

The evolutionary transition to coloniality promotes higher blood parasitism in birds

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Abstract

Parasitism has been argued as one of the major costs of breeding sociality in birds. However, there is no clear evidence for an increased parasite pressure associated with the evolutionary transition from solitary to colonial breeding. I used the pairwise comparative method to test whether colonial bird species incur in a greater risk of infection and if they must to face with a greater diversity of blood parasites (Metazoa), by comparing pairs of congeners that included one solitary and one colonial breeding species. The richness, both in terms of number of species and number of genera, as well as the prevalence of blood parasites resulted higher in colonial species than in their solitary breeding sisters, while controlling for differences in research effort and other potentially confounding effects. These results point towards higher transmission rates of blood parasites among colonial hosts. Given the detrimental effects of blood parasites on their host fitness, the higher risk of infection and the exposition to a more diverse parasite fauna may have imposed an important cost associated to the evolution of avian coloniality. This may help to explain why colonial species have larger immune system organs, as well as to explore differences in other host life history traits potentially shaped by blood parasites.

Introduction

Colonial breeding is a form of social reproduction widely extended in birds and other vertebrates, which has attracted a considerable amount of research effort during the last decades (Brown & Brown, 1996; Rolland et al., 1998). In species exploiting food uneconomical to defend, breeding aggregations may have arisen from social advantages such as food-finding enhancement and predator avoidance (see review in Brown & Brown, 1996), or may simply result from individuals looking for mates or good habitat patches (Wagner et al., 2000). Whatever the origin of coloniality, high breeding densities may impose costs to the individuals such as a higher transmission of parasites among them. Parasites are known to detrimentally affect a number of fitness components in birds (e.g. Møller et al., 1990), and

parasite loads may increase the higher the degree of host aggregation in colonial birds (reviewed in Brown & Brown, 1996). For instance, a long-term study has shown that ectoparasitism increases with colony size in cliff swallows (*Hirundo pyrrhina*), affecting host breeding success and first-year survivorship and thus representing a major cost of coloniality for this species (Brown & Brown, 1996).

Most evidence for parasitism being a cost of coloniality comes from intraspecific studies where host breeding aggregations varied in size (Brown & Brown, 1996). However, very few interspecific studies testing the prediction of higher parasite loads in coloniality than in solitary nesting species are available. Rózsa et al. (1996) found that the colonial breeding rook (*Corvus frugilegus*) has higher prevalence and species-richness of avian lice (Insecta: Phthiraptera) than the territorial hooded crow (*Corvus corax*), results which gained support when including 12 other bird species (Rékási et al., 1997). On the other hand, Gregory et al. (1991) did not find a relationship

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between richness of helminths (Platyhelminthes) and avian coloniality, and Poulin (1991) found no differences in louse fly (Diptera: Mippoboscidae) abundance between group-living and solitary passerines, whereas feather mite (Acarina: Proctophylodidae) prevalence was significantly greater on group-living ones. The former result, however, was later related to winter sociality but not to breeding coloniality (Figuerola, 2000). Therefore, the few available interspecific studies seem to offer little, or even controversial, support for parasitism arising as a cost associated to the evolution of coloniality in birds.

The relationships found between parasite loads and host breeding sociality may depend on the host-parasite systems studied, these relationships being largely shaped by the particular life histories of parasites and their strategies of transmission. Coloniality might promote the spread of parasites to hosts in the case of ectoparasites which need the direct body-to-body host contact for transmission, which is facilitated when hosts are aggregated (Rékási *et al.*, 1997). Most grouping, however, might provoke the opposite result in the case of parasites which rely on mobile vectors for transportation if group living provides an encounter-dilution effect (i.e. when the probability of detection of a group by the vector does not proportionally increase with group size, and vectors do not offset the encounter effect by attacking more members of the group; see Mooring & Mart, 1992). In fact, the per capita rate of attacks by blood-sucking flies decreases with group size in some herding animals (see review in Mooring & Mart, 1992). Therefore, comparative studies using parasites with different life strategies are needed to wholly assess whether or not coloniality is associated with a greater risk of parasitism. These kind of studies may help us to identify the potential costs derived from the evolutionary transition from solitary to colonial nesting in birds (Rolland *et al.*, 1998; Beauchamp, 1999), as well as to explain immunocompetence differences between species associated with their breeding sociality (Møller & Erritzøe, 1996; Sheldon & Verhulst, 1996).

In this paper, I tested whether colonial bird species incur in a greater risk of being parasitized and if they must face with a greater diversity of blood parasites (Maematozoa) than species breeding solitarily. A recent phylogenetic analyses showed that in all possible reconstructions of the evolution of avian coloniality, solitary breeding was the ancestral state (Rolland *et al.*, 1998). Therefore, larger parasitizations in colonial than in solitary species would be associated with the evolutionary transition from solitary to colonial breeding. I chose Maemoparasites for this study because they offer clear advantages for conducting comparative studies in birds. The amount of data available on the world avian haematozoa (Bennett *et al.*, 1982; Bishop & Bennett, 1992) allows to work with a high number of host species and thus to perform robust tests (Figuerola & Green, 2001), an advantage not easily offered by other parasite groups. Moreover, since the pioneering work of Mamilton & Zuk (1982), blood parasites have been the

focus of much interest on parasite-mediated sexual selection in birds (Clayton, 1991). Therefore, differences in risk of blood parasitization between solitary and colonial species might have implications on the evolution of certain hosts traits such as sexual dimorphism in showiness. On the other hand, avian blood parasites are transmitted from host to host mainly by highly mobile blood-sucking flies from the order Diptera (Atkinson & van Riper III, 1991). Therefore, blood parasitization might be higher in colonial species in the case that host grouping favours parasite transmission, but no differences between colonial and solitary species, or even greater parasitization rates in solitaries, could be expected in the case that host grouping would promote a reduction of parasite transmission through an encounter-dilution effect of vectors. For testing these hypotheses, I compared pairs of closely related bird species that included one colonial and one solitary breeding species to examine potential differences in parasite richness and parasite prevalence among hosts differing in their breeding sociality. This pairwise comparative method (Burt, 1989) controls for similarities among species because of common ancestry, and thus has long been recognized as a powerful tool for examining an array of ecological hypotheses in a phylogenetic context (e.g. Møller & BirKhead, 1992; Beauchamp, 1999; Cuervo & Møller, 1999; Figuerola, 1999; Figuerola & Green, 2001).

Methods

Data collection

I extensively searched the ornithological literature for selecting pairs of phylogenetically related species differing in their degree of breeding sociality. Since detailed phylogenetic information is not available for all species, I mostly relied on taxonomic information according to Sibley & Monroe (1990, 1992); see Figuerola (1999) and Cuervo & Møller (1999) for the same approach. Breeding sociality in birds ranges between species being strictly solitary to others being strictly colonial, with some species showing both behaviours and others breeding in loose groups (Brown *et al.*, 1990; Rolland *et al.*, 1998). When no pairs of species including one strictly solitary and other strictly colonial were obtained, I selected the most solitary and the most colonial one within each genus, when available, or within each subfamily in other case. The incidence of blood parasites may vary among geographical regions (see comparison in Bennett *et al.*, 1991a), broadly characterized habitats (Figuerola, 1999; Tella *et al.*, 1999), geographical range (Tella *et al.*, 1999), and host species with different migratory behaviours (Figuerola & Green, 2001). Therefore, I selected between all potential pairs of species those in which there are maximum overlaps both in the distribution, habitats, and migratory patterns of sister species. Other host-specific differences in haemoparasite susceptibility (Tella *et al.*, 1999) among sister species should be minimized through

this pairwise comparative method, since it controls automatically for potentially confounding variables because pairs of closely related species generally have a similar anatomy, physiology and ecology because of their common evolutionary past (Møller & BirKhead, 1992; Beauchamp, 1999).

After the construction of the pairs following the above criteria, I consulted the host–parasite catalogues of the world avian haematzoa (Bennett *et al.*, 1982; Bishop & Bennett, 1992), as well as a number of posterior host-specific publications, to record the number of parasite species reported for each bird species. Parasite richness was obtained in two ways: (1) as the total number of parasite species, including only nonspecific identifications when no other species of the same genus were reported for a given host, and (2) as the number of genera reported in each host species (see Figuerola, 1999 for the same approach). The world host–haemoparasite catalogues (Bennett *et al.*, 1982; Bishop & Bennett, 1992) do not report data on prevalence (number of birds infected/number of birds sampled). Prevalence was therefore obtained from several regional surveys and host-specific studies, and thus the resulted sample sizes (i.e. number of sister host pairs) were smaller than for parasite richness. When one host species is distributed across more geographical regions than its sister species, data on blood parasites was recorded only for the region of overlap. An exception to the above restrictions for the selection of species is the pair formed by *Pica nivalis* and the North American population of *Pica pica*, where both populations are close together but actually do not overlap their distributions. However, in this pair of species the parasite prevalence was larger in the solitary than in the colonial congener (see Appendix). Therefore, the exclusion of this pair of sister hosts from analyses just would lead to even stronger parasitization rates in colonial species (see Results), and thus the tests are conservative by keeping it. Finally, I only included pairs of host species for which at least one parasite species was recorded for each one. There are two reasons for this restriction. First, as indicated by Bennett *et al.* (1982), the above mentioned world host–haemoparasite catalogues only report one research source for bird species that are apparently free of blood parasites. Therefore, sampling effort for these species (see below) is clearly underestimated. Second, the lack of blood parasites in some pairs of bird species could be because of factors unrelated to breeding sociality, such as both species being out of the host–parasite coevolutionary process (Bennett, 1992) or both species living in habitats particularly free of haemoparasites (e.g. Little & Earlé, 199F; Figuerola, 1999; Jovani *et al.*, 2001a).

Statistical analyses

Estimations of parasite richness and prevalence are potentially influenced by research effort (Gregory &

Blackburn, 1991; Walther *et al.*, 199F). Therefore, I recorded the number of research sources (i.e. the number of papers looking for blood parasites at each host) and obtained the residuals of the regression of log-number of parasite species (or parasite genera) on log-number of sources as a measure of parasite richness controlled for research effort (Gregory, 1997). The number of research sources for each species was obtained from the world catalogues (Bennett *et al.*, 1982; Bishop & Bennett, 1992) and further publications (see Appendix). This method does not allow to control for potential differences in sample sizes among host studies, which could bias differences in parasite richness, an information that, on the other hand, is not provided by the haemoparasite world catalogues (Bennett *et al.*, 1982; Bishop & Bennett, 1992). Moreover, in the species included in this paper for which prevalence data was available, there was no difference in sample sizes between solitary and colonial species (Mann–Whitney test, $z = -1.06$, $P = 0.29$, $n = 60$). Therefore, my estimates of parasite richness are unlikely to be affected by biases in the number of sampled hosts.

To control for the potential influence of sample size on parasite prevalence (Gregory & Blackburn, 1991), I used two methods. First, statistical analyses were repeated including only species for which at least 10 individuals were sampled, since simulations using randomized sample sizes showed that prevalence values are consistent over 10 individuals sampled (R. Jovani, pers. comm.). Second, within each pair of hosts I subtracted the prevalence of the solitary species from that of the colonial one to calculate an effect size, such that negative and positive values indicate greater prevalence in solitary and colonials, respectively. Each effect size was then corrected for unequal sample sizes following Poulin (1996), so that comparisons with smaller sample sizes were given less weight than those with larger samples. In the case that prevalence would be not influenced by host breeding sociality, these standardized effect sizes should be randomly distributed and not significantly different from zero (Poulin, 1996). Haemoparasite infections usually increase during the breeding season (see Discussion), and so estimates of both prevalence and parasite richness could be potentially affected by seasonal differences in host trapping. Moreover, the great majority of research looking for blood parasites has been conducted during the breeding season, both for colonial and solitary species (Author, unpublished compilation).

Medians and percentiles (2F and 7F%) are reported for variables not normally distributed and medians and SD for those with a normal distribution. Statistical differences within pairs of host species were computed by Wilcoxon matched-pairs tests or by paired-J-tests, depending whether or not the variables were normally distributed. The tests were repeated for a subsample of paired species in which both members are social in winter (i.e. individuals of the species forage and/or roost

forming flocks), to discern between the effects of winter and breeding sociality on blood parasitization rates. All tests were two-tailed.

Results

I found 20 pairs of phylogenetically related species differing in breeding sociality, which met the restrictive criteria of maximum overlap of their range distributions, habitat preferences, and migratory behaviours, for which information on blood parasites is available. These pairs covered seven orders and 18 families of birds. Eighteen pairs were formed by species in the same genus and 12 by species in the same subfamily (see Appendix).

Parasite richness

The number of parasite species per host was lower in solitary (median = 2, quartiles = 1.7–4.2) than in colonial birds (median = 4.7, quartiles = 2–7). Colonials harboured larger number of parasite species in 21 of 20 pairwise comparisons, the contrary occurring only in three comparisons (Wilcoxon matched-pairs signed-rank test, $\zeta = -2.46$, $P = 0.014$). The same pattern was found for the number of parasite genera (solitaries: median = 2.7, quartiles = 1–4; colonials: median = 4, quartiles = 2–7); the number of genera was larger in colonials in 19 of 20 comparisons, whereas the contrary only affected to seven pairs of species ($\zeta = -2.90$, $P = 0.004$). Differences between solitary and colonial nesting host, however, could have been masked by differences in research effort among species. In fact, both the number of parasite species and the number of parasite genera significantly increased with the number of studies published on blood parasites for each host (parasite species: $r = 0.84$, $F_{1,19} = 128.6$, $P < 0.0001$; parasite genera: $r = 0.76$, $F_{1,19} = 79.2$, $P < 0.0001$; see Fig. 1). Accordingly, I used the residuals of these regressions as a measure of parasite richness corrected for sampling effort. This measure of parasite richness resulted to be much higher in colonial than in solitary species (Fig. 2). Most pairs of taxa (26 of 20) showed an increase in richness of parasite species associated with the transition to coloniality (Paired J-test, $J = -4.77$, $d.f. = 29$, $P < 0.0001$), as it was the case for richness of parasite genera ($J = -4.27$, $d.f. = 29$, $P < 0.0001$). The same trend was significant for those pairs of species ($n = 17$) in which both species are social in winter (species richness larger in colonials in 16 comparisons, $J = -2.86$, $d.f. = 16$, $P = 0.011$; genera richness larger in colonials in 12 comparisons: $J = -2.42$, $d.f. = 16$, $P = 0.027$).

Parasite prevalence

Data on haemoparasite prevalence was obtained for 27 out of the 20 pairs of phylogenetically related avian species (Appendix). Overall, the percentage of individu-

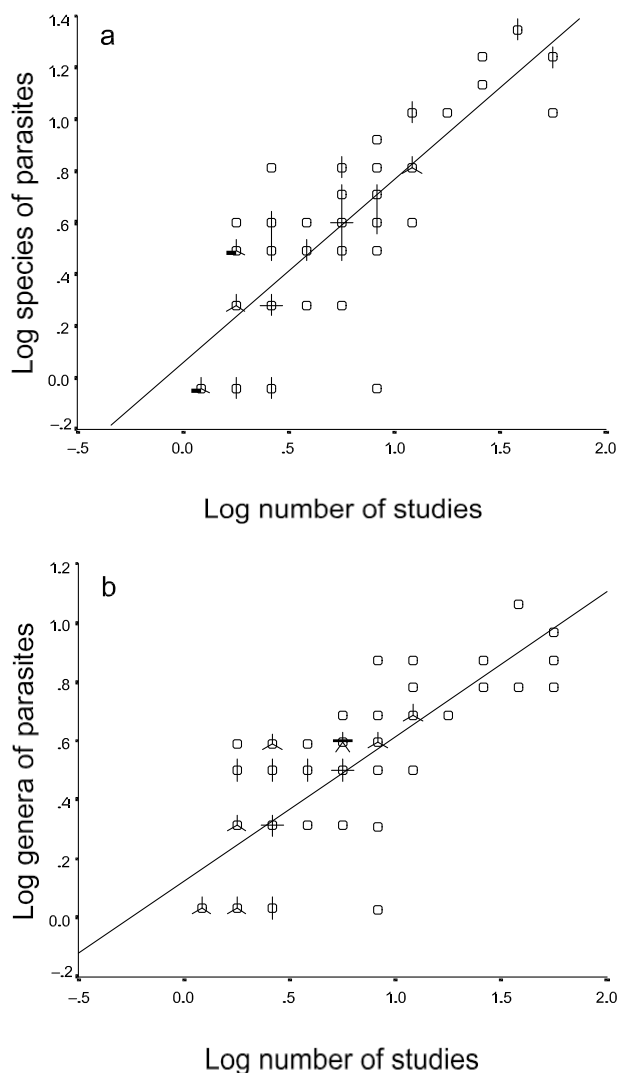


Fig. 1 Relationships between the number of studies on blood parasites published about a host bird species and (a) the number of species of blood parasites and (b) the number of genera of blood parasites reported to infect that host.

als infected by blood parasites was significantly lower in solitary species (median = 20%, quartiles: 7.7 and 46%) than in colonial ones (median = 21.7%, quartiles: 11.9 and 68.7%). Prevalence was larger in colonials in 18 of 27 pairwise comparisons (Wilcoxon matched-pairs signed-rank test, $\zeta = -2.14$, $P = 0.022$). Once again, unequal sampling effort among species could have influenced the above results. Moreover, differences between solitary and colonial species were also significant when considering those pairs of species for which at least 16 individuals from each species were sampled (solitaries: median prevalence = 18.42%, quartiles: 6 and 48.7%; colonials: median prevalence: 24.7%, quartiles: 19.2 and 68.7%; see Fig. 2). Most pairs of taxa (11 of 14) showed

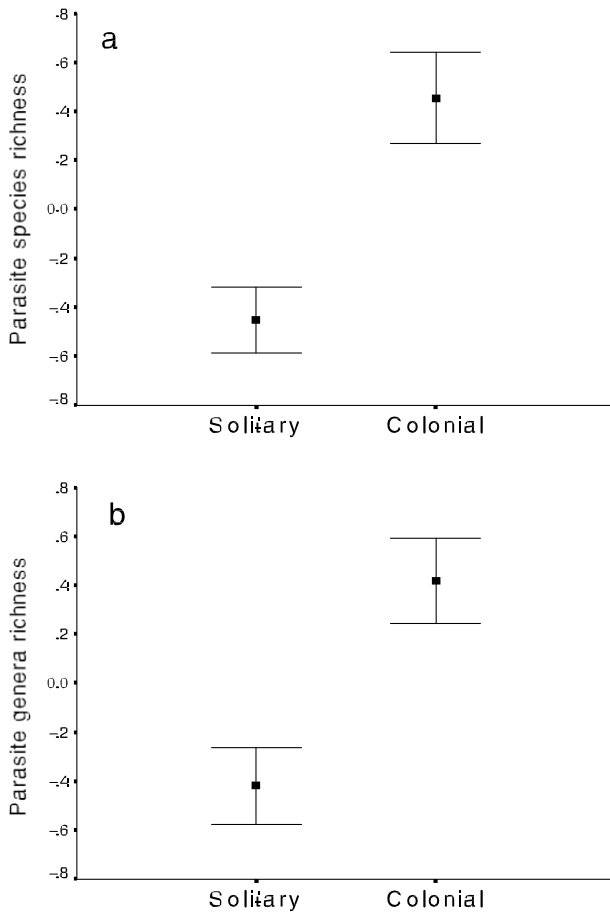


Fig. 2 Differences in (A) the number of species of blood parasites and (B) the number of genera of blood parasites, both corrected for research effort, between 20 pairs of phylogenetically related bird species differing in their breeding sociality.

an increase in haemoparasite prevalence associated to coloniality ($\zeta = -2.10$, $P = 0.02F$). Standardized effect sizes (i.e. the difference between the prevalence in the colonial species and that in the solitary one within each pair, corrected for sample sizes) were positive and significantly different from zero, both considering the 2F pairs of species (median difference: 11.5%, $\zeta = -2.11$, $P = 0.02F$) and only those 14 pairs with sample sizes of at least 1F individuals per species (median difference: 14%, $\zeta = -2.10$, $P = 0.02F$). The same significant result was found for all pairs of sister species which are social in winter ($\zeta = -2.17$, $P = 0.020$, $n = 16$ pairs). This last result, however, did not reach statistical significance ($\zeta = -1.28$, $P = 0.16$) when considering only species with sample sizes of at least 1F individuals per species, probably because of the resulting small sample size ($n = 10$ pairs), although the trend was the same (the standardized effect size was positive in seven out of 10 pairwise comparisons).

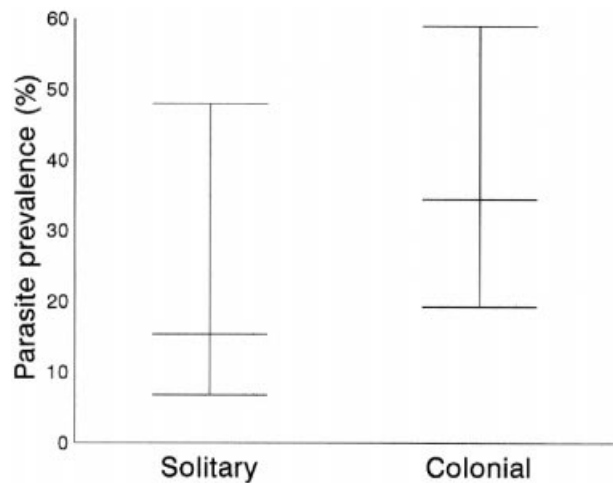


Fig. 2 Prevalence of blood parasites (median, 2F and 7F% quartiles) in 14 pairs of phylogenetically related bird species differing in their breeding sociality. At least 1F individuals were sampled from each host species.

Discussion

Comparisons between pairs of closely related species have been recommended to assess whether the evolutionary transition to coloniality has caused an increase in parasite infestation (Beauchamp, 1999). This study shows that the richness of blood parasites, both in terms of number of species and number of genera, was higher in colonial species than in their solitary breeding sisters, a result which was much stronger when differences in research effort among host species were controlled for. Moreover, the prevalence of blood parasites was also higher in colonial than in solitary species, despite that it is influenced by a number of intrinsic and extrinsic factors such as sex, age, season and geographical related variations (Weatherhead & Bennett, 1991, 1992; Merilä et al., 199F; Allander & Sundberg, 1997; Sol et al., 2000), which may induce sampling biases and thus mask the actual differences. Contrarily to the case of feather mites, in which prevalence was unrelated to coloniality when controlling for winter sociality (Figuerola, 2000), in the case of blood parasites coloniality was still associated with increased parasite richness and prevalence when considering only pairs of species in which both members are social in winter.

Differences in infestation trends between feather mites and blood parasites are likely to be related to their different modes of transmission. Feather mites are benign ectosymbionts transmitted by host-to-host body contact (Blanco et al. 2001; Jovani et al., 2001b), and the number of congeners that directly contact with an individual may be higher in winter flocks and communal roosts than in the nests, as transmission at the nests would be more

constrained to occur within family members (Blanco *et al.*, 1997, 2001; Jovani & Blanco, 2000; Blanco & Frias, 2001). Blood parasites, however, need of blood-sucking arthropods for their transmission among avian hosts. In the case of haemosporidians (Haemaphysalis, Leucocytozoon and Plasmodium, the most common haematozoa in birds), once infective sporozoites are inoculated to a suitable host by the vector, they undergo multiple cycles of asexual and sexual reproduction, multiplying quickly in the host and producing gametocytes which also are transmitted from one host to another by the same vectors (Atkinson & van Riper III, 1991). Infected birds later exhibit chronic or latent infections which may persist for years, when parasitemia is reduced to low levels in blood, but relapses occur each breeding season (Atkinson & van Riper III, 1991; Allander & Sundberg, 1997). Therefore, parasites circulating in blood reach their maximum abundance during the breeding season, coinciding also with a higher abundance of vectors such as flies and mosquitoes (Bennett & Fallis, 1960; Super & van Riper III, 1997), and thus transmission among hosts may be higher in breeding colonies than in winter flocks.

Coloniality seems to not provide protection from blood parasites through the potential encounter-dilution effect (Mooring & Mart, 1992), which would produce lower per capita attacks by flying haematophagous vectors, as parasite prevalence was higher in colonial than in solitary species. To my knowledge, Davies *et al.* (1991) provided the only related results when studying differences in prevalence of Plasmodium among Amazonian species of primates. These authors found that Plasmodium prevalence increased with the average annual sleeping group size of the species, suggesting that host grouping enhances odour production and thus attracts a greater number of mosquito vectors than expected by chance. Most odour, rather than visual cues, seems to be also important for the attraction of haemoparasite vectors in birds (Yezerinac & Weatherhead, 1997). As different blood parasite species are usually transmitted by different species of vectors (Atkinson & van Riper III, 1991), the aggregation of conspecific hosts during the breeding season could increase not only the attraction of large vector numbers but also its diversity, thus also explaining the relationship between avian breeding sociality and haemoparasite richness. Nonetheless, larger blood parasitizations in colonial birds could also be explained in the absence of a higher attraction of vectors and even in the case of acting an encounter-dilution effect. Assuming that flying vectors are randomly distributed with respect to host aggregation, the probability of a host being infected would be initially equal or even smaller for colonial than for solitary birds. In further steps of time, however, the likelihood of parasite transmission would be higher among host congeners breeding colonially, because of their close proximity, than among solitaries. This is because a flying vector (or haematophagous

ectoparasite, see, e.g. Sol *et al.*, 2000) acquiring parasite gametocytes by biting an infected colonial host would have a greater chance before to die of biting – and thus infecting – another host of the same species than in the case of territorial, isolated host breeders. Therefore, this scenario could also explain the larger prevalence found in colonial hosts.

The best evidence so far for larger parasite infections in colonial than in solitary bird species was provided by Rékási *et al.* (1997). Moreover, although these authors found larger lice prevalences in colonial than in solitary birds, they concluded that colonial hosts do not pay a higher price for being social because lice loads per individual did not differ between solitaries and colonials (i.e. lice were not more abundant, but more equally distributed among colonial hosts). Nonetheless, several studies from the same host species were included as independent data points and the conducted statistical analyses did not control for potentially confounding phylogenetic effects (Rékási *et al.*, 1997), facts that might have affected their results and interpretation. In any case, and contrarily to avian lice (Rékási *et al.*, 1997), a redistribution of haemoparasite numbers among colonial individuals is not plausible, because once a bird is infected the parasite undergoes reproductive cycles independently of the fate of neighbouring hosts (Atkinson & van Riper III, 1991; Sol *et al.*, 2000), so haemoparasite numbers by infected host are reasonably expected to be equal among colonial and solitary birds.

More I have shown that the evolutionary transition from solitary to colonial nesting in birds (Rolland *et al.*, 1998) is associated with a greater risk of acquiring haemoparasites. Although information on pathogenicity of blood parasites was mainly restricted until recently to domesticated birds (Atkinson & van Riper III, 1991; Bennett *et al.*, 1992), increasing observational and experimental studies in the field are showing a variety of detrimental effects on their hosts (ValKiünas, 1992; Merino *et al.*, 2000), including a higher risk of mortality both within (Richner *et al.*, 1997; Dawson & Bortolotti, 2000; Mora *et al.*, 2001) and between host species (Sorci & Møller, 1997). The larger prevalence in colonial species not only means that a higher number of individuals are infected, but may also increase the number of infectious clones per host (Read *et al.*, 1997), thus increasing the virulence of monospecific infections (Taylor *et al.*, 1998). Moreover, given that the degree of pathogenicity varies among blood parasite species (Atkinson & van Riper III, 1991), the larger diversity of haemoparasite fauna found in colonial birds adds a cost to the larger prevalence in terms of multiple parasite infections. Multiple haemoparasite infections not only increase the risk of holding the more virulent species, but also the potential impact on host fitness through additive or synergic effects of combined species (Atkinson & van Riper III, 1991). Blood parasites may have thus imposed an important ecological

cost derived from the evolutionary transition from solitary to colonial breeding.

The larger blood parasitization pressure in colonial birds could have selected for an improved immune system in this group of birds. Parasite virulence is thought to evolve in response to the mode of transmission. Horizontal transmission among unrelated individuals not involved in common reproductive activities, as it occurs in haemoparasites, is proposed to select for increased virulence, whereas vertical transmission from parents to offspring selects for reduced virulence (Ewald, 1982). Møller & Erritzøe (1996) hypothesized that, because coloniality should increase the horizontal transmission of parasites, colonial species should have developed larger immune organs to fight against parasites than their congeneric solitary ones. Accordingly, these authors showed through pairwise comparisons that two organs involved in immune defence were consistently larger in colonials. More recently, Møller et al. (2001) have shown through a comparative study of 11 swallows and martins that direct measures of T- and B-cell immune response increased with breeding sociality of the species, and that these immune responses were related to the pressure exerted by ectoparasites. Given that blood parasites are mainly transmitted horizontally, they may have also contributed to the evolution of immune defence of hosts in relation to their breeding sociality, a possibility that would require further research to be confirmed. Attending to these and other potential implications (Beauchamp, 1999), colonial breeding results a behaviour which must be considered both in studies dealing with the ecology of haemoparasites and the evolution of several parasite-related life history traits of their hosts.

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Appendix Richness of parasite Maematzoa and prevalence of infection in pairs of bird species differing in their breeding sociality. P: prevalence in percentage (sample size in brackets); S: number of parasite species; G: number of parasite genera; R: number of references; W: winter sociality.

Order and Family	Solitary species	P	S	G	R	Colonial species	P	S	G	R	W	Sources ^b
O: Ciconiiformes												
F: Ardeidae	<i>Egretta novaehollandiae</i> (S, C?) ^a		2	2	0	<i>Egretta intermedia</i> (C)		3	3	3	Y	1, 2
F: Ciconiidae	<i>Jabiru mysteryia</i> (S)	0 (3)	1	1	2	<i>Mysteria amerisana</i> (C)	11.1 (9)	3	3	6	Y	1, 2, 3
	<i>Ephippiorhynchus senegalensis</i> (S)	0 (2)	3	2	8	<i>Leptotilos srumeniferus</i> (C)	100 (10)	0	3	10	N	1, 2, Q
F: Threskiornithidae	<i>Bostrychia hagedash</i> (S)	20 (U)	2	2	6	<i>Threskiornis aethiopicus</i> (C)	26.7 (1U)	1	1	8	Y	1, 2, Q
	<i>Mesembrinibis sayennensis</i> (S)	10.2 (11)	2	2	3	<i>Theristisus saudatus</i> (C,S?)	0 (Q)	2	2	3	N	1, 2, 3
F: Accipitridae	<i>Torgos tracheliotus</i> (S)	31.2 (6Q)	Q	Q	6	<i>Gyps africanus</i> (C)	0 (U)	9	7	7	N	1, 2, Q, U; F:
Falconidae	<i>Falco subbuteo</i> (S)		10	U	20	<i>Falco vespertinus</i> (C)		Q	3	U	N	1, 2, 6, 7
O: Anseriformes												
F: Anatidae	<i>Anser albifrons</i> (S,LC)	12.U (8)	2	2	3	<i>Anser saerulesens</i> (C)	3.U (U77)	6	Q	U	Y	1, 2, 8
	<i>Melanitta nigra</i> (S)	2U (Q)	Q	Q	6	<i>Melanitta persipillata</i> (LC, S)	60 (U)	2	2	2	Y	1, 2, 8
O: Columbiformes												
F: Columbidae	<i>Zenaidura macroura</i> (S)	68.2 (2U18)	12	6	UU	<i>Zenaidura asiatica</i> (C, S?)	87.U (72)	7	U	10	Y	1, 2, 8-10
	<i>Ducula sarala</i> (S)	20 (U)	1	1	1	<i>Ducula bisolor</i> (C)	100 (1)	3	3	3	Y	1, 2, 11
O: Psittaciformes												
F: Psittacidae	<i>Tanygnathus lusionensis</i> (S)	100 (7)	2	2	3	<i>Prioniturus dissurus</i> (C)	12.U (8)	Q	Q	2	?	1, 2, 11
O: Apodiformes												
F: Apodidae	<i>Apus saffer</i> (S, LC)	1.9 (U3)	1	1	3	<i>Apus affinis</i> (C)	7.7 (17)	6	3	U	Y	1, 2, Q, U
O: Coraciiformes												
F: Meropidae	<i>Merops leschenaulti</i> (S, C)	6.2 (32)	1	1	3	<i>Merops viridis</i> (C)	31.7 (126)	3	2	2	Y	1, 2, 11
F: Alcedidae	<i>Alcedo cristata</i> (S)	7.6 (66)	3	3	Q	<i>Seryle rudis</i> (LC)	2Q.3 (37)	U	3	8	N	1, 2, Q
O: Passeriformes												
F: Hirundinidae	<i>Hirundo susullata</i> (S)	7.9 (88)	Q	Q	3	<i>Hirundo spilodera</i> (C)	Q7.U (278)	Q	Q	Q	Y	1, 2, Q, U
	<i>Riparia sinista</i> (S)	33.3 (6)	2	1	2	<i>Riparia paludisola</i> (C)	11.3 (133)	Q	Q	3	N	1, 2, Q, U
F: Turdidae	<i>Turdus philomelos</i> (S)	Q2 (162)	17	7	U0	<i>Turdus pilaris</i> (C,S)	U3.U (71)	11	6	11	Y	1, 2, 6
F: Meliphagidae	<i>Plectorhyncha lanceolata</i> (S)		1	1	2	<i>Manorina melanosephala</i> (C)		U	Q	8	N	1, 2, 11
F: Passeridae	<i>Estrilda erythronotos</i> (S)	33.3 (6)	2	2	2	<i>Estrilda astrild</i> (S)	U3.8 (26)	11	7	11	Y	1, 2, Q, U
	<i>Euplestes albonotatus</i> (S)	20 (2U)	3	3	6	<i>Euplestes afer</i> (C)	22.2 (QU)	6	U	7	?	1, 2, Q, U
	<i>Vidua shalybeata</i> (S)	2.9 (171)	Q	Q	7	<i>Quelea quelea</i> (C)	2 (1U0)	7	U	12	Y	1, 2, Q, U
	<i>Ploceus luteolus</i> (S)	7 (128)	U	Q	6	<i>Ploceus susullatus</i> (C)	37.3 (370)	1Q	7	30	Y	1, 2, Q, U
F: Sturnidae	<i>Aplonis santoroides</i> (S)		1	1	1	<i>Aplonis metallisa</i> (C)		3	3	2	?	1, 2, 11
	<i>Spreo superbus</i> (S)	12.9 (31)	6	U	12	<i>Sreptophora sinerea</i> (C)	7Q.Q (Q3)	6	Q	3	N	1, 2, Q, U
F: Icteridae	<i>Sasisus leusoramphus</i> (S)		1	1	1	<i>Sasisus sela</i> (C)		3	3	Q	N	1, 2,
	<i>Molothrus ater</i> (S)	17.9 (1613)	16	6	2U	<i>Agelaius phoeniceus</i> (C)	21.1 (2077)	20	6	33	Y	1, 2, 8, 9, 12, 13
F: Corvidae	<i>Sorvus sorone</i> (S)	88.U (10Q)	17	10	UQ	<i>Sorvus frugilegus</i> (C)	1Q (901)	21	11	39	Y	1, 2, 6
	<i>Pisa pisa</i> (S)	81.Q (307)	Q	Q	8	<i>Pisa nuttalli</i> (C)	77.1 (3U3)	U	U	6	Y	1, 2, 8
	<i>Syanositta stelleri</i> (S)	UQ.U (33)	Q	Q	6	<i>Gymnorhinus syanocephalus</i> (C)	71.Q (7)	3	3	2	N	1, 2, 8

^a S = solitary, C = colonial, LC = loosely colonial. When a species exhibits two breeding strategies, the first cited one is the most commonly reported in the literature.

^b I, Bennett et al. (1982); 2, Bishop & Bennett (1992); 2, White et al. (1978); 4, Bennett et al. (1992); F, Earlé et al. (1991); 6, Peirce (1981); 7, Tella et al. (1999); 8, Greiner et al. (197F); 9, Bennett et al. (1991b); 10, Mu11man & Cali (1982); 11, McClure et al. (1978); 12, Weatherhead & Bennett (1991); 12, Weatherhead & Bennett (1992).