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Speciation Patterns in Chewing Lice from *Catharus* Thrushes

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**Preface**

Cospeciation is an interwoven process that impacts many organisms. It is important to study because no organism lives in a vacuum by itself. All organisms interact with other organisms on a daily basis. Some interactions are fleeting, whereas others may become more and more important as time progresses. This study attempts to discover if the interactions between parasitic chewing lice and their avian hosts are important enough to cause cospeciation.

The first chapter of this work includes a literature review covering broad aspects that affect speciation. As this is a rather broad subject, I focused on antagonistic relationships and what I feel are the major factors that impact them: transmission and virulence. I focused especially on the specific interactions of chewing lice and their avian hosts, as they present an interesting system for a cospeciation study.

After the basics of cospeciation and the factors that influence it have been laid out, in chapter 1, I use phylogenetic analyses of two genera of chewing lice, *Brueelia* and *Myrsidea* from *Catharus* thrushes to experimentally test whether they have cospeciated. I chose *Catharus* thrushes because they are common captures at the Shaw Woods Avian Monitoring Project (SWAMP) and I knew that they were often heavily infested with lice. Also there was a published phylogeny of the *Catharus* thrushes for me to compare to my parasite phylogeny.

**Chapter 1: How do Ecological Features Influence Evolutionary Outcomes in Host-parasite Systems?**

This chapter focuses on close-knit relationships and the factors that influence the cophylogenetic history of two organisms. I attempt to draw links between ecological and evolutionary processes to elucidate the patterns of organisms that are likely to cospeciate. First, I introduce the basics behind coevolution and why it might lead to cospeciation. Next, I review the two most important ecological factors affecting two organism’s cophylogenetic history: virulence and transmission. I look at other cophylogenetic patterns that may arise in host-parasite systems, and offer an explanation for why these patterns may occur instead of cospeciation. Throughout this chapter, I focus heavily on bird-louse systems, but include selective examples from other systems.

**Coevolution And Specialization**

Coevolution occurs when organisms respond to each other’s adaptations with reciprocal adaptations. Where species of hosts and parasites have coevolved exclusively, there should be high host-specificity, concordant geographic ranges, and congruent phylogenies, i.e. cospeciation (Barker, 1991). Although coevolution does not necessarily always lead to cospeciation (Hoberg and Brooks, 1997), specialization is likely to increase the rate of speciation that may occur in both host and parasite (Price, 1980). The new species will likely have adaptations that make it better suited to its coevolved partner. Over time, these adaptations may accumulate so that one partner will not be able to survive without the other. Coevolution supports cospeciation, and enough specialization may lead to cospeciation.

**Coevolutionary Arms Races**

Highly coevolved antagonistic interactions are sometimes termed coevolutionary arms races, and these interactions were the inspiration for the coevolution concept. Coevolution was originally outlined by Ehrlich and Raven (1964) in a study on butterflies and their host plants. They found that the plants they studied were usually fed upon by a single, phylogenetically coherent group, or several closely related groups of butterflies, and that these butterflies and plants were specifically adapted to one another (Ehrlich and Raven, 1964). Through occasional mutations and recombinations, plants produce chemical compounds that protect them from attacks of phytophagous insects (Ehrlich and Raven, 1964; Farrell and Mitter, 1998). In response, the phytophagous insects may evolve a defense that neutralizes the chemical compound and leaves them free to feed on the plant (Ehrlich and Raven, 1964; Farrell and Mitter, 1998). As the plants and insects acquire adaptations, the number of species of insects that can consume the plant diminishes, as does the number of plants the insect can consume (Ehrlich and Raven, 1964). As these organisms become specifically adapted to each other, a certain dependence forms, and if the interaction is tight enough, cospeciation is likely to occur.

Coevolutionary arms races are also common in predator-prey relationships. In Lake Tanganyika there is a group of endemic gastropods and their predators, the potamonautilid crab (Thompson, 1994). These two organisms have acquired some obvious adaptations that showcase their coevolutionary history. The claws of the crabs are large and robust relative to other freshwater species and the gastropods have responded with thicker lips, more sculpting on their shells, and stronger shells compared to other freshwater species to defend against the larger claws of their predators (Thompson, 1994). As the gastropod developed a thicker shell, the crab developed larger claws to break that shell, and then the gastropod developed an even thicker shell, which led to selection for even larger claws in the crab. Although they are highly coevolved, as of yet, no one has tested to see if the two organisms have cospeciated.

Why parasites are likely to coevolve with their hosts  
Similar to the herbivore-plant and predatory-prey systems, the nature of the host-parasite relationship provides strong incentive for parasites and their hosts to coevolve. Parasites are organisms that depend upon

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other host organisms for food and shelter, and in the pursuit of these things they cause damage to the host. Extreme specialization is the norm in parasites due to a number of factors specific to living life on the body of another (Thompson, 1994). These factors include: long-term attachment to host, induced host defenses, unbalanced nutrition, intake of large amounts of one or several toxic compounds and avoidance of enemies (Thompson, 1994). When confronted with these factors, the parasite needs to be extremely well adapted to its host or it will die. At the same time, the host also faces selective pressures to adapt defenses against these harmful organisms and ensure their health. Throughout time, reciprocal adaptations by host and parasite lead to coevolution.

Coevolution leads to organisms with specific adaptations to each other. Over time, these adaptations may result in the two organisms becoming exclusive partners. Extreme specialization by parasites tends to result in the parasites only being able to survive on one or a few host species (Moller et al., 2005; Poulin, 1997). When this specialized parasite is transferred to a novel host, it may not be able to survive in the new habitat. The novel host may have a defense that the parasite is unable to defend against. Even if a parasite has evolved to detoxify the toxin of its original host, it is unlikely to be able to detoxify a wide variety of toxins. As the coevolutionary arms race draws parasite and host into a tight interaction, the likelihood that the two will co-speciate increases.

Chewing lice and their avian hosts
Of all parasites, lice may be expected to coevolve with their hosts. These insects are found on virtually all bird species and many of these are host specific, occurring on only one host (Johnson and Clayton, 2003; Janovy, 1997). Lice might be expected to coevolve with their hosts for reasons such as: they lack a free-living stage in their life cycle, they are wingless, they are completely dependent upon their host, and transmission is generally only through direct contact (Barker, 1991). The obvious, coevolved characteristics between lice and their hosts make them perfect for coevolutionary studies.

Bird Defenses
Birds have developed a variety of defenses in their fight to control parasite infestations. Unfortunately for birds, parasites evolve more quickly than their hosts, and this may result in their anti-parasite defenses being perpetually obsolete (Hafner et al., 1994; Whitman et al., 2005). For the most part, louse populations are controlled through host grooming as well as a number of other defenses including anting, dust-bathing, sunning, and potential avoidance behavior through sexual selection (Johnson and Clayton, 2003; Marshall, 1981). Some birds will even go so far as to leave a heavily infested nest, even if it has eggs or nestlings in it (Emlen, 1986). A coevolutionary balance between host defense and parasite resistance may explain why most birds have small populations of lice that have little or no negative effects on the birds, because lice generally only reduce the host's fitness when they are in large numbers (Clayton, 1991b). The defenses birds have evolved help them to keep louse populations from approaching levels where they would become harmful.

Once a bird has become infested with lice, the most obvious and effective defense for their removal is grooming. Selective pressure is exerted by the lice for efficient preening ability (Clayton et al., 1999). Birds that are host to a large number of parasites must spend more time preening and this leads to less time available for foraging or other important activities (Hart, 1997). The time overhang on the beak is specially adapted for rootning out and damaging lice and defects in bill shape often lead to increased parasite load (Clayton et al., 2005; Moyer, Peterson, and Clayton, 2002; Clayton and Walther, 2001). Birds have adapted this deadly overhang specifically to root out louse infestations and keep their populations from getting out of hand. Unfortunately, the lice are also well-adapted to the body of their host, and it is unlikely that a bird will be able to remove every last louse.

Having a healthy mate is essential to the success of a pair's offspring. In species where pairs mate for a season, or life, it is worth the effort to ensure an unparasitized mate. These mated pairs may allopreen, or preen each other, often in places they cannot reach themselves such as the head (Hart, 1997). Birds that do not have an allopreening partner are sometimes able to damage parasites on their head by scratching with their feet, however this treatment is not as effective (Marshall, 1981). Unmated birds are unlikely to invest in the health of another bird unless it has a direct benefit for them, such as the increased health and reproductive ability of their mate.

Anting is a rather unique adaptation that has been shown to decrease louse loads. Anting is when a bird exposes itself to acid- or toxin-secreting ants, or to other pungent substances such as limes (Clayton and Vernon, 1993). Clayton and Vernon (1993) observed a common grackle (Quiscalus quiscula) preening with bits of lime. They experimentally tested louse susceptibility to limes in a Petri dish and found that lice exposed to limes were killed (Clayton and Vernon, 1993). Anting is a way for birds to kill lice without rootning out each one individually. It is kind of similar to dousing themselves with a pesticide and may be an effective way to get rid of lice.

Another rather amazing adaptation for reducing louse infestations is sunning. Moyer and Wagenbach (1995) observed Black Noddies (Anous minutus) sunning in large groups with one wing extended and their tail feathers fanned. They experimentally reproduced these wings and placed ischnoceran lice on them and found that air temperatures slightly above 40 degrees Celsius can be lethal to lice and their eggs. Birds were observed to groom extensively preceding or following sunbathing, likely to remove the dead lice (Blem and Blem, 1993; Moyer and Wagenbach, 1995). Sunbathing in Swallows (Hirundinidae) can often lead to heat stress, including behaviors such as gaping and panting (Blem and Blem, 1993). Obviously, these birds are not comfortable; it is unlikely adaptation to warm themselves, but an adaptation to kill lice (Blem and Blem, 1993). Blem and Blem (1993) treated a number of birds with pesticide and then observed the behavior of the birds and found that the treated birds spent less time sunning than untreated birds. Sunning, like anting, is a way to kill a large number of lice without spending the time to root out each one individually while preening.

Secondary sexual characteristics may have evolved to cue females to the parasite levels of males. Species with the most evident sexually selected traits are often the most subject to attack by debilitating parasites (Hamilton and Zuk, 1982). Although lice are
Generally not debilitating, there may be heritable genetic resistance to louse infestations (Potti and Merino, 1995; Clayton, 1991a). However, low parasite load does not necessarily mean that an individual is resistant to parasites; it may only mean that this particular individual was never exposed (Clayton, 1991a). Parasite infestation can actually lower the testosterone levels in the host, preventing it from developing secondary sexual characteristics (Hilgarth and Wingfield, 1997). Testosterone has been shown to be an immunosuppressant and increased levels may result in a decreased ability to fight infections (Hilgarth and Wingfield, 1997). If a young male bird is infested with parasites, he must reduce the amount of testosterone in his system to fight the infestation and therefore he will not be able to develop his secondary sexual characteristics. If the testosterone is not reduced, the secondary sexual characteristics can develop but he would leave himself open to infestation and may be overcome by it.

Reduced reproductive success is correlated with male parasite infestation in some birds (Lehmann, 1993). Female barn swallows (Hirundo rustica) are attracted to long tails in their mates (Kose and Moller, 1999). The number of holes in tail feathers caused by lice is negatively correlated with tail length in male barn swallows, and therefore reduced reproductive success (Kose and Moller, 1999). Lice preferred white spots to other areas of the tail feathers and males with longer tails had less damage to white-spots, possibly due to genetic resistance (Kose and Moller, 1999). Females also chose to mate with males with longer tails and these males may have been chosen because they have genetic resistance to louse infestations that the females would like to pass on to their offspring.

Infestation level does not always reduce the mating chances of males. Increased parasite load does not always equal decreased showiness in passerines; sometimes there are no signs that point to a heavily infested individual (Walther et al., 1999). In these cases, females do not seem to prefer unparasitized males (Walther et al., 1999). Brown et al. (1995) found no relationship between fleas or chewing louse load and the quality of their host, the Cliff Swallow’s (Hirundo pyrrhonota) phenotype, which suggests that is not sexual selection for parasite resistance. The theory that secondary sexual characteristics developed to alert females to parasite infestations in males has not been proven. If this theory is true, parasites that inflict obvious damage may be selected against and less damaging parasites may thrive.

Chewing Lice

Just as birds have adapted to remove lice, lice have adapted to thwart these defenses. Lice have evolved many resistance tactics to counter a bird’s preening bill including: small size, flattened shape, heavily sclerotized integuments, spines, ctenidia, numerous setae, strong mouthparts, grasping claws, and avoidance behavior (Clayton, 1991b; Lehane, 2005). These adaptations allow the louse to hide from the bill and prevent them from being dislodged.

Host-specificity in lice may be partially due to extreme specialization to the body of their host. Lice tend to stay within a specific feather barb diameter and are only able to survive upon hosts of a particular size (Tompkins and Clayton, 1999). The main reason lice are unable to survive on hosts of varying size is their inability to escape a preening bill when they no longer fit between the host’s feather barbs (Clayton et al., 2003). Lice are only able to survive on birds of a particular size, which leads to high host-specificity.

Grooming-imposed selections upon lice differ with the area of the body the louse inhabits. Lice on the wings, which are the most vulnerable to grooming, tend to be elongate, compressed forms that flatten against feathers or insert between the barbs very quickly (Clayton, 1991b). Those that live on the head and neck tend to be round-bodied and sluggish with no apparent adaptations for avoidance (Clayton, 1991b). These lice are safe from the beak of the bird and therefore have not adapted to get away from it quickly like the lice on the wings have. The lice that live on the wings and body of their host are forced to conform to the topology of the host in order to be able to avoid the host’s defenses (Kethley and Johnston, 1975). Host body size is the major selection factor acting upon lice, but where they occur on the body also affects the lice.

After molting, there appear to be fewer lice, but actually the number has not decreased, they are just hidden from human eyes. Lice have evolved to actively seek refuge inside the sheath that encases developing feathers when the bird begins molting (Lehane, 2005; Moyer, Gardner, and Clayton, 2002). By hiding in the sheath, they are not dropped with the feather and are able to continue on their host. This is a significant adaptation for survival on an avian host. If they dropped with the feathers every time the bird molted, the louse populations would be significantly decreased every molting cycle.

Hosts also adapted behaviors that make them better able to infest the next generation. Some blood-feeding lice may synchronize their life cycle with that of their host (Janovy, 1997; Moller et al., 2003). *Ricinus picturatus* and *Menacanthus* sp. showed peak reproduction during their host’s, the Orange-crowned Warbler (*Vermivora celata*), nesting period (Janovy, 1997). This way they are able to increase the chances of nestlings picking up their parent’s lice. Non-blood-feeding lice reproductive-cycles were not dependent upon the host; the blood-feeders may be responding to host hormones that signal when they should start reproducing (Janovy, 1997). These types of adaptations can only occur when the lice are in contact with the host’s blood. Lice are well-adapted to living life on the body of their host and consequently are not well-equipped to survive off of the host. Louse populations are extremely sensitive to changes in temperature and humidity, and by living so near to the host’s skin, there is some control of these factors as compared with the outside environment (Moyer, Drown, and Clayton, 2002; Johnson and Clayton, 2003). Birds that live in humid regions are likely to have a greater number of lice than those that live in dry regions (Moyer, Drown, and Clayton, 2002; Johnson and Clayton, 2003). These lice are so adapted to the temperature and humidity controls on the body of their hosts that few can survive for more than a few days off of their host (Johnson and Clayton, 2003). Rem and Zlotorzycka (1981) found that lice lived 3-11 days in an empty tube at room temperature with unknown humidity, although it is unknown how long they retain the ability to infest another host. Although these lice were able to survive a surprisingly long time without food, they likely did not experience extreme changes in temperature or humidity, which could have killed them, so the study may not represent an accurate representation of how long a louse can live off of its host.
Amblycerans and Ischnocerans
The two main suborders of lice that infest birds are Amblycera and Ischnocera. Amblycerans feed mainly on host skin as well as blood and skin secretions; however, they may also eat other lice and feather mites especially when they are in high abundance (Marshall, 1981; Moller and Rozsa, 2005; Whiteman and Parker, 2004a). Blood has high nutritional value and it is easy to digest, which allows blood feeders to have greater fecundity (Lehane, 2005). Amblycerans are generally less host-specific, less restricted to a particular region of the host’s body, more vagile than ischnocerans and when they do co-occur with ischnocerans, amblycerans are the more abundant (Whiteman and Parker, 2004a). Although there are major differences between amblycerans and ischnocerans, both suborders respond to selective pressures imposed by their hosts, and both show evidence that they have coevolved with their hosts.

Ischnocerans live on their hosts’ feathers and, unlike amblycerans, they have no contact with their host’s immune system. Ischnocerans feed on feathers and/or skin debris, but not blood (Marshall, 1981; Moller and Rozsa, 2005; Crompton, 1997). They have no direct contact with the host’s immune system and mainly encounter the host’s mechanical defenses (Whiteman et al., 2005). Since ischnocerans have no contact with the host’s immune system, there may be more selective pressure for birds to evolve defenses against amblycerans.

Although there may be more selective pressure for a host to adapt to amblycerans, amblycerans are thought to be better able to find new hosts. Amblycerans are generally more mobile than ischnocerans and will often abandon a dead host in search of a new one, whereas the ischnocerans will die with their host (Johnson and Clayton, 2003; Kierans, 1975; Marshall, 1981). Amblycerans are known to migrate to the head feathers of dead hosts even though they are not normally found there and were able to survive for up to 14 days, just hoping a chance would come along for them to find a new host (Rem and Zlotoryzcka, 1981). It is possible that although amblycerans try to find new hosts, they are frequently denied the chance.

Factors that hinder cospeciation
Chewing lice and their hosts have coevolved, but have they coadapted? Extreme specialization by both host and parasite will not always lead to cospeciation. Factors such as parasite virulence and transmission ability may hinder cospeciation. Phylogenetic congruence may be hidden by sorting or duplication events (Banks et al., 2006). False congruence could come from a series of sequential host switches successively colonizing the host’s closest relatives and then speciating, although this is unlikely to be common (Banks et al., 2006; Paterson and Gray, 1997; Paterson et al., 2000). Furthermore, a large founding population of hosts would be necessary for all louse species to be present when speciation occurs (Paterson et al., 1999). House Sparrows (Passer domesticus) were introduced to North America and only 35 of the original 69 ectoparasite species of the European species are present on the North American species (Paterson et al., 1999). With factors working for and against cospeciation, partially congruent phylogenies may be common.

Paterson et al. (2000) demonstrated partial congruence between a louse phylogeny and their seabird hosts. Cospeciation is also the main explanation for the history of seabirds and their lice (Paterson et al., 2000). It is not strict cospeciation however; there is some intrahost speciation and also some sorting events with little host-switching (Paterson et al., 2000). Host-switching is rare due to limited contact between hosts and the lack of a vector (Paterson et al., 2000). These organisms have partially cospeciated, but other cophylogenetic patterns explain the rest of the relationships.

Virulence
Traditionally, virulent pathogens/parasites were thought of as those that had been associated with their host for only a short period of time. Pathogens were thought to evolve towards non-virulence the longer they were associated with a host, because non-virulence ultimately benefits the pathogen (Smith, 1934; Swellengrebel, 1940). This view predicts that non-virulent pathogens are more likely to have cospeciated with their hosts than virulent ones.

Although, in theory, a pathogen has high fitness if it is benign, the view that all pathogens are evolving toward becoming more benign has lost favor in recent decades. Even in the 1940’s, some believed that long associations could also lead to increased virulence (Ball, 1943). In the 1990’s Paul Ewald really revolutionized the field. By showing that easily transmitted pathogens tend to be highly virulent (Ewald, 1993). He showed that the length of the association between host and parasite/pathogen is not the determining factor; long associations are just as likely to result in non-virulence as virulence (Ewald, 1983, 1998). A pathogen or parasite that has been associated with its host for a long period of time can still have high fitness while being virulent if it is easily transmitted to a new host.

The mode of transmission and the ability to survive outside/off of the host greatly influence the evolution of virulence (Ewald, 1993, 1998). The more difficult it is for a pathogen or parasite to be transferred to a new host, the less virulent it can afford to be. If it incapacitates its host, its host will be unable to transfer it to a new host and the pathogen or parasite will die with its host. However, if there is a vector that facilitates the transfer of the pathogen or parasite between host individuals, the pathogen or parasite can afford to incapacitate the host, because it can still colonize a new host (Ewald, 1983). Along the same lines, if a pathogen or parasite is able to survive for a long time off of the host, it can afford to be more virulent. It can sit and wait for a new host to come along without being adversely affected (Ewald, 1995). Hosts and parasites will not ultimately end up in a coexisting state with neither harming the other in all cases; it depends a lot on transmission (Anderson and May, 1982). Essentially, the more easily something is transmitted, the more virulent it can afford to be. These easily transmitted, virulent organisms may have been associated with their hosts for a short or a long period of time, but there is certainly incentive for the host to adapt defenses to protect against them.

Parasite virulence
Although a lot of work has been done on the virulence of pathogens, ectoparasites have not received as much attention. Ectoparasites generally do not kill their host, so virulence in parasites may be measured as parasite
reproduction, parasite infectiousness or parasite-induced mortality rate of the host (Toft, 1981). Ectoparasites may harm their hosts by lowering body mass, blood loss, feather loss; they may serve as vectors for other pathogens, and may also increase time spent in self-maintenance behavior and, therefore, reduce the amount of time that the host can spend on other activities (Brown et al., 1995). Although parasites generally do not kill, they do have a negative impact on their hosts. A host with few parasites is bound to be healthier than a host with many parasites.

**Virulence and Chewing Lice**

As discussed before, lice generally have small populations on a host due to their host's defenses. Lice are also the only parasitic insects that complete their entire life cycle on a host and show only low levels of pathogenicity (Moller and Rozsa, 2005; Crompton, 1997). However, much of this data has come from studies that merely correlate host condition with parasite loads, and therefore may not tell the whole story (Booth et al., 1993). The effect of infestations may not be evident until a burst of energy is needed, such as when the host needs to escape from a predator (Hart, 1997). Unfortunately, heavily infested birds are uncommon in nature which makes them difficult for correlational studies to observe.

On the other hand, experimental studies that have manipulated the louse loads on birds have been able to look at many heavily parasitized individuals. Booth et al. (1993) showed that birds with high loads of ischnoceran lice suffered significant feather mass reduction and an increase in metabolic rate and whole thermal body conductance. Barbosa et al. (2002) found a significant positive relationship in barn swallows between the number of lice and the percentage of time spent in flapping flight. Since lice are not thought to produce any mechanical constraints on flight, these high parasite loads have been linked to increased thermoregulation costs and therefore lower fat stores, which lead to less energy that can be devoted to flying. Although lice likely have a negative impact on their host, it is generally not readily detectable.

**Are Amblycercans or Ischnocercans More Virulent?**

There is some debate over whether amblycercans or ischnocercans are more virulent, and since most studies measuring virulence are correlational, there is not a lot of data to definitively support either as more virulent. Large populations of either louse suborder can induce a significant positive relationship in barn swallows with a decreased feather mass of 30% and increased metabolic rate of 8.5% (Booth et al., 1993). The pigeons increased their metabolic rate to compensate for increased thermal conductance and maintain body temperature, so high-load birds steadily lost body mass and appeared unable to compensate for increased metabolic rate (Booth et al., 1993). Ischnocercans certainly seem capable of inflicting major harm; however, in most cases the host's defenses will keep them in small enough numbers to prevent major harm.

**Transmission**

Transmission not only has an influence on virulence, it also has a more direct impact on the cophylogenetic histories of hosts and parasites. Hosts act as temporary islands for parasites and effective transmission to a new host is essential for the survival of the parasite genes (Ewald, 1983). There are three main types of transmission patterns: vertical, horizontal and host-switching. Each of these supports a different cophylogenetic history which will be outlined below.

**Vertical Transmission**

Vertical transmission is the transfer of parasites from parents to offspring through direct contact. This common dispersal method essentially guarantees the survival of the parasite in the next generation, resulting in high fitness. Vertically transferred organisms, whether they be parasite or symbiont, are relatively benign since they rely on their host to pass them to their offspring (Lipsitch et al., 1996). A solely vertically transferred organism is likely to cospeciate with its host. Vesicomyid clams have had a long term association with endosymbiotic sulfur-oxidizing bacteria (Peek et al., 1984). These bacteria are transferred cytoplasmically through the eggs and there has been nearly completely vertical transmission for as long as they have been associated with one another (Peek et al., 1984). These two organisms have cospeciated almost strictly (Peek et al., 1984). Although strict
vertical transmission will not always result in cospeciation, cospeciation is extremely likely. Another example of strict vertical transmission also results in cospeciation. Aphids and their endosymbiotic bacteria, Buchnera have cospeciated (Moran, 2001; Clark et al., 2000). Buchnera are transferred from mother to progeny and there has been strict vertical transfer over the last 100 million years (Moran, 2001). There is not even any evidence of horizontal transmission among closely related groups (Moran, 2001). Vertically-transmitted endosymbionts tend to cospeciate with hosts to a greater extent than do ectoparasites, because they are tied to their hosts and have few transmission opportunities.

**Horizontal Transmission**

Some parasites that are vertically transferred can also be horizontally transferred. Horizontal transfer is transfer between individuals of the same species. It can occur through direct contact during mating, copulation, pair preening, pair feeding, working in a nest chamber, chick feeding, or phoresy (Darlova et al., 2001). Since they are not dependent upon living on individual host organisms for long periods of time in order to be transferred to the next generation for survival, they can also afford to evolve to become more virulent. Furthermore, since they are able to transfer between unrelated individuals, there are more opportunities for a chance switch to a new species to occur, resulting in incongruent phylogenies of host and parasite. When looking at an evolutionary time scale, unlikely everyday events become commonplace. An extremely rare, chance encounter between two unrelated species may be enough to transfer a parasite to a novel host, thereby changing the cophylogenetic history of the organisms. Although horizontal transfer does not necessarily entail switching between host species, it may make it more likely.

**Host-switching**

When a parasite is transferred to a novel host species it is called host-switching. Vectors are a common implement in host-switching as they provide an easy way for parasites to be transferred to novel hosts and this relatively easy transfer often allows for greater virulence in vector-borne parasites (Day, 2002; Sol et al., 2000). Some parasites, like malaria are transferred solely by vectors such as mosquitoes (Rickles and Fallon, 2002). Mosquitoes have broad host ranges and this creates ample opportunities for host-switching in mosquito-carried blood pathogens (Rickles and Fallon, 2002). This rampant host-switching would probably result in a phylogenetic tree of malaria parasites looking nothing like a phylogenetic tree of their hosts.

**Transmission in Chewing Lice**

Direct contact is the main mode of transmission for lice. Lice are generally transmitted as nymphs or adults through direct contact between parents and their young and between mates (Janovy, 1997). Horizontal transfer through direct contact may be the most common mode of transfer. Louse loads correspond on mates, suggesting that when the mates come into direct contact, their lice are able to transfer from one body to the other and the loads become evenly split over time. (Potti and Merino, 1995). Common Cuckoos (Cuculus canorus) also support frequent transfer through direct contact. They are brood parasites, so their young have no contact with their parents. Although there is no direct contact between the two, there are multiple cuckoo-specific lice that seem to be acquired through direct body contact before and after the hatch (De L. Brooke, 1998; Lindholm et al., 1998). Direct contact, whether it is vertical or horizontal, is believed by most to be the main way lice find new hosts.

Horizontal transmission is not limited to direct contact. Additional non-vertical routes for louse transmission between birds of the same species include: dispersal of lice or eggs on detached feathers, shared dust baths or shared nest holes or stolen nest material (Johnson and Clayton, 2003; Whitteman and Parker, 2004b). If a louse does manage to get on a new host through one of these methods, competition among the lice already present on that host may limit the success of host-switching (Barker, 1994). While these methods are unlikely to be common, they may occasionally result in horizontal transfer of lice or even a host-switch.

Since lice are transferred mainly through direct contact, they should be confined to their host species. Valera et al. (2003) found that mites and C. hemapterus parasites were able to transfer between European bee-eaters (Merops apiaster) and Rock Pigeons (Columba livia) living in a mixed colony, whereas the lice species remained exclusively on their respective hosts. It is possible that the other two parasites were transferred via a vector that was unavailable to the lice. However, if the two species were coming into direct contact with each other, it is possible that lice were being transferred but were unable to survive on novel host species.

Horizontal transmission may be a more important dispersal route for amblycercans than ischnocerans (DeVaney et al., 1980, Whiteman and Parker, 2004b). Amblycercans may be more adept at transfer during brief periods of direct contact. This speed would allow them to make use of even a brief point of contact between two hosts. The amblyceran levels were similar between individual birds living in a polyandrous group, whereas the ischnoceran levels differed, suggesting a greater ease of transmission for amblycercans than ischnocerans (Whiteman and Parker, 2004b). However, this may only be true for polyandrous species that come into direct contact with their mates on a regular basis. Species that do not come into frequent direct contact may not share this characteristic and horizontal transfer of amblycercans among them may be no more common than in ischnocerans.

**Phoresy on Hippoboscid Flies**

The one relatively common event that may prevent cospeciation between some chewing lice and their hosts is phoresy on hippoboscid flies. Ischnocerans are able to attach to hippoboscid flies (Hippoboscidae)
and hitch rides between birds (Kierans, 1975). Amblyceroans, on the other hand, are unable to attach to hippoboscid flies due to the shape of their mandibles (Marshall, 1981; Kierans, 1975). Ischnoceroans are quite capable of attaching to hippobosciids; in fact, there is an account of 31 ischnoceroans being found on a single fly (Marshall, 1981). *Brueelia* and *Sturniidae*, both ischnoceroans, are the louse genera most often collected from flies (Kierans, 1975). In contrast, there has only been one record ever of an amblodyneran on a hippoboscid fly (Kierans, 1975). The host-switching opportunity provided by phoresy may result in *Brueelia* and *Sturniidae* having fewer cospeciation events with their hosts than do amblodyneran lice.

There is no hippoboscid phoresy in the two chewing louse systems in which host-louse cospeciation has been demonstrated. Gopher and swiftlet lice (*Amblycera*) have cospeciated with their hosts, and this may be due to all of the factors that have been discussed that make lice ideal for cospeciation, and the lack of a vector that would enable host-switching (Hafner et al., 1994; Johnson, Williams, et al., 2002). If the lack of a vector, like the hippoboscid fly, results in less cospeciation in lice, amblyceroans should cospeciate. However, ischnoceroans, with their well-documented ability to phoresy on hippoboscid flies, should not cospeciate with their hosts.

Hippoboscid flies are generally considered to be generalist parasites similar to mosquitoes. However, Tella et al. (1998) found that hippoboscid flies are only another form of horizontal transfer. If the lack of a vector, like the hippoboscid fly, results in less cospeciation in lice, amblyceroans should cospeciate. However, ischnoceroans, with their well-documented ability to phoresy on hippoboscid flies, should not cospeciate with their hosts.

Cospeciation has been demonstrated for *Brueelia* and helminthes (Johnson, Williams, et al., 2002). If the lack of a vector, like the hippoboscid fly, results in less cospeciation in lice, amblyceroans should cospeciate. However, ischnoceroans, with their well-documented ability to phoresy on hippoboscid flies, should not cospeciate with their hosts.

Possible Cophylogenetic Patterns of Amblyceroans and Ischnoceroans

Current host-parasite associations can be explained by one of two overarching cophylogenetic histories. Association by descent is when associations have in the absence of host-switching (Banks and Paterson, 2005; Hoberg and Brooks, 1997). This association often results in cospeciation. Weckstein (2004) suggested that association by descent should be rare in bird lice because of factors such as host-switching, extinction, failure to speciate, or independent speciation of the parasite (Weckstein, 2004). Each of these factors can change the topology of the parasite tree and prevent congruence with the host tree.

The other overarching cophylogenetic history is association by colonization. Association by colonization occurs when host switching is the predominant explanation for the parasite’s distribution (Banks and Paterson, 2005; Hoberg and Brooks, 1997). Generally when association by colonization is predominant, the host and parasite phylogenies will not be congruent. However, there is the extremely unlikely possibility that the parasites colonized each new host species as they speciated and therefore it appears as if the two have coevolved (Banks and Paterson, 2005).

**Amblycera:** *Myrsidea*

Amblyceroans are more likely to cospeciate with their hosts than ischnoceroans are. They feed on the blood of their hosts, which may make them more virulent than ischnoceroans (Marshall, 1981; Whiteman and Parker, 2004a; Brown et al. 1995; Clayton and Tompkins, 1994). They are also incapable of attaching to hippoboscid flies, which may result in them being more host specific than ischnoceroans (Kierans, 1975). Increased virulence and the inability to easily transfer to a novel host increases the likelihood that these lice will cospeciate with their hosts.

However, phylogenetic congruence is imperfect or absent for most kinds of interactions because even a very low rate of horizontal transfer among host lineages over long periods of time would reduce or eliminate the pattern of cospeciation (Clark et al., 2000; Barker, 1991). Incongruence does not necessarily suggest host-switching, though (Banks and Paterson, 2005). A false incongruence could be caused by parasite lineage sorting events such as extinction, absence from founding population or sampling error (Paterson and Gray, 1997; Paterson et al., 2000). It is unlikely that the parasite and host tree will be perfectly congruent in this case, especially since the main mode of transfer for amblyceroans seems to be horizontal. Over an evolutionary time scale, there will likely be opportunities for a host-switch to occur, thus preventing total congruence between the host and parasite tree.

**Ischnocera:** *Brueelia*

*Brueelia* are even less likely to cospeciate with their hosts. *Brueelia* feed on feathers and are frequently transferred among birds by hippoboscid flies (Marsh, 1981; Kierans, 1975). The relative non-virulence of *Brueelia* likely results in less cospeciation with their hosts. Despite this, approximately 90% of *Brueelia* species are believed to occur on only a single host species (Johnson, Williams, et al., 2002). However, strict cospeciation will only occur when opportunities for host-switching are absent (Barker, 1994). *Brueelia* phoresy on hippoboscid flies reduces the likelihood of much congruence between the parasite and host trees.

Cruickshank et al. (2001) suggested that ischnoceroans should be host specific, and therefore should cospeciate. However, Johnson, Adams, and Clayton (2002) found that *Brueelia* do not appear to have cospeciated with their hosts. They found a general lack of phylogenetic congruence between *Brueelia* and their hosts, which they attributed to host switching events that might have occurred through hole-nests or by phoresy on hippoboscid flies (Johnson, Adams, and Clayton, 2002). Based on transmission ability and virulence, *Brueelia* should cospeciate with their hosts less frequently than *Myrsidea*. 
Chapter 2: Comparative Phylogenetic Histories of Two Louse Genera Found on Catharus Thrushes and Other Birds

Abstract

I reconstructed phylogenies of Brueelia (Ischnocera) and Myrsidica (Amblycera) chewing lice from five species of North American thrushes, and additional Neotropical migrant species, captured or collected in Northeastern Illinois in the spring of 2006. I extracted DNA from the lice, amplified and then sequenced three genes: COI, 12s (mitochondrial), and EF1α (nuclear). I reconstructed the louse phylogenies from these DNA sequences using maximum parsimony, maximum likelihood, and Bayesian methods. Brueelia do not appear to have speciated, much less cospeciated with their thrush hosts. Myrsidica show a greater degree of diversification than Brueelia, but also do not appear to have cospeciated with thrushes. The lack of differentiation and/or cospeciation suggests that host switching or failure to speciate is rampant in this system. The relationships between chewing lice and their hosts may be better explained by biogeography, habitat, or even barb-size correspondence.

Introduction

Chewing lice are prime candidates for cospeciation studies because they lack a free-living stage which makes these parasites completely dependent upon their host (Crompton, 1997). Specific adaptations such as dorsoventral flattening and hiding in the sheath of developing feathers during molting allow lice to survive the defenses of their hosts (Lehane, 2005; Tompkins and Clayton, 1999; Moyer, Gardiner and Clayton, 2002). The strong selective pressure to conform to the topology of the host body to avoid defenses limits the number of host species on which a louse can survive (Kethley and Johnson, 1975; Clayton et al., 2003). Lice are fit to live on their specific hosts, but not many other places.

Not only have lice adapted to living their entire lives on birds, but birds have responded with adaptations of their own to defend against these parasites. Preening is a bird’s first line of defense (Marshall, 1981; Hart, 1997), and the bill shape is specifically adapted for removal of lice (Clayton et al., 2005; Moyer, Peterson, and Clayton, 2002). Other defenses include anting (Marshall, 1981), sun bathing (Moyer and Wagenbach, 1995; Blem and Blem, 1993), and dust bathing (Marshall, 1981). Also, sexual selection may cue potential mates to infestation levels and potential genetic resistance to louse infestations (Hilgarth and Wingfield, 1997; Read, 1988; Potti and Merino, 1995; Moller, 1988; Kose and Moller, 1999; Hamilton and Zuk, 1982; Clayton, 1991a). This highly specialized, coevolved system is an ideal arena for cospeciation between chewing lice and their hosts.

Coevolution may lead to exclusivity and cospeciation, as it has between gophers and their chewing lice (Hafner et al., 1994).

Of the two suborders of lice present on birds: Ischnocera and Amblycera, amblycerans are more likely to cospeciate with their hosts. Ischnocerans, that eat only feathers, are seen as less virulent than amblycerans, which feed on blood (Marshall, 1981). The more virulent amblycerans may exert a stronger selection pressure on their host which would make them more likely to cospeciate with their hosts than ischnocerans. Lice of both suborders are generally transmitted through direct contact by parent-offspring interaction, sexual contact or predator-prey contact (Potti and Merino, 1995; Rozsa, 1993, Janovy, 1997; de L. Brooke et al., 1998; Lindholm et al., 1998). However, ischnoceran lice are also capable of being transmitted through phoresy on hippoboscid flies (Kiers, 1975; Marshall, 1981). The ability of ischnoceran lice to hitch a ride on hippoboscid flies may result in enough host switching or gene flow opportunities to prevent cospeciation. Amblyceran lice, on the other hand, are unable to attach to hippoboscid flies due to their mandible shape, and may therefore be more likely to cospeciate (Kiers, 1975; Marshall 1981). Many host-switches presumably end with death due to non-host specific hosts, potential competitors, and few, if any, reproductive opportunities (Rozsa, 1993). However, a few studies have found high host specificity in louse flies (Kiersan, 1975, Tell, et al., 1998) suggesting that phoresy on flies might allow for a successful switch to a host of the same or similar species.

Based on transmission ability, ischnoceran lice seem to have greater opportunities for host switching and amblyceran lice, therefore, should be more likely to cospeciate. Although amblycerans are unable to attach to hippoboscid flies, they are generally thought to be less host-specific than ischnocerans (Whiteman and Parker, 2004a). They are possibly transferred through loose feathers or shared dust baths (Whiteman and Parker, 2004b). Lice may also be transferred through chance contact and amblycerans are much more likely to leave a dead host than are ischnocerans (Marshall 1981; Kiersan 1975). However, lice are unable to survive for an extended period of time off a host (Rem and Zlotoryczka, 1981), so presumably most lice die when their host dies.

Decreased transmission ability of amblyceran lice seems to be the only factor that may contribute to them cospeciating with their hosts. The greater virulence of amblycerans may also make them more likely than ischnocerans to cospeciate. Amblyceran lice come into direct contact with the host’s immune system through their blood meals, whereas ischnoceran lice are restricted to feeding on feathers, and therefore have no contact with the host’s immune system (Marshall 1981; Crompton 1997; Moller and Rozsa, 2005). Amblyceran lice are known to induce an immune response in their hosts (Lehane 2005; Whiteman et al. 2005; Mumcuoglu et al. 1997) and it has been found that as the immune response increases against fleas, the number of host species parasitized decreases (Moller et al. 2005). This interaction has led many to believe that amblycerans are more virulent than ischnocerans (Whiteman and Parker, 2004a; Barbosa et al. 2002). However, this has been challenged by the negative effects ischnocerans cause by increasing the metabolic rate of their host through feather mass reduction (Booth et al. 1993; Hart 1997). Amblycerans are generally believed to be more virulent than...
ischncerans, but it is possible that in heavy infestations ischnocerans are just as virulent as amblycerans.

Although some louse groups are known to cospeciate with their hosts (Hafner et al., 1994; Paterson et al., 2000), other cophylogenetic patterns can occur. In ischnocerans, the general lack of virulence and frequent transfers through hippoboscid flies may result in the lice infesting many of the hosts in a particular region, regardless of the host's taxonomy. For example, Austrophilopterus (Ischnocera) lice, which are known to ride on hippoboscid flies, inhabit multiple species of Ramphastos toucans in a given geographic area (Weckstein, 2004). Biogeography, not cospeciation, is the major factor influencing speciation in these lice. The overarching factor that may limit successful host-switches between avian species in a particular area may be barb correspondence (Clayton et al., 2003; Tompkins and Clayton, 1999). Lice hide from preening bills in between feather barbs, so size correspondence with the space between barbs is important.

The louse genera Myrsidea (Amblycera) and Brueelia (Ischnocera) both infest New World Thrushes in the genus Catharus. Multiple data sets indicate that Catharus thrushes are a monophyletic group (Outlaw et al., 2003; Winker and Pruett, 2006). Therefore, I chose to use this monophyletic group of hosts to explore patterns of speciation with their chewing lice. I used phylogenies of Brueelia and Myrsidea to assess patterns of host specificity and their phylogenetic history with respect to the host’s phylogenetic history. Based on Brueelia’s increased transmission abilities and lesser virulence I predicted that Brueelia would cospeciate less than Myrsidea, which are less able to transfer to a new host and more virulent due to contact with the host’s immune system.

Methods

Mist-netting

Birds were captured in Shaw Woods at the Skokie River Nature Preserve in Lake Forest, IL (42° 15’ 37.2” N, 87° 51’ 34” W) as part of the Shaw Woods Avian Monitoring Project (SWAMP) (Gordon et al., 2002). Twelve standard mist nets (35mm mesh and 12 meters in length) were set up in brush-cleared lanes. The nets were open from 5 am to 10 am 27 days between May 1st and May 31st, 2006. Captured birds were removed from the nets and placed in cloth bags to be carried back to the banding station. The five focus species of my study, Hylocichla mustelina, Catharus minimus, Catharus ustulatus, Catharus fuscens, and Catharus guttatus, were banded with standard bands from the U.S. Federal Bird Banding Laboratory, deloused, and then released. Following the procedure of Walther and Clayton (1997) and Clayton and Drown (2001), thrushes were dusted with pyrethrin flea powder (Hartz), which was then rubbed into their feathers for approximately 5 minutes. As the lice were killed, they fell off the bird onto a white piece of paper. They were then collected with a paint brush and placed in a vial of 95% ethanol and stored frozen at -20 °C.

Delousing Salvaged Specimens

Window-killed thrushes, and other Neotropical migrant species, salvaged by the Field Museum of Natural History in spring, 2006 from the downtown Chicago area, were placed in ziplock bags for 5-10 minutes with a drop of ethyl acetate on a cotton ball to kill the lice. The specimen’s feathers were then rigorously ruffled over a clean piece of white paper until no more lice fell off the bird. Then the lice were picked up with a paint brush and placed in a vial of 95% ethanol and stored frozen at -20 °C.

Louse Specimens

Louse identifications were made using the Price et al. (2003) chewing lice checklist and the taxonomic descriptions cited within. DNA was amplified and sequenced for 39 Brueelia chewing lice. Lice included: 12 individuals from Catharus thrushes of 4 different species, and 26 other Brueelia and Stumidocetus lice, from a range of host species (Table 1). Stumidocetus was included because there is evidence that it is actually a Brueelia (Johnson, K. P., unpublished data). Outgroup (ischnceran) taxa for the Brueelia phylogeny included Paragoniocotes, Neopsittaconirmus, and Struthiolipeurus. DNA from 34 Myrsidea chewing lice from 6 individual Catharus hosts was amplified and sequenced, and the other 28 lice were from a range of hosts (Table 2). Outgroup (amblycera) taxa for the Myrsidea phylogeny included Ricinus and Dennyus.

Louse DNA extraction

Each louse to be extracted was placed in a clean dish of fresh ethanol under a dissection scope and the head and body were plucked from the body using a set of sterilized forceps. The head and body were then placed in a 0.5 mL tube which was left open until the ethanol dried. The genomic DNA was then extracted using the Qiagen DNeasy micro-kit following the manufacturer’s protocols. All specimens were extracted, amplified and sequenced in the Pritzker Laboratory at the Field Museum of Natural History. The head and body of each specimen from each extraction was mounted on a slide and placed in the Field Museum’s insect collection.

Amplification of Louse Genes

379-385 base pairs (bp) of the mitochondrial gene cytochrome oxidase I (COI) were amplified with primers L6625 and H7005 (Hafner et al. 1994) using the temperature protocols in Weckstein et al. (2004). 483 bp of 12s were amplified using 12sai and 12sbi (Simon et al., 1994). 347 bp of the nuclear elongation factor 1α (EF-1α) gene were amplified using primers EF1-For3 and EF1-Cho10 (Danforth and Ji, 1998) using the temperature protocols in Weckstein et al. (2004). Most PCR products were amplified using Taq Gold (AmpliTaq Gold; Perkin-Elmer Corporation, Foster City, CA) and Taq beads (Promega, Madison, WI) were used to amplify a few EF-1α sequences. PCR-products were purified with either Exonuclease and Shrimp Alkaline Phosphotase enzymatic reactions (United States Biochemical) or by cutting bands from a low melt Biochemical) or by cutting bands from a low melt agarose gel and digesting them with gelase (Epicentre Technologies, Madison, WI).

Sequencing of Louse Genes

I cycle sequenced 1µL of purified PCR product with 1µL ABI Big Dye kit (version 3.2, Applied Biosystems, Foster City, CA) and 1µLxµM primer, and ran these sequenced products on an ABI Prism 3730 automated DNA sequencer (Perkin-Elmer Applied Biosystems). Sequencer (version 4.5, GeneCodes Co., Ann Arbor, MI) was used to reconcile and align double-stranded
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<th>Locality</th>
<th>Habitat</th>
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Table 1: Voucher numbers, host associations and host habitat and range information for all Brevella house specimens used in this study. Habitat and range information was taken from Martinson and Pilatti (1993).
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<td>Myr.6.14.2006.5</td>
<td>Tetrabrachidae</td>
<td>Cathusus suturalis</td>
<td>Illinois</td>
<td>Cook Co, old 1st growth, above-ground forager</td>
<td>Mexico and N.S. Am. to Canada</td>
</tr>
<tr>
<td>6</td>
<td>Miridae incerta</td>
<td>Myr.6.14.2006.6</td>
<td>Tetrabrachidae</td>
<td>Hybridae suturalis</td>
<td>Illinois</td>
<td>Lake Co, forest and edge, understory</td>
<td>Middle Am., Mexico to Canada</td>
</tr>
<tr>
<td>7</td>
<td>Miridae incerta</td>
<td>Myr.6.14.2006.7</td>
<td>Tetrabrachidae</td>
<td>Cathusus suturalis</td>
<td>Illinois</td>
<td>Lake Co, old 1st growth, above-ground forager</td>
<td>Mexico and N.S. Am. to Canada</td>
</tr>
<tr>
<td>8</td>
<td>Miridae incerta</td>
<td>Myr.6.14.2006.8</td>
<td>Tetrabrachidae</td>
<td>Cathusus suturalis</td>
<td>Illinois</td>
<td>Lake Co, second growth and understory</td>
<td>S. Am. to N. Alaska, and N. Canada</td>
</tr>
<tr>
<td>10</td>
<td>Miridae sp.</td>
<td>Myr.6.14.2006.12</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus albus</td>
<td>Ghana</td>
<td>open savanna, shrub-gross</td>
<td>Middle of Africa</td>
</tr>
<tr>
<td>11</td>
<td>Miridae sp.</td>
<td>Myr.6.14.2006.15</td>
<td>Tetrabrachidae</td>
<td>Gymnephora calcar</td>
<td>Ghana</td>
<td>forest and secondary growth</td>
<td>W. Africa</td>
</tr>
<tr>
<td>12</td>
<td>Miridae esculenta</td>
<td>Myr.7.15.2005.9</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus castaneus</td>
<td>Madagascar</td>
<td>swampy shrubland, understory</td>
<td>Madagascar</td>
</tr>
<tr>
<td>13</td>
<td>Miridae westfalicus</td>
<td>Myr.7.15.2005.10</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus sp.</td>
<td>Madagascar</td>
<td>swampy undergrowth, mist, and canopy</td>
<td>Madagascar</td>
</tr>
<tr>
<td>14</td>
<td>Miridae parviflori</td>
<td>Myr.6.15.2006.5</td>
<td>Tetrabrachidae</td>
<td>Anthocraea convolvulacea</td>
<td>Ghana</td>
<td>closed canopy forest</td>
<td>W. Africa</td>
</tr>
<tr>
<td>15</td>
<td>Miridae flava</td>
<td>Myr.6.14.2006.6</td>
<td>Tetrabrachidae</td>
<td>Monocolea oligoleuca</td>
<td>Panama</td>
<td>shady ravines with heavy thatch</td>
<td>Costa Rica to N. Venezuela and S. Peru</td>
</tr>
<tr>
<td>16</td>
<td>Miridae cashmeri</td>
<td>Myr.6.15.2006.2</td>
<td>Tetrabrachidae</td>
<td>Ctenoprax barbatissima</td>
<td>Ghana</td>
<td>understory and gallery forest</td>
<td>W. Africa</td>
</tr>
<tr>
<td>17</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.3</td>
<td>Tetrabrachidae</td>
<td>Tyrannidae</td>
<td>Panama</td>
<td>lowland woodlands</td>
<td>C. Panama to N. Bolivia and Amazonia</td>
</tr>
<tr>
<td>18</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.4</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus vittatus</td>
<td>South Africa</td>
<td>shrubland, savanna</td>
<td>South Africa</td>
</tr>
<tr>
<td>19</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.5</td>
<td>Tetrabrachidae</td>
<td>Anthocraea vittata</td>
<td>Panama</td>
<td>forest in lower highlands</td>
<td>S. Mexico to N. S. Am.</td>
</tr>
<tr>
<td>20</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.6</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus nitidus</td>
<td>Panama</td>
<td>shrubland, wooded borders</td>
<td>SE Mexico to W. Panama</td>
</tr>
<tr>
<td>21</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.7</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus nitidus</td>
<td>Panama</td>
<td>evergreen and semideciduous forest</td>
<td>Mexico and Argentina</td>
</tr>
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<td>22</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.8</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus nitidus</td>
<td>Panama</td>
<td>forest, deciduous and second growth</td>
<td>Costa Rica to Bolivia and Amazonia</td>
</tr>
<tr>
<td>23</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.9</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus nitidus</td>
<td>Panama</td>
<td>forest and forest borders of highlands</td>
<td>Costa Rica to W. Panama</td>
</tr>
<tr>
<td>24</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.10</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus nitidus</td>
<td>Panama</td>
<td>scrub, deciduous forest</td>
<td>Costa Rica to W. Panama</td>
</tr>
<tr>
<td>25</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.11</td>
<td>Tetrabrachidae</td>
<td>Phalacrinus nitidus</td>
<td>Panama</td>
<td>scrub, deciduous forest</td>
<td>N.S. Am.</td>
</tr>
<tr>
<td>26</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.12</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Mexico</td>
<td>humid to semiarid forest, semi-open areas</td>
<td>E. Mexico to W. Panama</td>
</tr>
<tr>
<td>27</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.13</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Panama</td>
<td>shrubland, riparian woodland</td>
<td>S. Honduras to Bolivia, Paraguay and S. Br.</td>
</tr>
<tr>
<td>28</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.14</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Panama</td>
<td>woodland, clearings, ridgelines</td>
<td>N. Colombia, Mexico to Panama</td>
</tr>
<tr>
<td>29</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.15</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Panama</td>
<td>canopy and borders, forstlands</td>
<td>C. Panama to NW Venezuela and NW Peru</td>
</tr>
<tr>
<td>30</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.16</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Panama</td>
<td>dry savannas, brushy desert lands</td>
<td>SW Africa</td>
</tr>
<tr>
<td>31</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.17</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Ghana</td>
<td>deciduous and gallery forest</td>
<td>W. Africa</td>
</tr>
<tr>
<td>32</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.18</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Ghana</td>
<td>deciduous and gallery forest</td>
<td>W. Africa</td>
</tr>
<tr>
<td>33</td>
<td>Miridae sp.</td>
<td>Myr.6.15.2006.19</td>
<td>Tetrabrachidae</td>
<td>Anthocraea confectionis</td>
<td>Madagascar</td>
<td>deciduous and humid evergreen forest</td>
<td>Madagascar</td>
</tr>
</tbody>
</table>

Table 2: Voucher numbers, localities, host associations and host habitat and range information for all Miridae species specimens used in this study. Habitat and range information was taken from MacKinnon and Phillips, 1991; Metz and Hawkins, 1968; Eakle et al., 1985; Ridgely and Gwynne, 1989; Hoelzle and Kriebel, 1992; Howell and Webb, 1995; Sinclair and Ryan, 2003; Ridgely and Tudor, 1990; Evans-Mack and Yong, 2001; Jones and Donovan, 1992; and Fish et al., 1968.
sequences for COI and EF1α. 12s gene sequences were aligned using Clustal X and then manually aligned with MacClade v4.05. All of the sequence data generated by this study have been submitted to Genbank (pending acceptance), and the 12s alignment was submitted to Treebase (pending acceptance).

Phylogenetic Analysis

Maximum parsimony heuristic searches were performed with 100 random addition sequence replications (PAUP*, version 4.0b10; Swofford, 2002). Branch-swapping was by stepwise addition using TBR swapping algorithm. 1000 bootstrap replications were performed with 10 random addition sequence replications.

I used the partition homogeneity test (ILD statistic, Farris et al. 1994, 1995) as implemented in PAUP* (version 4.0b10; Swofford 2002) to test for incongruence in the sequence data sets. For Brueelia we analyzed two data sets, one including only samples sequenced by me for COI, EF1α, and 12s, and another including COI and EF1α sequences from Johnson, Williams, et al. (2002). For the Brueelia data set including 12s, three different ILD tests were run, comparing all three genes, 12s to CO1 and 12s and CO1 to EF1α. All parsimony uninformative characters were removed prior to the test.

I used Akaike Information Criterion in Modeltest 3.5 (Posada and Crandall 1998) to determine the best likelihood model for each data set. Maximum likelihood analyses were run using Garli v0.951 (Zwickl, 2006, unpublished Ph.D. dissertation; http://www.zo.utexas.edu/faculty/antisense/Garli.html). I ran 5 independent runs and chose the best tree. 1000 bootstrap replicates were performed to assess statistical support for nodes in the likelihood tree.

Bayesian inference analysis was performed using Mr. Bayes 3.1.1 (Ronquist and Huelsenbeck 2003). Mr. Modeltest (Nylander 2004) was used to determine the likelihood model for each of the seven data partitions. These partitions included 3 codon positions for each protein-coding gene and 1 partition for the non-coding 12s gene. We ran two analyses of 5,000,000 generations and 4 Markov chains with every 500th tree sampled. The first 500 trees were discarded as the burn-in and the consensus of the remaining trees was used. Neighbor-joining analyses were also performed on the Brueelia data set with a 16 parameter Log Det model to determine whether the complexity of the model of molecular evolution might affect the tree topology.

Biogeographic Analyses

MacClade (version 4.05; Maddison and Maddison, 1992) was used to map and reconstruct biogeographic distributions of the hosts onto the louse phylogenies. To test whether biogeography contained significant phylogenetic signal, I used Maddison and Slatkin’s (1991) randomization procedure of 1,000 randomize biogeographic regions 1000 times on each of the louse phylogenies. These randomized character distributions were compared to the empirical character distributions mapped onto the Brueelia and Myrsidea louse trees to obtain a P-value for the test.

Results

Phylogenetic Analyses

Brueelia

Maximum parsimony, maximum likelihood and Bayesian analyses of the Brueelia data set with sequences from COI, EF1α, and 12s show that Brueelia from Catharus hosts are monophyletic. Clade 1 (Figure 1) is a well supported clade (Maximum parsimony (MP) = 100%, Maximum likelihood (ML) = 93%, and Bayesian posterior probability (B) = 100%) that includes all of the individuals from migratory Catharus hosts. Price et al. (2003) lists 3 species of Brueelia found on Catharus hosts. However, among the Brueelia that we sampled from Catharus species there is little to no genetic variation with only 0-0.55% uncorrected sequence divergence. These levels of nuclear and mitochondrial variation are consistent with all of these Brueelia collected from Catharus thrushes being a single biological species.

The well-supported clade 2 (Figure 1: MP, ML and B = 100%) includes a single louse from Slaty-backed Nightingale-thrush (Catharus fuscator), a tropical resident Catharus thrush. This Sturnidoeus shows little genetic distinction from the Sturnidoeus species that inhabits Wood Thrush (Hylocichla mustelina), a close relative of the Catharus and Rappole, 1988). These lice differ by only 0.28% uncorrected sequence divergence. Clade A (Figure 1) is dominated by lice from Catharus hosts. Two lice, from non-Catharus hosts come out between the Catharus clades. The louse, Brueelia brunneinucha, is from a Gray Catbird (Dumetella carolinensis) a Mimid that has similar habitat and range to the Catharus thrushes. The sister relationship of B. brunneinucha with Brueelia from migratory Catharus is not well supported by maximum parsimony (47%) or maximum likelihood (64%), but is well supported by Bayesian posterior probabilities (100%). These Brueelia differ by an average of 10.08% uncorrected sequence divergence. The other louse separating the two Catharus clades is from the Asian Fairy-bluebird (Irena puella). This Asian species obviously does not share a range with any of the birds in the larger clade and yet this rather odd biogeographic placement is well supported in Bayesian and maximum parsimony analyses (MP = 75% and B = 100%).

Clades 3 and 4 (Figure 1) also make up a larger, well-supported clade (MP, ML and B = 100%) with the lice from the Bobolink (Dolichonyx oryzivorus) and Brown Thrasher (Toxostoma rufum). Small birds such as sparrows and warblers dominate these clades. Clade 3 is very well supported by all analyses (MP, ML and B = 100%). It consists of a genetically indistinct Brueelia that is found on three different sparrow species, the White-crowned Sparrow (Zonotrichia leucophrys leucophrys), Dark-eyed Junco (Junco hyemalis), and White-throated Sparrow (Zonotrichia albicollis). The uncorrected sequence divergence differs by an average of 0.19%. These three host species are closely related (Spicer and Dunipace, 2004) and they inhabit similar habitats and ranges, with the two sparrows being very similar. The Brueelia from the Swamp Sparrow (Melospiza georgiana) and the Ovenbird (Seiurus aurocapillus) make up clade 4, also strongly supported by all analyses (MP = 89%, ML = 95%, B = 100%). There are some genetic differences between these two lice, but not much, they likely constitute one species. The uncorrected sequence divergence of Brueelia from Swamp Sparrow and Ovenbird is only 0.69%. Clades 3 and 4 are well supported as sister clades (MP = 89%, ML = 95%, and B = 100%) and all share hosts with small body size,
Neotropical migration and some of the same habitat preferences. These have an average uncorrected sequence divergence of 6.67%.

I also analyzed a *Brueelia* data set that includes a number of additional taxa but only has DNA sequences from COI and EF1α (Figure 2) to help further elucidate some of the relationships among *Brueelia*. The *Cattharus* louse clades appear as they did in Figure 1: two distinct clades, one of *Brueelia* inhabiting migratory *Cattharus* and one for *Sturnidocus* of the tropical *Cattharus* together with the *Sturnidocus* sp. from Wood Thrush. Clade 3 (Figure 2) includes a number of taxa present in Figure 1, plus 4 additional *Brueelia* from Asian hosts. *B. brunneinucha*, from the Gray Catbird, and the *Brueelia* from the Asian Fairy-bluebird (*Irena puella*) share similar relationships with the *Brueelia* of clade 1 as they did before, however now the *Brueelia* from the Asian Fairy-bluebird is joined by the well-supported clade (MP = 100%, ML = 99%, and B = 100%) of genetically indistinct *Brueelia* from the four other Asian hosts. These four birds belong to four different families: Paridae, Dicruridae, Sittidae, and Muscicapidae. These four *Brueelia* have 0% uncorrected sequence divergence. This Asia clade is sister to the *Brueelia* from the Asian Fairy-bluebird (MP = 74%, ML = 96%, and B = 100%), however, the sister relationship of these 5 lice from Asian birds with respect to clade 3 is not strongly supported by maximum parsimony (49%) or maximum likelihood (55%) analyses, even though Bayesian posterior probabilities do support it (90%).

Two hosts that share similar habitat and range, as well as the same family, do not have closely related lice. *B. brunneinucha* from the Gray Catbird and *B. dorsale* from the Brown Thrasher come out in clades 3 and 9 respectively (Figure 2). These two *Brueelia* are only distantly related, which is surprising considering the close taxonomy and biogeography of their hosts.

In the maximum likelihood and Bayesian analyses the outgroups sometimes came out as sister to the louse from the Bar-bellied Cuckoo-shrike (*Coracina striata*).

**Myrsidea**

The phylogenetic analyses for *Myrsidea* shows relatively higher levels of genetic differentiation than that among taxa in the *Brueelia* tree (Figure 3). Clade 1 (MP = 100%, ML = 96%, and B = 100%) consists of three individuals of *Myrsidea incerta* collected from two different host species, Gray-cheeked Thrush (*Cattharus minimus*) and Swainson’s Thrush (*Cattharus ustulatus*). Gray-cheeked and Swainson’s Thrushes are not each other’s closest relatives (Figure 4). Uncorrected sequence divergence between *M. incerta* differs by an average of 0.55%. Clade 2 (Figure 3: MP = 100%, ML = 98%, and B = 100%) is also of a single species, *Myrsidea pricei*, except these two individuals are from the same host species, the Hermit Thrush (*Cattharus guttatus*). The uncorrected sequence divergence between these two individuals is 0.69%.

Clades 1 and 2 from *Cattharus* thrushes are monophyletic. Clade A (Figure 2) includes all lice from *Cattharus* hosts, however, it also includes *Brueelia* from a number of non-*Cattharus* hosts encompassing different sizes, biogeographies, and habitats. For example, the *Brueelia* from the C. fuscator, a tropical resident, is genetically indistinct (uncorrected sequence divergence differs by 0%) from the *Sturnidocus* species from the Wood Thrush (clade 4). This clade is sister to clade 5 (Figure 2: MP, ML, and B = 100%), which includes 2 individual *B. laticeps* from the Black-billed Mountain-toucan (*Andigena nigrirostris*) and Emerald Toucanet (*Aulacorhynchus prasinus*). Although there is strong support for clade 5, there is no support for this clade being sister to clade 4. Neither is there strong support for the placement of the *Brueelia* from the Mountain Barbet (*Megalaima monticola*) as sister to clades 4 and 5.

Clade 8 (Figure 2) consists of *Brueelia* from small Neotropical-nearctic migrants and White Woodpecker (*Melanerpes candidus*). These relationships are similar to those shown in Figure 1. However, *Brueelia* of the House Finch (*Carpodacus mexicanus*) and the House Wren (*Troglodytes aedon*) have been added. *Brueelia anamariae*, from the House Wren, is well supported (MP = 94%, ML = 93%, and B = 99%) as sister to the rest of clade 7, and the uncorrected sequence divergence differs by an average of 3.75%. It is interesting to note that lice from the larger of these birds comprise clade 6, whereas the *Brueelia* from smaller-bodied birds comprise clade 7. The majority of the hosts in this clade are Neotropical-Nearctic migrants. However, a *Brueelia* from a Neotropical resident, the White Woodpecker, is basal to the rest of the group and this placement is fairly well supported (MP = 72%, ML = 94%, and B = 100%). Most of the hosts in this clade have similar habitat preferences and distributions, except for the White Woodpecker.
Figure 1: Molecular phylogeny of the genus Brueelia based on 385 bp of CO1, 483 bp of 12s and 347 bp of EF1α. Maximum likelihood values are above the node (<50% support of 1000 bootstrap replicates), maximum parsimony values are beside them (<50% 1000 bootstrap replicate support), and Bayesian posterior probabilities are below the node (consensus of 5,000,000 samples trees < 0.90). Bold taxa are parasites from Catharus hosts.
Figure 2: Molecular phylogeny of the genus Brueelia based on 385 bp of COI and 347 bp of EF1α. Maximum likelihood values are above the node ([less than] 50% support of 1000 bootstrap replicates), maximum parsimony values are beside them ([less than] 50% 1000 bootstrap replicate support), and Bayesian posterior probabilities are below the node (consensus of 5,000,000 samples [less than] 0.90). The hash marks represent a shortening of the Struthiolipeurus nandu branch. Bold taxa are parasites from Catharus hosts.
Phylogenetic relationships within both louse groups are not congruent with the host thrush tree (Figure 4). If the trees were congruent, I would expect monophyletic groups of lice from Catharus thrushes, and I would expect the branching events of the parasite tree to mirror the branching events of the host tree. Instead, Brueelia from migratory Catharus thrushes form a genetically distinct clade, whereas Sturnidoecus from the tropical Slaty-backed Nightingale-thrush is indistinct from the sister group of Catharus, the Wood Thrush. Myrsidea from migratory Catharus form a number of distinct species; Myrsidea incerta and Myrsidea pricei have an average uncorrected sequence divergence of 6.86%. However, Myrsidea incerta is found on two distantly related Catharus thrushes. In the Myrsidea tree, lice from the Wood Thrush form a distinctly separate clade, but this clade (4; Figure 3), is not closely related to any of the lice from Catharus thrushes.

Geographic Analyses

Using the Maddison and Slatkin (Maddison and Maddison, 1992) test, I found that host biogeography mapped onto the louse topologies was significantly different than expected by random chance (Brueelia P<0.001, Myrsidea P<0.000). Therefore, biogeographic region has significant phylogenetic signal when mapped onto the Brueelia and Myrsidea phylogenies.

Discussion

Cospication

If Brueelia and Myrsidea were cospicating with their Catharus thrush hosts, I would expect to see monophyletic groups of Brueelia and Myrsidea from Catharus and the parasite tree’s branching events should mirror those of the host. However there is no genetic differentiation among Brueelia from Catharus hosts. The lice from migratory Catharus species all come out in an undifferentiated clade, which may suggest ongoing gene flow which causes the phenomenon of failure to speciate in parasites (Banks et al., 2006; Johnson, Williams, et al., 2002). Ischnoceran lice, in particular Brueelia, are able to attach to hippoboscid flies and hitch a ride to a new host (Kierans, 1975). This mode of dispersal may allow a single Brueelia species to move freely among individuals of all of the migratory Catharus species. Phoresia may also be the mechanism by which the tropical resident C. fuscator and migrant Wood Thrush share identical Sturnidoecus. Sturnidoecus is also well known for its phoretic relationship with hippoboscid flies (Kierans 1975). In this case, a North American Neotropical migrant might be picking up its Sturnidoecus louse from a tropical resident host. This is the first definitive demonstration of such a pattern for lice.

Myrsidea are unable to phores on hippoboscid flies (Kierans, 1975). For the most part, Myrsidea differs from Brueelia in that distinct Myrsidea species inhabit the Catharus thrushes. However, these species do not match the phylogenetic history of Catharus thrushes. For example, Swainson’s and Gray-cheeked thrushes, although not each other’s closest relative (Winker and Pruett, 2006), share the same species of louse, M. incerta. These results suggest that M. incerta has failed to speciate on Swainson’s and Gray-cheeked thrushes due to ongoing dispersal/gene flow between hosts. Swainson’s and Gray-cheeked thrushes have overlapping wintering and breeding ranges, so dispersal between these hosts is possible. However, the mechanism by which they do this is unknown.

Neither is it known how the host-switch occurred between the Myrsidea from Catharus thrushes and the Ovenbird. The Myrsidea from Ovenbird comes out in the middle of the two Myrsidea species from Catharus thrushes. These hosts share similar habitat preferences and geographic distributions and therefore these hosts could potentially come into physical contact. The Myrsidea tree had longer branch lengths, which likely indicates less frequent host-switching. Since Myrsidea are unable to attach to hippoboscid flies, dispersal between species is less frequent.

Biogeography

Varying levels of host switching and gene flow, not cospication, may account for the patterns shown on the Brueelia and Myrsidea trees. Both trees show significant phylogenetic signal when biogeographic regions are mapped onto the louse phylogeny. There is some overlap in both the breeding range and the wintering range of the Neotropical migrant Catharus clade. This overlap may create enough opportunities for host-switching and gene flow to result in a single louse species infesting all of these hosts. The same is true for the sparrow and warbler lice clades (clades 6 and 7 in Figure 2) in the Brueelia tree and the Asian clade (clade 2 in Figure 2) that comes out between the two Catharus clades. However, if biogeography were the sole reason for the speciation patterns, the lice from Neotropical warblers and sparrows should be more closely related to lice from Catharus, and the Asian clade should not come out between the two Catharus clades. The two Mimidae species (Gray Catbird and Brown Thrasher) that share similar breeding and wintering ranges should also share a louse.

It is possible that the Wood Thrush picked up its Sturnidoecus louse when it was on its wintering grounds from the Neotropical residents there. Although other migrant Catharus species also inhabit the same wintering grounds as the Slaty-backed Nightingale-thrush. Why would the Wood Thrush pick up a tropical louse, while the other Catharus thrushes don’t? It is possible that the Slaty-backed Nightingale-thrush and the Wood Thrush are close in size, whereas the other migratory Catharus thrushes are smaller, perhaps the Sturnidoecus louse is unable to hide from the preening bill on the migratory Catharus thrushes.

Biogeography explains the majority of the relationships in Myrsidea. All of the Myrsidea from Neotropical migrants sampled, except for the lice from the Wood Thrush, form a monophyletic clade. Also, the rest of the clades tend to exhibit a biogeographic pattern as well. This strong biogeographic signal suggests a more extensive taxon sampling is necessary in order to resolve these lice phylogenies.

Habitat

Louse speciation may be limited to hosts that occupy the same biogeographic regions and also use the same type of habitat. If two birds are in the same region but one is high up in the canopy of the forest and the other is in the understory, there may be less chance for lice to move from one host to another. Of the Brueelia from Neotropical migrants, the Catharus are more likely to be found in dense forest understory whereas a number of the sparrow migrants prefer grassy, open areas. This
Figure 3: Molecular phylogeny of the genus *Myrsidae* based on 379 bp of CO1 and 347 bp of EF1α. Maximum likelihood values are above the node (<50% support of 1000 bootstrap replicates), maximum parsimony values are beside the maximum likelihood values (<50% 1000 bootstrap replicate support), and Bayesian posterior probabilities are at the below the node (consensus of 5,000,000 samples trees < 0.90). Bold taxa are lice from *Catharus* hosts.
Figure 4: Phylogeny of the *Catharus* hosts from Winker and Pruett 2006, based on cytochrome *b* and ND2 genes and a β-fibrinogen intron. The bold represents Neotropical migrants.
may explain why the lice from these two groups are only distantly related. Habitat may also explain the speciation pattern of the Myrsidea from Ovenbird. In the Myrsidea tree, the louse from Ovenbird is nested between the Catharus clades. However, this result might be confounded by the fact that there are no lice from sparrow species in the Myrsidea tree.

Habitat does not explain everything though, the Brueelia from the Ovenbird prefers the same type of habitat that the Brueelia from thrushes do and yet its louse is closely related to the sparrow lice, not the thrush lice. Considering that Brueelia are more easily transferred between hosts, it would suggest that Brueelia would match their host’s habitat more closely than the less easily transferred Myrsidea would. It is possible that the Brueelia are being transferred to more hosts but they are unable to survive on these novel hosts whereas the Myrsidea may be transferred less frequently but are more able to survive when they are transferred.

**Host size**

Biogeography and habitat may influence what hosts lice are able to get to, but one limiting factor of a successful host transfer may be host size. Lice may be able to transfer to a number of different hosts but are unable to hide from the host’s defenses if the barbs of the new host are too big or small. Ultimately the determining factor of a successful host switch and therefore louse speciation may be host size.

**Brueelia Paraphyly?**

In the maximum likelihood and Bayesian analyses, the outgroups were coming out in the middle of the tree, sister to B. sp off of the Bar-bellied Cuckoo-shrike. I ran a neighbor-joining tree analysis and the outgroups did come out as an ingroup which supports long-branch length attraction as the explanation for why the outgroups get pulled in, because B. sp off of the Bar-bellied Cuckoo-shrike has an especially long branch length. This is the Felsenstein concept. Over a long evolutionary time convergence tends to happen and with the long branch lengths, this can produce false affinity between long branches (Felsenstein, 1985). This concept may explain why the outgroups were appearing inside the ingroup.

Also, the model we used may not be complicated enough. Lice are AT rich (Simon et al., 1994) and we used the GTR model that assumes all changes are reversible with equal probabilities. It assumes that A to G and G to A are equally likely and occur at the same rate. When actually G to A is likely more frequent. Another explanation for the outgroups coming in is that Brueelia may not be monophyletic. It is possible that the group is paraphyletic and those outgroups belong there, however, the neighbor-joining analysis suggests that long-branch length attraction is the reason for the outgroups being pulled in.

The placement of the Sturnioidea clade may also suggest that Brueelia is paraphyletic. Sturnioidea comes out deep inside the Brueelia tree, as sister to B. laticeps from Anigena nigrorostris and Aulacorynchus prasinus (clades 4 and 5, Fig. 2). However, this and unpublished data of Kevin P. Johnson’s suggests a reclassification of Sturnioidea may be necessary, and that Sturnioidea should be considered a member of the genus Brueelia.

**Conclusion**

Neither Brueelia nor Myrsidea appear to have cospeciated with their Catharus hosts. For Brueelia, dispersal on Hippoboscid flies has led to a failure to speciate which resulted in a single species infesting all of the migratory Catharus thrushes. Although Myrsidea lice show greater genetic differentiation than do Brueelia, the phylogenetic relationships do not correspond with those of their hosts. In Myrsidea, the hosts seem to act like islands, allowing speciation for the development of species. Host-switching events are likely not as common in Myrsidea as in Brueelia, but they do occasionally happen, which leads to unrelated hosts having closely related lice. It is also possible that the greater ease of transmission in Brueelia does not explain everything. Since Myrsidea interacts with the immune system, it is possible that they have fewer successful host transfers when they come into contact with a novel immune system (Moller and De Lope, 1999; Moller and Rozsa, 2005). Perhaps they are adapted to their host’s immune system and are not generally able to survive a novel host’s immune system. Although it is thought that lice are extremely likely to cospeciate with their hosts, this does not hold true in the case of Sturnioidea in lice seem more likely to correspond with their host’s biogeography, habitat, or potentially, barb size. In the future more attention should be paid to these possible speciation patterns instead of just looking for cospeciation.

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