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ABSTRACTS

SATELLITE SYMPOSIUM

Evolutionary aspects of mite parasitism

House dust mites from the urban area of Tychy, Upper Silesia (Southern Poland). Risk of exposure to the allergenic mite taxa.

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Domestic mites, including the house-dust mites from the family Pyroglyphidae may cause atopic diseases in humans. In Poland, the knowledge of the occurrence of these house dust mites is still poor.

The aim of this study was to extend our knowledge of the occurrence of pyroglyphid mites and other allergenic mites in dwellings in certain cities of Poland. The faunistic study was carried out in September and October 2006 in Tychy (Upper Silesia, Poland). A total of 50 house-dust samples from 10 dwellings were examined for the occurrence of allergenic or parasitic mites. The dust samples were taken from the same 5 places in each dwelling, namely from beds, bedroom carpets, upholstery furniture, living-room carpets and kitchen floors. Mite density was calculated as the number of specimens per 1 gram of dust. Damaged mites were assumed dead at the time of sampling, whereas intact mites were determined as alive at this time. Information on various parameters which could influence mite numbers was obtained by questioning the residents and analysed using a correlation test. Mites were found in 78% of the samples collected. A total of 716 mites were isolated, including 705 of the family Pyroglyphidae (98.5%). More than 6 mite species were found, all known as allergenic. *Dermatophagoides farinae* [DF] was predominant (56.4%), followed by *Dermatophagoides pteronyssinus* [DP] (34.5%). DF was also more frequent (70.0%) and distinctly more abundant per 1 gram of dust (54.96) than the second species, DP (26.0% and 24.7, respectively). Unidentified *Dermatophagoides* spp. constituted 7.54% of the total count. Moreover 3 species (or genera) were identified – *Acarus siro* (Acaridae), *Gohieria fusca* (Glycypahgidae) and *Cheyletus* sp. (Cheyletidae). The mean number of domestic mites per 1 gram of dust was 88.2 ± 159.7 (for live mites: 22.17 ± 40.1). Mean values of indoor relative humidity and temperature were 64.6% RH and 24.3°C, respectively. The greatest densities of mites per 1 gram of dust were found in bed-dust samples (mean = 167.8) and in samples from upholstery furniture (104.8). The abundance of mites was influenced mainly by the following parameters – type and age of building, type of place examined (beds), type of sleeping accommodation (bed mattress), type of upholstery furniture, presence of a housewife (unemployed resident) and milder temperature.

External mites (Acari) found on bumble-bees (Insecta, Apoidea, Bombinae)

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Mites often occur on insects of various orders, including hymenoptera. They are often observed on bumble-bees during the whole year (esp. in the autumn). In the winter, their phoretic, survival instars are attached to the body surface of their hibernating hosts, i.e. *Bombus* queens. After overwintering, the surviving mite specimens start the spring season in new established bee nests and continue their development and activity.

Material (adult insects) for this study was collected from the flowers of both wild and cultivated plants in the Puławy area. Sampled insects were examined for mites using stereoscopic light microscopy and SEM. In the survey, a total of over 400 bumble-bees were examined comprising 288 workers, 123 drones and 14 queens, from the following *Bombus* species: *B. lapidarius* (L.), *B. lucorum* (L.), *B. pascuorum* (Scopoli) and *B. terrestris* (L.). The prevalence of mites was greatest in queen bees (over 90%) and the overall occurrence was around 50%. The number of mites per host varied enormously, ranging from one to over a hundred specimens per bee. The following genera and species of mites were recorded: *Kuzinia laevis* (Duj.), *Scutacarus acarorum* (Goeze),

Parasitellus fucorum (De Geer), *Parasitus* spp. and several other genera of mesostigmatid mites, together with other unidentified acaroid (Acaroidea) and anoetoid (Anoetoidea) hypopi. Some larger mite individuals, such as those belonging to *Parasitus*, Laelapidae and other Mesostigmata found on bumble-bees, were often settled on by *S. acarorum*, which were usually found on the legs of these larger mites as well as on the bees themselves, mainly on the back of the thorax and at the base of the insect's wings. Adaptations of external bumblebee-philous mites to life on the body surface of bees include suckers, tactile setae, sensillae, curved and powerful claws as well as a dorso-ventrally flattened body. Majority of these mites occur and develop in *Bombus* nests and are considered the associates, commensals and/or nest parasites of these insects. Phoretic relations of these arachnids with insects can be acknowledged as a kind of transport parasitism, especially when their number on the bodies of the carriers/hosts is so great that it makes their flight and movement impossible. Whereas the typical endoparasitic mite *Locustacarus (Bombacarus) buchneri* (Stammer) (fam. Podapolidae), infesting the tracheal system of bumble bees, hasn't previously been registered in Poland, it is known to be present in some other countries such as France, Germany and the USA.

The evolution of ectoparasitic feather mites (Actinotrichida, Astigmata) revealed by molecular tools

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Feather mites (FM) belong to the most ecologically diverse taxon of mites (Actinotrichida: Astigmata). These ectoparasites and commensals inhabit the body surface of birds, mainly their plumage. The huge FM group, over 2500 described species, displays complex morphological adaptations to living in strong air-flows on the feather surface, among the threads of down feathers, in quills and on/in the skin. The striking phenomenon is the close association of particular mite taxa with particular bird taxa, which suggests a close evolutionary parallelism between parasites and their hosts.

The recent rapid development of molecular tools, specifically DNA sequencing techniques, together with sophisticated analytical tools of phylogenetics and population genetics have made possible the resolution of various evolutionary questions concerning these tiny animals. The lecture will be devoted to the main events of FM evolution which act on various levels of the taxonomic diversity. Firstly, the general position of FM on the tree of life of mites will be presented together with the phylogenetic relationships among the main lineages of these ectoparasites. The reversibility of mite parasitism (the case of dust mites) will be discussed, and the speciation mechanisms driving diversification at the population level will be shown.

Finally, the results of the co-phylogenetic analyses of the bird-mite complexes will be presented. It will answer the question of whether the co-speciation is a key factor in the origin of the observed FM-birds associations or whether other evolutionary events (e.g. horizontal transfer, sorting event, duplication, and evolutionary inertia) have more significantly influenced their evolution.

Ectoparasitic quill mites of the family Syringophilidae (Acari: Prostigmata: Cheyletoidea): evolutionary considerations

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Syringophilids (Acari, Prostigmata, Cheyletoidea) are a group of obligatory ectoparasitic mites inhabiting the quills of various types of feathers in many bird species. Molecular data (DNA sequences of the mitochondrial cytochrome c oxidase subunit I gene (COI), domene D2 of the nuclear gene 28S rDNA and a fragment of the nuclear 18S rRNA gene) were applied for the first time in this group to reconstruct the phylogenetic relationships among mites (on various taxonomic levels – subfamilies, genera and species) and to investigate the possible coevolutionary processes responsible for the recent host-parasite associations.

The results of these research changed entirely the previous view on the syringophilid phylogeny and, to some extent, calls into question the reliability of morphological features even in systematic studies. The analyses carried out on subfamily level deny the hypothesis of basal divergence of taxa belonging to the two subfamilies and show different evolutionary scenarios in quill mites. On the generic level molecular results do not confirm the separation of the sister genera *Syringophiloidus* Kethley – *Betasyringophiloidus* Skoracki and *Aulonastus* Kethley – *Neoaulonastus* Skoracki and suggest the synonymization necessity in these two cases. Also on the species level, molecular and morphological data generate different results. Two morphologically well distinguishable “species” *Torotroglia merulae* Skoracki, Dabert and Ehrnsberger and *T. rubeculi* Skoracki inhabiting different hosts proved to be conspecific according to molecular data. Most probably this is a case of phenotypic plasticity showed by one genome. DNA barcodes also reveals the first incident of female dimorphism in syringophilids showing that *Stibarokris phoeniconaias* Skoracki and O’Connor and *Ciconichenophilus phoeniconaias* Skoracki and O’Connor co-occupying the quills of secondaries, coverts and body feathers of The American Flamingo *Phoenicopterus ruber* L. are conspecific. Inversely, in some cases of multihost mite species the molecular information allowed to detect the genetic isolation between well-defined populations living on different hosts (species *in statu nascendi*).

The cophylogenetic analysis reconstructing the evolutionary history of association patterns of the mites and their hosts indicate very low level of cospeciation and suggest the sorting events as the main driving force influencing recent associations. This phenomenon is explained by low prevalence index of syringophilids and suggest that their current distribution is rather a result of “missing the boat” (mites absence on the host founder population at a speciation event) or “drowning on arrival” (because of small size of the initial population they have gone extinct after the divergence of host species). Additionally, the possible connection between the unbalanced sex-ratio in syringophilids with the presence of endosymbiotic bacteria *Wolbachia* and *Spiroplasma* (known as the key factors inducing numerous reproductive alterations in host organisms) is discussed.

Host specialization in eriophyoid mites: *Aceria tosichella*, *Abacarus hystrix* and *Aculodes mckenziei*: are these plant parasites generalists or specialists?

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The evolution of host specialization is a result of long-term and complex interactions between parasites and hosts, and is influenced by a variety of factors. For example, host specificity can be seen as an outcome of environmental conditions defined by the ecology and physiology of both parasites and hosts. Furthermore, the life histories of both parasites and hosts (e.g. relatedness between hosts) may have an impact on the evolving interactions between them. The specialization of parasites may be considered as high (i.e. they have narrow host specificity) or low (wide host specificity) and also they may have an intermediate host range. The level of host specificity is a result of mutual interactions between hosts and parasites as well as influence of various ecological and historical factors. Eriophyoid mites are obligate plant parasites. They are characterized by an extremely narrow host plant specificity. Only a few species of eriophyoid mites with a potential wide host range are known, and in this sense they are regarded as exceptions among other eriophyoids. *Aceria tosichella* (Keifer), *Abacarus hystrix* (Nalepa) and *Aculodes mckenziei* (Keifer) have been considered as such exceptions.

The great development of molecular techniques in the last several years has made testing hypotheses about host specificity in many parasite taxa feasible and easy. Phylogenetic analyses based of the mitochondrial cytochrome c oxidase subunit I (COI) gene fragment, supported by analyses of a fragment of the nucleotide DNA sequences (ITS and D2 region of 28S rDNA) have shown that *A. tosichella*, *A. hystrix* and *A. mckenziei* represent genetically differentiated biotypes with diverse host specificity, that is narrower than previously assumed. Specifically, the results showed that *A. tosichella* is a complex of cryptic lineages, with those characterized by wide host specificity being more virulent. *Abacarus hystrix* is a complex of cryptic species with narrow host ranges, within which *Abacarus lolii* (Skoracka) has been described so far. The level of genetic variation among the host population of *A. mckenziei* suggests the host race formation.

A thorough investigation into the host specificity of eriophyoid parasites can significantly contribute to such practical goals as parasite management and control, and biological control, as well as taxonomic and evolutionary considerations.

The ecology and evolution of parasitism in terrestrial parasitengone mites (Actinotrichida: Prostigmata)

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The cohort Parasitengona is among the most diverse mite taxa and traditionally includes Hydrachnidia and Trombidia, the so-called terrestrial Parasitengona.

Their protelean life style resulting from the different feeding strategies of their larvae and post-larval stages, combined with the heteromorphism of their developmental stages, favours describing new species on the basis of selected stages and represents a major obstacle when trying to unravel the phylogenetic relationships within the group. The number of nominal species vastly exceeds the number of actual ones because of the system of so-called double systematics, which is independent for the larval and heteromorphic post-larval stages; the great majority of species are known exclusively as larvae.

The important apomorphies of Parasitengona include calyptostatic proto- and tritonymph and the switching of originally predatory larvae to parasitism. Due to their association with mobile hosts, the larvae of Parasitengona are the main stages prone to dispersal.

Terrestrial Parasitengona include three distinct superfamilies: Calyptostomatoidea, Erythraeoidea and Trombidioidea; because of the great structural and ecological diversification, their representatives constitute good objects of evolutionary studies. The concept of phylogenetic relationships between family-level as well as subordinate taxa is in a state of flux. The contradictory nature of life history characters results in an array of evolutionary trade-offs, and renders phylogenic reconstruction difficult.

The present study aims at a review of life strategies in terrestrial parasitengone mites, which facilitate the success of parasitism in an evolutionary sense.

Co-parasitism of mites of the superfamily Trombidoidea (Actinotrichida: Parasitengona) – a host-specificity-related phenomenon?

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The problem of co-parasitism is closely associated with recognition of inter- and intraspecific variation of parasites and their site preferences which result in occupation of different niches.

Narrow and highly specific niches may result from the history of acute competition among parasite species or may be due to the lack of competition associated with the absence of niche overlap.

Trombidoidea, one of the three superfamilies of terrestrial Parasitengona, are represented by ca. 4000 nominal species. Larvae of members of most of the families (13) are obligatory parasites of arthropods; two families are associated with vertebrates and the host spectrum of one (Yurebillidae) remains unknown.

Co-parasitism is rare among the arthropod-associated Parasitengona. The phenomenon has been confirmed for ca. 3% of cases of invasion. The cohabitation is accompanied by distinct divergence of site preferences.

Several cases of co-parasitism have been observed in vertebrate-associated families (Trombiculidae, incl. Leuwenhoekidae, and Walchiidae). However, the actual frequency of this phenomenon remains unknown. It can be due to various factors, among which unrecognized interspecific variation can play a crucial role.

During our studies on bat- and rodent-associated trombiculids, cases of co-invasion were observed for three host species. The co-parasitic mites belonged to the same or different genera, which was confirmed by morphological and molecular analyses.

The present study aims at finding the possible evolutionary background for co-parasitism, with special reference to vertebrate-associated trombiculids.