addressing factors affecting the individual development of perfume phenotypes. How well are volatiles stored and preserved in hind leg pouches of males, and how is retention related to molecular characteristics? How much of their tibial perfume do males expose during display in relation to how much they have stored? What is the resulting relationship between individual age and perfume traits like volatile quantity, complexity, or the proportion of head and base not compounds? I discuss results in the context of the evolution of male perfume signals.

Implications of the karyotypic study for integrative taxonomy and cytogenetics of parasitoid Hymenoptera

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Nowadays chromosomal characters are beginning to be used in integrative taxonomy of parasitoid Hymenoptera. For example, our karyotypic research of a supposedly well-known cosmopolitan parasitoid of a wide array of coleopteran stored-product pests, *Anisopteromalus calandrae* (Howard) (Pteromalidae), revealed that some strains of this species had = 7, whereas the others had n = 5. Further study has demonstrated that this name harbored two different reproductively isolated species. These species also had alternative life-history strategies which were best interpreted in terms of the r/K continuum. Moreover, differences in life-history features between those parasitoids correlated with the corresponding characteristics of their preferred hosts. In addition, the species with n = 5 appeared to be new to science and was later described as *A. quinarius* Gokhman & Baur. Analogously, two different species with n = 5 and 6 were also found in another pteromalid, *Lariophagus distinguendus* (Förster) having similar biology. Nevertheless, these species are closer to each other in terms of karyotypic characters than those of the genus *Anisopteromalus*. Moreover, they can hybridize under certain conditions, and this situation therefore constitutes the first known case of hybridization between two parasitoid species with different chromosome numbers. The above-mentioned results, together with a number of similar cases, call for wider application of chromosomal analysis to parasitoid stocks cultivated for both industrial and laboratory use, and this kind of analysis can therefore provide means of express identification of particular strains.

Karyotypic study is very important for determining numbers of linkage groups in parasitoid Hymenoptera. This method is especially valuable when certain chromosomes are small or relatively inert in terms of genetics, e.g. B chromosomes. Recent data suggest that these elements are substantially more abundant among parasitic wasps than it was previously supposed. Specifically, a few years ago we detected up to six B chromosomes per diploid karyotype in *Pnigalio gyamiensis* Myartseva & Kurashev (Eulophidae). Chromosomes of that kind were also found in the chromosome sets of several other parasitoids including certain members of the genus *Pnigalio* and a particular strain of *Aphidius ervi* Haliday (Braconidae). Although these chromosomes sometimes carry sex-ratio distorters in parasitic wasps, this is probably not the case in *P. gyamiensis*, thus providing a possible explanation for the presence and accumulation of B chromosomes in this species as well as in a

few similar cases. For example, some individuals of *Eurytoma cynipsea* Boheman apparently carry four dotlike B chromosomes, whereas other individuals do not (2n = 20+0-4B).

Staining with base-specific fluorochromes and fluorescence *in situ* hybridization (FISH) are efficient tools used for the cytogenetic study of parasitic wasps. In parasitic wasps, AT-binding fluorochromes, e.g. DAPI and Hoechst 33258, usually provide homogeneous chromosome staining, except for obvious gaps in the nucleolus organizer regions (NORs) which constitute clusters of ribosomal DNA (rDNA). Accordingly, GC-binding fluorochromes, such as chromomycin A3, usually stain NORs in parasitoid Hymenoptera. Haploid chromosome sets of this group mostly carry one or two rDNA sites, although three and even six of these clusters can be found within karyotypes of certain members of the superfamily Ichneumonoidea (i.e. Ichneumonidae and Braconidae). Since this parameter generally corresponds to the chromosome number, and the latter value often decreases in advanced parasitoids, so does the number of rDNA sites. However, certain exceptions to this rule, e.g. varying numbers of rDNA clusters in different members of certain genera sometimes having the same chromosome number, also occur. Specifically, among chalcid wasps of the genus *Eurytoma*, *Eu. compressa* (Fabricius) with n = 5 has two rDNA sites, whereas both *Eu. serratulae* (Fabricius) with n = 6 and *Eu. robusta* Mayr with n = 7 have single clusters that are situated on two apparently different chromosomes. Analogously, n = 5 in all members of *Trichogramma* (Chalcidoidea: Trichogrammatidae), although *T. pretiosum* Riley and *T. kaykai* Pinto & Stouthamer have one and two rDNA sites respectively. Moreover, we have found that multiple CG-rich chromosome segments are characteristic of terminal regions of all chromosomes of another chalcid wasp, *Trichospilus diatraeae* Cherian & Margabandhu (Eulophidae) with n = 7. However, rDNA sites in this species were not studied using FISH, and therefore their precise number and localization are currently unknown.

In addition, our views on the phylogenetic distribution of the TTAGG telomeric repeat in the order Hymenoptera have dramatically changed during the last years. Specifically, the $(TTAGG)_n$ telomeric motif was initially considered characteristic of the Hymenoptera in general, but it was actually found only within the families Formicidae and Apidae (Aculeata). Furthermore, we failed to detect the TTAGG repeat in telomeres of all studied parasitoids of the superfamilies Ichneumonoidea, Cynipoidea and Chalcidoidea. In addition, all other main groups of aculeate Hymenoptera were later shown to lack this motif. On the other hand, our recent finding of the TTAGG telomeric repeat in the clade Eusymphyta, i.e. in two members of the family Tenthredinidae (Symphyta: Tenthredinoidea), *Tenthredo omissa* (Förster) and *Taxonus agrorum* (Fallén) both having n = 10, proves an ancestral nature of this motif in the order Hymenoptera. Taken together with all previously accumulated information, these data also suggest a subsequent loss of the TTAGG telomeric repeat somewhere among the basal lineages of the clade Unicalcarida as well as its independent reappearance in the Apidae and Formicidae.