Postdoc Fellowships for non-EU researchers

Final Report

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Selection	2011
Host institution	Institut Royal des Sciences Naturelles de Belgique
Supervisor	Patrick Grootaert
Period covered by this report	from 18/04/2012 to 17/10/2013 (2x 6 months)
Title	Mites of the family Psoroptidae (Acariformes: Astigmata) – permanent parasites of mammals: phylogeny, host-parasite relationships, and systematics

1. Objectives of the Fellowship (1/2 page)

The main goal of the project was the phylogenetic analysis of the family Psoroptidae (i) and the analysis of their relationships with hosts based on the reconstructed phylogeny (ii). The final aim of the project was the monographic revision of the family, including illustrated re-descriptions of all known species (about 70) based on all postembryonic instars, keys to all species, geographical distribution, host ranges, and summated information about pathogenesis and control of these mites.

Mites of the family Psoroptidae (about 70 species in 30 genera) are highly specific parasites of marsupial and placental mammals belonging to12 orders. Some of them have high veterinary importance causing serious and sometimes lethal dermatitis in wild and domesticated mammals. Psoroptid mites, being specialized and mostly mono- or oligoxenous parasites (Fain, 1994), are non-randomly distributed on their hosts demonstrating a phenomenon of phylogenetic parallelism with mammals (Bochkov et al. in press). It is well known that host-parasite associations, if evolved in a highly predictive fashion, may be used as a valuable data source to validate a host phylogenetic hypothesis (Klassen, 1992; Whiteman and Parker, 2005; Hypsa, 2006), especially if non-co-speciation events (host switches, extinctions, speciation within a host lineage, and failure to speciate) can be accounted for. Pphylogenetic relationships in psoroptid mites have been studied so far only in few psoroptid taxa (Bochkov and OConnor, 2006; Bochkov and Wauthy, 2009; Bochkov and OConnor, 2010; Bochkov et al., 2011) that does not allow to undertake a well-grounded parsimonial analysis of their historical associations with their hosts. It is paradoxical, but the systematics of the most economically important psoroptid genera, *Psoroptes* and *Chorioptes*, is weakly developed and their species accounts was still disputable due to troubles with species discrimination (Zahler et al., 2000; Pegler et al., 2005; Bochkov, 2010). Finally, modern taxonomic revision of this family and illustrated keys to all currently recognized psoroptid species were absent.

2. Methodology in a nutshell (1/2/ page)

Phylogeny of the family Psoroptidae is based mostly on external morphological characters because fresh materials suitable for DNA extraction are unavailable for most “key” representatives of the family. Many psoroptid species are represented by few specimens only and parasitize exotic hosts like Malagasy lemurs or some marsupials. It should be mentioned that the absence of such morphology based analyses seriously impedes the zoological phylogeny and systematics causing "phylogenies without synapomorphies" (see review by Mooi and Gill, 2010). Whereas the morphology based analyses serve as external tests for molecular-based phylogenies which are often contradict to each other and form the ground for the systematics of the group. In our project, molecular data were used to validate the principal phylogenetic lineages of some closely related species of the genera *Psoroptes*, *Chorioptes*, and *Otodectes* having high economic importance.

Mite morphology was examined with light microscopy using DIC (Nomarsky) optic and SEM. External morphology of immature instars of psoroptids were investigated in detail for the first time. History of host-parasite associations was reconstructed with the last versions of respective software for some taxa of the target group (TreeMap).

3. Results (6-8 pages)

The systematics and phylogeny of mites belonging to the close outgroups to the family Psoroptidae were investigated.

1. The family Listropsoralgidae Fain, 1965 (Acariformes: Sarcoptoidea) is represented by the permanent skin ectoparasites associated with South American and Australian marsupials (most species of the family) and South American rodents of the family Echimyidae (1 species). It formerly was concluded that the family Psoroptidae as a separate subfamily. The phylogenetic relationships of these mites (12 ingroup and 2 outgroup species) are reconstructed on the basis of the maximum parsimony (MP) and Bayesian analyses (BA) of 76 morphological characters. MP analysis confirmed monophyly of the listropsoralgid genera, the strict consensus of 3 trees generated by MP has the following pattern: *Petauralges* (*Listropsoralgoides*, *Didelphialges*, *Listropsoralges*) with poor resolution among species of the genus *Listropsoralges*. The same tree is generated by BA. Both successive and implied weightings revealed a single MP tree: *Petauralges* (*Listropsoralgoides* (*Didelphialges* (*Listropsoralges*))). The relationships between species of the genus *Listropsoralges* received the full resolution: *L. caenolestes* ((*L. monodelphis*-*L. vossi*) ((*L. faini*-*L. brevisetosa*) (*L. thylamys* (*L. marmosa*-*L. caluromys*)))))). The host-parasite relationships of listropsoralgids are briefly discussed. The family Listropsoralgidae is taxonomically revised and to date includes 13 species in 4 genera. Six species and 1 genus are described as new for science: *Listropsoralges brevisetosus* **sp. n**. from *Marmosa murina* Linnaeus (Didelphimorphia: Didelphidae) from Peru, *Listropsoralges similis* **sp. n**. from *Caluromys derbianus* (Waterhouse) (Didelphidae) from Panama, *Listropsoralges thylamys* **sp. n**. from *Thylamys venustus* (Thomas) (Didelphidae) from Bolivia, *Listropsoralges vossi* **sp. n**. from *Monodelphis domestica* (Wagner) (Didelphidae) from Brazil, *Listropsoralges caenolestes* **sp. n**. from *Caenolestes fuliginosus* (Tomes) (Paucituberculata: Caenolestidae) from Ecuador, and *Didelphialges metachirus* **gen. n**., **sp. n**. from *Metachirus nudicaudatus* (E. Geoffroy) (Didelphidae) from Peru. Female of *Listropsoralges faini* Bochkov and Wauthy, 2009 is described for the first time.

Results are published in a monograph.

2. The subfamily Onychalginae Fain, 1988 (Acariformes: Pyroglyphidae) is a monophyletic lineage comprising the closest parasitic relatives of the free-living pyroglyphid house dust mites. Onychalgine mites parasitize passerine birds of the families Estrildidae, Passeridae, and Ploceidae in Africa and South America (a single record of *Onychalges spinitarsis* from the piciform bird requires confirmation). Here we revise this subfamily based on external morphology of adults and immature stages using light and scanning electron microscopy and give a key to species.

Onychalginae includes 2 genera: *Onychalges* Gaud and Mouchet, 1959 (6 species) and *Paramealia* Gaud, 1968 (1 species). The genus *Kivuicola* Fain, 1971 **syn. nov**. is synonymized with *Onychalges*, and its single species *K. kivuana* Fain, 1971 **syn. nov**. is considered as a putative synonym of *O. odonturus* Gaud, 1968. *Onychalges spinitarsis* (Fain and Gaud, 1984) is considered as a *species inquirenda*.

Results are published in a paper.

Direct investigations of psoroptid mites are reflected in four following works.

1. The external morphology of adult and immature stages of mange mites of the genus *Chorioptes* was investigated with the aid of light and scanning electron microscopy. A molecular phylogeny of this genus was inferred based on 6 genes (18S, 28S rDNA, EF1-α, SRP54, HSP70, and CO1). The validity of 4 species (*Ch. bovis*, *Ch. panda*, *Ch. texanus*, and *Ch. sweatmani* sp. nov. described from the moose from Sweden, Finland, and Russia) was confirmed based on morphology and a Bayesian species delimitation analysis incorporating both gene tree uncertainties and incomplete lineage sorting via the coalescent process model in BPP. Sequence data for *Ch. crewei* and *Ch. mydaus* was not available but their morphology strongly suggests their validity. The 6 valid *Chorioptes* species are diagnosed using type and non-type specimens, and a key to species is provided. *Ch. sweatmani* differs from closely related *Ch. texanus* by the following features: in males, the body length, including the gnathosoma, is 380-405 µm (vs. 220-295 in *Ch. texanus*), the idiosoma is 3-4 times longer than setae *cp* (vs. 1.3-1.6 times longer), legs III are approximately 3 times longer than setae *sR*III (vs. 1.8-2 times longer), the apical spur of tarsus III is curved (vs. straight), a spur near seta *f*III base is not developed (vs. small but distinct); in females, setae *h2* are 1.4-1.5 times shorter than legs IV (vs. about 2 times longer). Hosts and distribution records of *Chorioptes* species are summarized.

Results are published in a paper.

2. A new species of the genus *Lemuralges* Fain, 1963 (Acariformes: Psoroptidae: Makialginae) is described from the Malagasy lemur *Propithecus diadema* (Bennett, 1832) (Primates: Indriidae) based on all postembryonic instars. This new species differs from the only known species in this genus, *Lemuralges intermedius* Fain, 1963 by the following features. Both sexes of *L. propithecus* sp. n., show a pair of ventro-median projections of the subcapitulum (vs. without projections in *L. intermedius*) and the propodonotal shield is slightly ornamented (vs. unornamented); in males the hysteronotal shield is completely covered by longitudinal striae (vs. median part without striae), setae *c2* are 120–140 long (vs. 200–210 long), and femur III has a short transverse furrow dorsally (vs. a longitudinal furrow); in females, setae *h2* are, at least, 2 times shorter than *h3* (vs. slightly longer, or subequal to, *h3*), tibia IV has a ventro-apical projection (vs. without projection). Larvae and protonymphs of the new species show some unique developmental delays. Female and male tritonymphs differ by their external morphology.

Results are reflected in a paper accepted for press (Folia Parasitologica).

3. Morphology based phylogeny of the family Psoroptidae was reconstructed. Only qualitative characters, such as the presence/absence of a structure or certain form of anatomical features were used in the analysis. Characters having multiple states were interpreted as unordered and were not modified into binary characters. In total, 64 species (among them 20 species are outgroups

representing all families of the superfamily Psoroptoidea and Zachvatrkinia stercorarii (Avenzoaria) as a distant outgroup) and 249 characters were included in the data matrix. The reconstruction of the phylogenetic relationships was performed with PAUP 4.0b.10 for IBM (Swofford 2001). All characters were initially unordered and unweighted. The heuristic search option was used because of the relatively large number of taxa (addition sequence random, tree bisection-reconnection as branch-swapping algorithm, 'MulTrees' option in effect). We used the stepwise addition option, with 1000 random replicates, to reduce the chance of hitting local optima. The results of the PAUP initial analysis were checked with NONA implemented in WINCLADA (Nixon 1999): three independent ratcheted analyses with 100 000 iterations each and other options by default. Analysis of character distributions, drawing, and editing of the trees were conducted using WINCLADA (Nixon 1999). 85 maximum parsimonious trees were received at the first step of the analysis. This analysis confirmed monophyly of the all psoroptid genera and most its subfamilies. However relationships between the psoroptid subfamilies remained unresolved. Moreover, the monophyly of the family and its largest subfamily Psoroptoidinae sensu Fain (1963) were not supported. The subfamily Psoroptinae is represented by two not related clusters – genera from artiodactylids and perissodactylids normally included in Psoroptinae and the genus *Hyracoroptes* (from hyrax). Additionally the genus *Echimyalges* (Psoroptinae sensu Fain) forms a common cluster with the genus *Coendalges* (Psoralginae) (both from South American rodents) and the genus *Trouessalges* (from peccary; Psoroptinae sensu Fain) was placed to the subfamily Psoralginae. Two monobasic subfamilies Marsupialginae and Nasalialginae appeared sister to the genera remained in Psoroptinae.

Although the obtained CI is significantly far from random, the unweighed analysis demonstrated the high rate of homoplasies (HI 0.65) and highly inconsistent results expressed in unresolved relationships between subfamilies of the Psoroptidae. Psoroptids of different phylogenetic branches, having undergone similar selective pressures in the course of adaptation to particular microhabitats on the host body and having a common genetic background, often developed similar morphological adaptations (Klimov and OConnor 2008). This situation is even more complicated, because the most common evolutionary tendency of these highly specialized symbionts is the progressive reduction or complete loss of some external structures (Fain 1994). The independent disappearance of many structures is very difficult to detect, and as the result, many false homologies affecting tree pattern could be "established".

For this reason we applied to our data the successive weighting (Farris 1969) according to RC indices. To check for the presence of a secondary phylogenetical signal, which could be suppressed by this procedure, all characters with CI 1 were excluded. The trees received under the same conditions as in the previous PAUP analysis were almost unresolved and, thus, the application of the successive weighting is quite defensible in our case. Tree length became stabilized after three successive reweightings and a single most parsimonious tree was finally obtained (Fig. 1).

In this tree the family Psoroptidae is a monophyletic group sister to the family Pyroglyphidae (nidicolous mites). Both these families are sister to the family Psoroptoidinae. The similar familial pattern is observable in molecular works by (Klimov and OConnor, 2008, 2012). The pattern of the family Psoroptidae is fully resolved and includes the following clades which we give subfamily status: Hyracoptinae subfam. nov., Makialginae, Psoroptinae, Psoralginae, Coendalginae subfam. nov., Cebalginae, and Paracoroptinae. The subfamily Psoroptinae includes three tribes: Nasalialgini (former Nasalialginae), Marsupialgini (former Marsupialginae), and

Psoroptini. The tribe Psoroptini can be separated on two subtribes, Otodectina (*Otodectes* and *Caparinia*) and Psoroptina (other genera).

The following hypothetical scenario of psoroptid evolution could be derived from the received phylogenetic tree. Mites of the family Psoroptidae probably independently passed from parasitism on birds to different groups of mammals. This hypothesis is supported by the fact, that the basal branches of all main psoroptid clades are represented by parasites from arboricolous hosts which probably received these parasites from birds. This family, nevertheless, should be considered as monophyletic because all these host switches were realized by mites closely related to each other. Thus, a common ancestor of the family parasitized on birds and was closely related (originated) to feather mites of the family Psoroptoididae. Simultaneously, nidicolous mites of the family Pyroglyphidae inhabiting bird nests are also descendants of a bird parasite closely affined with an ancestor of Psoroptidae and could be considered as another derived branch of the psoroptoidid-like mites.

Mites of the subfamily Hyracoptinae are represented by a single species from African host *Dendrohyrax dorsalis* (Hyraqcoidea: Procaviidae) climbing trees. These mites kept the second solenidion on genua II and in the family Psoroptidae are probably descendants of the first wave of migration from birds on mammals.

Mites of the subfamily Makialginaes are associated with primates of the suborder Strepsirrhini and are, probably, representatives of the second wave of mammal colonization by these mites. Some makialgin species are monoxenous parasites, for example, *Daubentonia madagascariensis*, whereas some others are associated with hosts belonging to different host genera or even families (*Lemuralges intermedius*). Many lemur species are still not examined for psoroptids, however, these mites are presently known from all recent families of lemurs (Bochkov and OConnor 2006).

The suborder Strepsirrhini is subdivided onto three infraorders, Lorisiformes (Lorisidae and Galagidae), Chiromyiformes (Daubentoniidae), and Lemuriformes (Cheirogaleoidea: Cheirogaleidae; Lemuroidea: Lepilemuridae, Lemuridae, and Indridae) (Groves 2005).

The most widely accepted hypothesis of strepsirrhin phylogeny based mostly on morphological data was proposed by Groves (2001, 2005). According to his hypothesis (Groves 2001), the family Daubentoniidae (infraorder Chiromyiformes) is the sister group to all other strepsirrhines or less likely to the infraorder Lemuriformes only. Most molecular data, however, support the direct sister relationships between Chiromyiformes and Lemuriformes (Del Pero et al. 2001, Pastorini et al. 2003, Poux et al. 2005; Karanth et al. 2005). These two infraorders are represented exclusively by Malagasy lemurs and, probably, form a monophyletic clade, the common ancestor of which presumably colonized Madagascar in the early Tertiary period (Karanth et al. 2005). The system of the infraorder Lemuriformes proposed by Groves (2001, 2005) can be transformed into the tree mode as Cheirogaleidae (Lepidolemuridae (Indridae-Lemuridae)). The recent molecular studies of lemur phylogeny (cytochrome b), including extinct species, by Karanth et al. (2005) yielded the similar results with exception for an unresolved node jointing the clades Cheirogaleidae, Lepilemuridae, and Lemuridae-Indriidae.

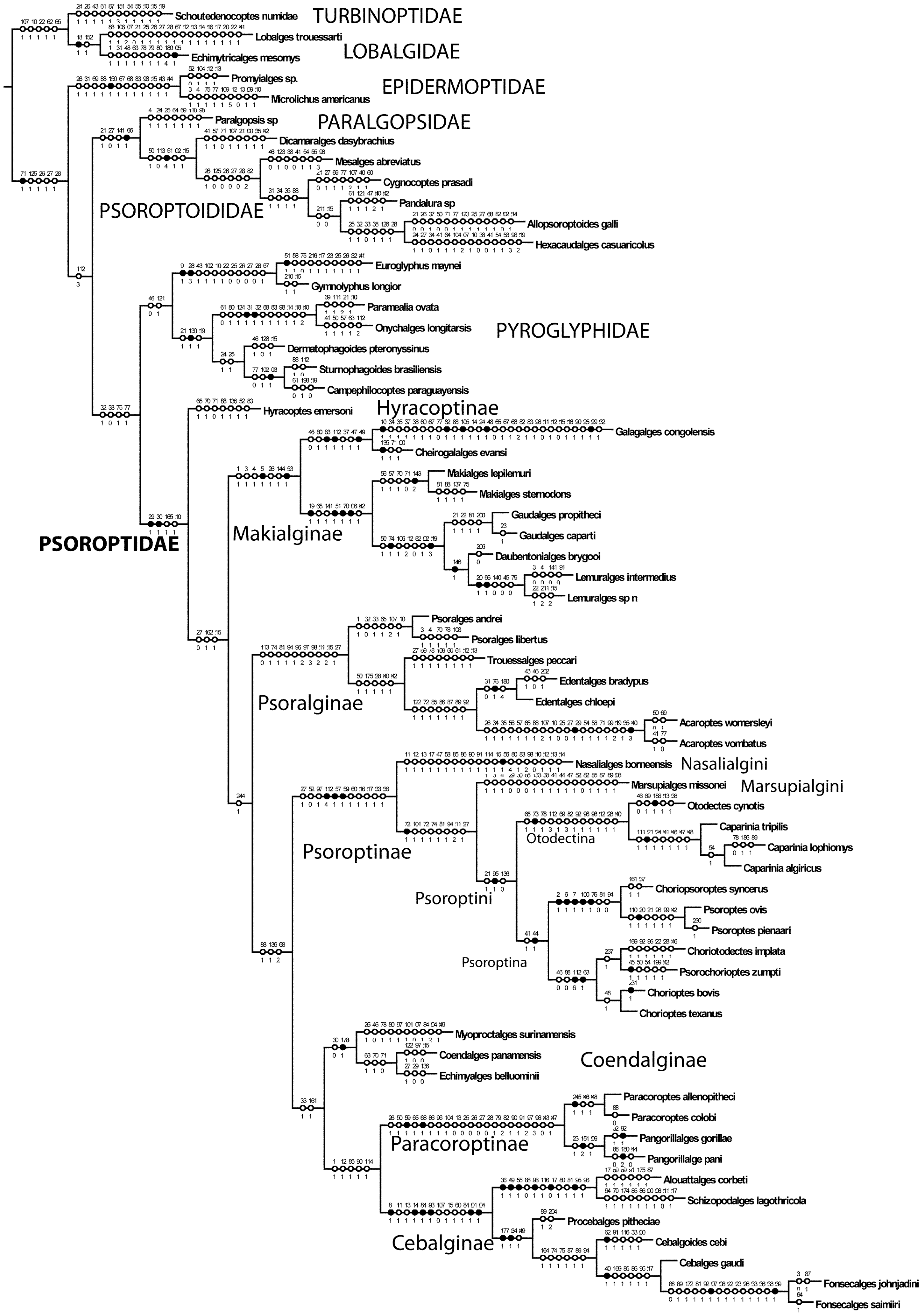

Fig. 1. Phylogeny of the family Psoroptidae

Makialgins do not show clear co-phylogenetic pattern with their hosts. Besides of extinctions, these mites demonstrate two duplications, failure of speciation observed in *Lemuralges*, and one host switch from lemuroids to daubentoniids. Because of this "disappointing" switch we cannot make any conclusions about position of the family Daubentoniidae on the strepsirrhin phylogenetic tree and to prove the monophyletic origin of all Malagasy lemurs. Instead of this, some conclusions about the host phylogeny derived from the obtained results can be done. First at all, our cladogram supports the hypothesis of the monophyletic origin of the infraorder Lemuriformes *sensu* Groves (2005). The parasitism of different species belonging to the genus *Gaudalges* on Indriidae (*G. propitheci*) and Lemuridae (all other species), respectively indirectly supports the sister relationships between these host families. Finally, parasitism of *Lemuralges intermedius* exclusively on the hosts of the superfamiy Lemuroidea and well-grounded monophyly of the clade *Makialges* (*Gaudalges* (*Lemuralges-Daubentonialges*)), whose representatives parasitize hosts of this superfamily, excluding mites of the genus *Daubentonialges* secondarily switched on daubentoniids, are indirect evidences for the lemuroid monophyly. Host distribution of *Lemuralges intermedius*, however, needs in the additional investigations. It is quite possible that parasitism of this species on hosts belonging to the three families is, actually, result of several host switches.

Mites belonging to the subfamily Psoralginae are descendants of the third wave of host colonization happened in South America. Mites of the genera *Psoralges* and *Edentalges* are associated with endemic South American hosts - anteaters and slots (Pilosa). A single representative of the genus *Trouessalges* probably secondarily shifted on peccary from these hosts. However the records of Acaroptes (mites certainly belonging to this South American subfamily) on possums in Australia looks very strange. We provide the following explanation of such host-distribution pattern. It was shown that hosts of the order Pilosa and some ancestors of Australian marsupials could co-occurr in Antarctica (Black et al. 2012) and the mite host shift from edentates to marsupials could have happened there.

Mites of the subfamilies Psoroptinae, Coendalginae, Cebalginae, and Paracoroptinae represent the fourth wave of mammalian colonists underwent the many following secondary shifts in limits of these new hosts.

Mites of the subfamily Psoroptinae are associated with strongly different hosts but the most archaic representatives of the subfamily are associated with arboreal ones. A single representative of the tribe Nasalialgini parasitizes *Nasalis larvatus* (Primates: Cercopithecidae) from Malaysia. A single representative of the tribe Marsupialgini is associated with South American arboreal marsupials. It was also recorded from *Nasua narica* (Carnivora: Procyonidae) in Panama and Brazil. This carnivorous host actively climbs trees and, probably, received the psoroptids preying on arboreal marsupials. This shift seems to be relatively recent because mites from *N. narica* have not undergone speciation on this new host. Mites of the subtribe Otocoptina parasitizing small mammals (Caparinia) or carnivores. It is probably that mites of the genus *Caparinia* were initially associated with hedgehogs of the subfamily Erinaceinae. Most species of this genus are associated with hedgehogs belonging to the genera *Erinaceus* (recorded on 1 from 4 extant species) and *Atelerix* (recorded on 3 from 4 species) and were registered on these hosts from various localities in Eurasia and Africa. Some *Caparinia* spp. were recorded also on *Erinaceus* sp. (*Caparinia* sp.) in

USA Zoo (Gerson and Boever 1983) and introduced *Erinaceus europaeus* (*C. tripilis*) in New Zealand (Brockie 1974). Two species of this genus, *C. setifera* and *C. ictonyctis* probably transferred from hedgehogs on the African carnivores, *Hyaena hyaena* and *Ictonyx striatus*, respectively. These hosts sometimes preying on hedgehogs. Moreover, *C. erinecei*, normally parasitizing the African hedgehog *Atelerix frontalis* was recorded on a mustelid, *Ictonyx striatus* (present paper). Finally, one species *C. lophiomys* transferred on an African rodent, *Lophiomys imhausi*, mostly hedgehogs or rarely rodents or carnivorous in Africa. Ancestors of the genus Otodectes are associated exclusively with carnivore hosts and probably switched from small mammals which are preys of these hosts. Mites of the tribe Psoroptini are associated with hosts of the orders Artiodactyla and Perissodactyla. They also secondary switched on some domesticated hosts, like rabbits or Guinea pigs. It is not clear how and there these mites shifted on ruminant hosts.

All three species of the subfamily Coendalginae parasitize a few South American rodents of the species reach infraorder Caviomorpha, including about 250 species. Hosts of these mites belonging to three not closely allied families, Dasyproctidae (Cavioidea), Echimyidae (Octodontoidea), and Erethizontidae (Erethizontoidea) (Blanga-Kanfi *et al*. 2009; Upham and Patterson 2012). Mites of the genera *Coendalges* and *Echimyalges*, forming separate clade, are associated with arboreal hosts, The Rothschild's porcupine *Coendou rothschildi* (Erethizontidae) and the Atlantic bamboo rat *Kannabateomys amblyonyx* (Echimyidae), respectively. Whereas, *Myoptoctalges surinamensis* was recorded from both species currently recognized in the genus *Myoprocta* (Dasyproctidae). There is also a record from hosts of the genus *Dasyprocta* needing, however, confirmation. The acouchis are terrestrial rodents, but agoitu (*Dasyprocta*) often climbing trees. It is possible that South American rodents received these mites from ancestral primates (close to a common ancestor of Catarrhini and Platyrrhini) migrated to South America.

The sister relationships between the subfamilies Paracoroptinae and Cebalginae probably reflect the phylogenetic links between their hosts, primates of the parvorder Platyrrhini and parvorder Catarrhini, respectively.

All species of the subfamily Cebalginae parasitize the South American primates of the parvorder Platyrrhini (New World monkeys). The parvoders Catarrhini and Platyrrhini diverged about 40 MYA, and later on, ancestors of the New World monkeys colonized South America (Goodman 1999). Accordingly, the sister subfamilies Paracoroptinae and Cebalginae probably diverged during this time along with their hosts.

Each of three generic groups established in the subfamily Cebalginae (OConnor 1984) is associated with the respective platyrrhine family. The groups *Procebalges* includes a single species *Procebalges propitheciae* associated with host from the family Pitheciidae - *Pithecia monachus*. This family includes about 40 species in four genera and, therefore, new psoroptid records from them are quite possible.

The group *Cebalges* (4 species in 3 genera) is associated with monkeys of the speciose family Cebidae (56 species in 6 genera). Both species of the genus *Fonsecalges* parasitize monkeys of the subfamily Callithricinae: *F. johnjadini* is associated with the Atlantic Forest marmosets (*Callithrix*) and *F. saimirii* - with tamarins (*Saguinus*). *Fonsecalges saimirii* also parasitizes the Common Squirrel monkey *Saimirii sciureus* belonging to the another cebid subfamily Saimiriinae.

This association is a probable result of the secondary shift from marmosets. The both monobasic genera *Cebalges* and *Cebalgoides* are both associated with capuchins (*Cebus*). Hosts of *Cebalges gaudi* belong to two different species groups within the genus *Cebus*, *C. capucinus* (*capucinus* group) and *C. apella* (*apella* group), whereas *Cebalgoides cebi* is known in the wild only from *Cebus albifrons* (*capucinus* group). The fact that to most cebid species have not been explored for psoroptids, several new species are expected in this generic group from these hosts.

The group *Schizopodalges* associated with monkeys of the family Atelidae (24 species of 5 genera). It includes two monobasic genera, *Schizopodalges* and *Alouattalges* associated with *Lagothrix lagotricha* (Atelinae) and *Alouatta seniculus* (Alouattinae), respectively.

The reliable psoroptid records from the night monkeys of the genus *Aotus* (8 species), a solely member of the family Aotidae, are absent.

According to all recent molecular phylogenetic hypotheses of Platyrrhini, the New World monkeys constitute three main clades: (Cebidae [including Callithricinae and Aotidae], Atelidae and Pitheciidae (Wildman *et al*. 2009; Perelman *et al*. 2011; Perez *et al*. 2012). The generic groups of cebalgin mites correspond well to these main platyrrhini clades. In the same time, the links of cebalgin generic groups in the cladogram received *Schizopodalges* group (*Cebalges* group-*Procebalges* group) and links of the three platyrrhin clades based on molecular hypotheses (Wildman *et al*. 2009; Perelman *et al*. 2011; Perez *et al*. 2012) are incongruent. Based on molecular estimations, the radiation between main platyrrhini clades underwent almost at the same time 22-16 MYA (Schneider 2000) and the observable pattern of the phylogenetic relationships between generic group of Cebalginae could be a result of the ancient host shifts.

All species of the subfamily Paracoroptinae parasitize the African representatives of the parvorder Catarrhini (Old World monkeys). It was suggested that the ancestor of this mite group changed to parasitism on the African primates from birds (Bochkov and Mironov 2011; Bochkov 2011).

Five of six species known in the genus *Paracoroptes* are associated with monkeys of the family Cercopithecidae. The record of *Paracoroptes natalensis* on the cane rat is obvious a mechanic contamination during the animal transportation and this species is undoubtedly a monkey parasite (Fain and Segerman 1978). The family Cercopithecidae is separated into two subfamilies. Three *Paracoroptes* spp. are known from representatives of the type subfamily. Among them, *Paracoroptes gordoni* is narrowly oligoxenous parasite being associated with guenons of the genus *Cercopithecus*. It was recorded on three of 25 species currently discerned in the genus *Cercopithecus*. Two other mite species, *Paracoroptes allenopitheci* and *P. miopithecus* are recorded so far on one host species each. The first species parasitizes the Allen swamp monkeys of the monobasic genus *Allenopithecus* and therefore, probable, is monoxenous. Whereas *P. miopithecus* could also been recorded on the Gabon talapoin *Monopithecus ogouensis* Kingdon, the second representative of this genus. The two remaining species *Paracoroptes colobi* and *P. pilicolobus* are morphologically close to each other and are both associated with monkeys of the subfamily Colobinae being recorded from a single species of the genera *Colobus* and *Pilicolubus*, respectively. Both of them, however, could be narrowly oligoxenous actually because the genus *Colobus* includes five and *Pilicolobus* eight extant species. The family Cercopithecidae unites several

African genera which are not explored on paracoroptids, therefore, many new species could be recognized in the genus *Paracoroptes* yet.

Both species of the genus *Pangorillalges* parasitize the great apes (Hominidae). The first species *Pangorillalges pani* is recorded on *Pan troglodytes* but we could also expect its records on *Pan paniscus* Shwartz, the second species of this genus. The similar situation is observable for *Pangorillalges gorillae*, which is known so far only from *Gorilla gorilla*, but could parasitize also *Gorilla beringei*.

A paper is submitted based on material of these investigations.

4. The comprehensive monograph concerning external morphology, systematics, and host-parasite relationships of all species of the family Psoroptidae is submitted.

4. Perspectives for future collaboration between units (1 page)

Collaboration between RBINS and the Zoological Institute in St. Petersburg does not end with the end of the present visit as can be seen by the large output that has been performed by now.

(1) Further visits to study of materials housed in RBINS (famous collection of A. Fain) and MRAC collections are mandatory. During this visits we will also work on new papers on the phylogeny of these parasitic mites.

(2) exchange experience in some methodical aspects with researchers of JEMU at RBINS molecular lab.

5. Valorisation/Diffusion (including Publications, Conferences, Seminars, Missions abroad...

Published monograph

Bochkov, A.V., OConnor B.M. and Grootaert P. 2013. Revision of the family Listropsoralgidae Fain, 1965 (Acariformes: Sarcoptoidea) —skin parasites of marsupials and rodents. *Zootaxa*, 3611: 1–69.

Published papers

Bochkov, A.V., Klimov, P.B., Grootaert, P. 2014. Revision of the subfamily Onychalginae Fain, 1988 (Acariformes: Pyroglyphidae)—ectoparasites of passerine birds. *Zootaxa*, 3785 (2): 175–200.

Bochkov, A.V., Klimov, P.B., Hestvik, G., Saveljev A.P. 2014. Integrated Bayesian species delimitation and morphological diagnostics of chorioptic mange mites (Acariformes: Psoroptidae: Chorioptes). *Parasitology research*, 113(7): 2603–2627.

Accepted papers

Bochkov, A.V., Klompen, H., Junge, R.E., Williams, C.V. 2015. *Lemuralges propithecus* sp. n. (Acariformes: Psoroptidae) – an ectoparasite of the diademed sifaka *Propithecus diadema* (Primates: Indriidae). *Folia Parasitologica*.

Submitted monographs

Bochkov, A.V., OConnor B.M., Grootaert P. Mites of the family Psoroptidae (Acariformes: Astigmata) – permanent parasites of mammals: phylogeny, host-parasite relationships, and systematics. Zootaxa. This monograph comprise more than 400 pages.

Submitted papers.

Bochkov, A.V., Klimov P.B., OConnor B.M., Grootaert P. Morphology-based phylogeny of the parasitic mite family Psoroptidae (Acariformes: Astigmata) – complicate “puzzle” consisting of co-speciation events and numerous host shifts. *Cladistics*.

6. Skills/Added value transferred to home institution abroad (1/2 page)

Added value for the home institution abroad is that the grantee acquired more experience in morphological, phylogenetic and molecular techniques that will be communicated to students and colleagues at the Zoological Institute in St. Petersburg. Collaboration with Dr. Serge Mironov from St. Petersburg was also renewed resulting in a visit to RBINS in October 2014.

Some results are also: Collection exchange (i); the collaborative work on the phylogeny and systematics of parasitic acariform mites associated with vertebrates and their applications for various home (RFFI, RNF) and foreign grants (Poland, NCN) (ii); two seminars about phylogeny and systematics of acariform mites in ZISP (iii).

Brussels, 8 December 2014

Dr. André Bochkov and Dr. Patrick Grootaert