters, but does not support higher taxa. Phytophagy and predation appear early in syrphid evolution and are exceptions among an otherwise uniform saprophagous feeding mode. Habitat diversification within saprophagous taxa is characterised by repeated transitions between wet, decaying vegetation and decaying tree sap and heartwood. Morphological transitions in structures of the thorax, anal segment and locomotory organs are numerous and gradual in nature. They explain most of the morphological diversity of larval Syrphidae.

Key words: larvae, syrphid, phylogeny, outgroup, character transitions.

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Animal blood meal sources of *Glossina pallidipes* and *G. longipennis* collected at Nguruman, south-west Kenya (Glossinidae).

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All the 3,050 individuals of tsetse flies belonging to *Glossina pallidipes* Austen and *G. longipennis* Corti were collected in the survey carried out at the two different vegetations of two suppressionally different areas at Nguruman, south-west Kenya during the dry season of 1992. In total, females of *G. pallidipes* was predominant (1,255 individuals, 41%) followed by males of *G. pallidipes* (697 indiv., 23%), females of *G. longipennis* (560 indiv., 18%) and males of *G. longipennis* (538 indiv., 18%). According to the collecting points, 43% (1,296 individuals) were collected at non-suppression area forest (NF) and the traps at the other three points; suppression area forest (SF), suppression area savannah (SS) and non-suppression area savannah (NS), collected nearly the same individuals of flies and the numbers were 539 (18%), 630 (20%) and 585 (19%) respectively. Females of *G. pallidipes* were collected predominantly (SF: 429 indiv., 80%; SS: 381 indiv., 65%) and in contrast, only a few of *G. longipennis* were collected (2 individuals of females at SF and 7 males and 6 females at SS) in suppression area. On the other hand, *G. longipennis* (males: 217 indiv., 37%; females: 289 indiv., 50%) was collected dominantly at NS. The points where the most number of individuals collected for both sexes and species were NF for *G. pallidipes* males, SF for *G. pallidipes* females, NF for *G. longipennis* males and NS for *G. longipennis* females.

339 individuals out of the 3,050 (11.1%) were considered to be engorged. Of these, males of *G. pallidipes* were 6.6% (46 out of 697), females of *G. pallidipes* were 12.5% (157 out of 1,255), males of *G. longipennis* were 9.7% (52 out of 538) and females of *G. longipennis* were 15.0% (84 out of 560). The ten kinds of conjugates used in this study were reacted against those blood meals, but anti-