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Bird communities and wind farms: a phylogenetic and morphological approach

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Abstract The undeniable environmental benefits of wind energy are undermined by the negative effects of wind farms on bird populations through mortality by collision with the energy-generating structures. Studies have documented morphological, ecological, and behavioral traits associated with vulnerability to wind turbines. However, practically all studies have concentrated on the effects on particular populations, and community-level analyses are lacking. Here we assess the susceptibility of species on the basis of their morphology, and examine the effect of selective mortality on the topology and dispersion of phylogenies, and on the structure and volume of the ecological morphospace of bird assemblages. Using an extensive database of bird occurrences and fatalities in a wind farm located in southern Mexico, and performing null models to establish statistical significance, we compared sets of affected and unaffected species in terms of their wing morphology and position in a phylogeny. We found that birds more likely to fly in the risk zone tend to be smaller, with longer wings, and with heavier wing loadings. Within this group,

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species more likely to collide with blades and die are smaller, with short wings, and supporting lighter wing loadings. These patterns determine that the set of species less affected distribute in morphospace leaving noticeable holes (morphologies not represented). Birds flying in the risk zone tend to be related to each other, but species that actually collide with turbines belong to several separate clades. These differential effects on morphology and phylogenetic diversity pose important and complex challenges to the conservation of birds in areas where wind farms are being established.

Introduction

Facing the energy production crisis, the harnessing of wind energy has been regarded by some as one of the great success stories in the use of renewable resources, and today wind farms are well established worldwide (Gross et al. 2003). However, the negative impact of wind facilities on wildlife has also been documented, pointing to pressing conservation challenges (Kuvlesky et al. 2007; Fargione et al. 2012; Martínez-Abraín et al. 2012). The spinning blades of turbines represent not only artificial obstacles for flying animals, but also constitute direct lethal threats to individual birds and bats, due to fatal collisions or to barotrauma caused by sudden and excessive pressure changes (Baerwald and Barclay 2011; Drewitt and Langston 2006; Baerwald et al. 2008). Although long-term studies are still few and not entirely systematic (de Lucas et al. 2008), it is clear that wind farms can have a substantial impact on some populations of bats and birds.

From the published studies on the impact of wind farms on birds, it is clear that this impact varies widely among species, due to differences in behavioral responses (Barrios and Rodríguez 2004), ecological features (Carrete et al. 2012), sensorial perception (Martin 2011), and morphological traits (Janss 2000). While some diverse groups show different levels of risk (e.g., passerine birds, Hüppop et al. 2006), others are clearly more vulnerable (e.g., birds of prey, Barrios and Rodríguez 2004; Ferrer et al. 2012).

Differential mortality caused by human activity among plant or animal groups has been proven to produce changes in the composition and structure of communities, for instance through selective local extinction caused by habitat fragmentation or through defaunation via hunting (Peres 2000; Holbrook and Loiselle 2009). These changes can have severe consequences along trophic levels (Pace et al. 1999) or in the functional diversity of whole ecosystems (Bihn et al. 2010). Selective impact can also produce a decrease in the phylogenetic diversity of taxa, as has been shown for tropical trees in forest edges (Santos et al. 2010). These changes, in turn, could trigger a cascade of indirect effects, because higher phylogenetic diversity is linked to ecosystem stability (Fonseca and Ganade 2001; Cadotte et al. 2012) and a lower probability of biological invasions (Gerhold et al. 2011). Changes in phylogenetic diversity also alters the content of the phylogenetic signal (sensu Blomberg et al. 2003) that species assemblages carry as a consequence of thousands or millions of years of evolution (Faith 1992). This perspective allows the incorporation of the evolutionary and functional traits of species in conservation strategies, as has been suggested recently (Hartmann and André 2013).

If mortality caused by wind farms is in fact selective, it could lead to changes in the bird and bat assemblages by lowering the population levels of the species that are affected the

most. Depending on the identity of the affected species, the phylogeny of the surviving assemblage could show overdispersion or clustering (Webb et al. 2002), in most cases showing also a lowered level of phylogenetic diversity. Similar effects can be documented with measures of morphological structure and diversity (Weiser and Kaspari 2006; Ricklefs 2012) if in fact vulnerability to wind turbines is related to wing morphology, which in turn is directly determined by the ecological and behavioral features of species (Ricklefs and Miles 1994). In this way, selective mortality of birds can produce shifts in the distribution of species within the ecological space defined by morphological traits (i.e., the "ecological morphospace"). This ecological conception about the distribution of species inside axis representing features and the morphological distance has been also considered a proxy for ecological relationships (Ricklefs 2012). Moreover, the synthesis provided by morphospace allows understanding ecological processes which lead the communities and their performance (e.g., species packing, Ricklefs and Travis 1980).

In this paper, we evaluate the potential impact of wind farms on the morphological and phylogenetic structure and diversity of bird assemblages. With data from a site in Mexico's Isthmus of Tehuantepec, we assess the susceptibility of species based on their morphology, and examine the impacts of selective mortality on the topology and dispersion of phylogenies and on the volume and structure of the ecological morphospace. To our knowledge, this is the first analysis of the impact of wind turbines on bird assemblages from a morphological and phylogenetic perspective.

Methods

Study site and field work

The study area is located in the lowlands of the narrowest stretch of land that exists in Mexico between the Pacific Ocean and the Gulf of Mexico, in the biogeographical province called the Tehuantepec Isthmus (Huidobro et al. 2006). The nominal vegetation of the area is tropical forest, but most of the original cover has been removed and replaced with croplands and cattle fields (García-Romero et al. 2005). We carried out this study in the wind farm named La Venta II, located in the vicinity of La Ventosa, in the southern part of the Isthmus of Tehuantepec, municipality of Juchitán, state of Oaxaca (16°34′N, 94°50′W, altitude 74 m above sea level; Villegas-Patraca et al. 2012). This wind farm consists of 98 wind turbines Gamesa G-52, with nominal capacity of 850 kW, each having three 26-m blades attached to a monopole at a height of 44 m above the ground. Units are arranged along four parallel lines, with a separation of 130 m from each other; the distance between lines is 600 m (Villegas-Patraca et al. 2012).

We established a monitoring station within La Venta II in a location that allowed an excellent peripheral vision of incoming birds. We collected data daily during both spring and fall migrations (March–April and September–November, respectively) on 2010 and 2011. We started every sampling day 3 h after dawn and continued observation for 8 h. At every moment, at least two experienced observers recorded all birds encountered in the area using field guides (Howell and Webb 1995; Sibley 2000), 10× magnification binoculars and 32× magnification spotting scopes. With prior knowledge about migration routes and field conditions within the wind farm, we designed the sampling schedule in such a way that fatigue of observers was minimized. Surveyors alternated sampling routes and schedules so they were not assigned to the sites with more challenging conditions in consecutive occasions. By following this protocol, we avoided biases caused by tiredness

of observers. Each record contained the species identity, number of individuals (in case of a flock), and the flight risk category, which could be (a) flight risk, when the bird was flying at a height where the collision with blades is likely (25–75 m), and (b) no risk, when the bird was flying at a different height.

To document collisions, we conducted searches of carcasses along routes perpendicular to the lines of wind turbines (Villegas-Patraca et al. 2012). Every 4 days during 2010 and 2011, five observers separated from each other by 10 m looked for bird remains on the ground. To avoid overlooking dead birds scattered in areas of dense vegetation and poor visibility, special attention was paid during searches in these areas. Carcasses were preserved for laboratory examination and confirmation of species identity. To minimize biases in our sampling procedure due to differential carcass removal by scavengers, we scheduled our searches to be more frequent than the mean time of persistence of carcasses measured in a previous study in the same site (Villegas-Patraca et al. 2012). This design, coupled with the fact that the size of removed carcasses is not correlated with their removal rate (Villegas-Patraca et al. 2012) allowed us to control the effect of scavengers.

Species pool

We defined a pool of bird species with potential geographic distribution in the study area by considering all species potentially occurring in the Isthmus of Tehuantepec, based on the information and maps of Binford (1989) and Howell and Webb (1995), and retaining those that have been observed in habitats similar to the one around the study site. For each species, we compiled the following morphological measurements: body length (m), body mass (kg), wingspan (m), and wing loading (N m^{-2}), calculated as the ratio between weight (body mass × 9.8 m s^{-2}) and the area of wing elements (Tennekes 1996). We obtained measurements directly from museum specimens (four to ten individuals of each species, Colección Nacional de Aves, and Museo de Zoología "Alfonso L. Herrera", both of the National University of Mexico, UNAM), from the literature, and, for a few species, from allometric functions, taking into account the taxonomic membership (Evered 1990; Morgado et al. 1987).

We constructed a phylogeny including all the species in the pool. We used one sequence of the mitochondrial gene COI (Hebert et al. 2003; Alif et al. 2011) for each species from the Gen Bank (NCBI, September–October 2011). Sequences for species that were not represented in the Gen Bank (about 20 %) were replaced with the available sequence of the closest relative, according to previous studies reported in the literature. We made the alignment in Clustal W, an accessory tool of BioEdit 7.0.9.0 and using JModelTest 0.1.1 we found that TPM3uf+I+ G was the best nucleotide substitution model based on Akaike's information criterion (AIC). We performed the phylogenetic tree reconstruction by maximum likelihood in PhyML v 3.0 (Guindon and Gascuel 2003). We were unable to obtain sequences for four of the species or for closely related taxa (*Herpetotheres cachinnans*, *Micrastur semitorquatus*, *Sarcoramphus papa*, and *Trogon violaceus*), so we inserted them manually into the phylogenetic tree with Mesquite 2.74 software based on previous phylogenetic reports (Griffiths et al. 2004; Brightsmith 2005).

Data analysis

Analyses were conducted at four levels defined by a series of nested sets of species: (1) the geographic species pool described above, (2) species actually recorded within La Venta II ("locality set"), (3) species flying in the collision risk zone ("risk set"), and (4) species

with documented fatal collisions ("collided set"). We also examined the complement of the "collided set", that is, those species with no documented collisions (the "survivors set"). We tested the null hypothesis that each set is a random subset of the previous set, developing simple null models, which are tests based on the randomization of the parameter of interest, retaining some of the biological information (Gotelli and Graves 1996; Gotelli and Ulrich 2012). Null models and analyses were performed in R 2.12.1 (R Development Core Team 2010) alongside PICANTE (for measuring phylogenetic structure; Kembel et al. 2010) and VEGAN (for calculating the minimum spanning tree (MST); Oksanen et al. 2011) packages.

In a test examining for differences in morphology and in phylogenetic structure of the "collided set", we took 10,000 samples from the pool of species, with no replacement, of the same number of species as in the "collided set". For each sample, we measured the mean of each morphological trait and its phylogenetic structure using two metrics: (1) mean pairwise distance (Mpd), which reflects general dispersion of species throughout the whole tree, and (2) mean nearest taxon distance (Mntd), which describes the structure closer to the tips, as it measure distances between closely allied species (Webb et al. 2002). We used equiprobable null models, in which each species had the same probability of being selected and weighed models in which the probability of each species being selected was proportional to its relative abundance (frequency of sightings) in the study area. We used the two sampling procedures because available data on the relationship between abundance and probability of collision with turbines is equivocal: even in the same study area, some studies have found no such correlation (de Lucas et al. 2008) or have detected a positive relationship (Carrete et al. 2012).
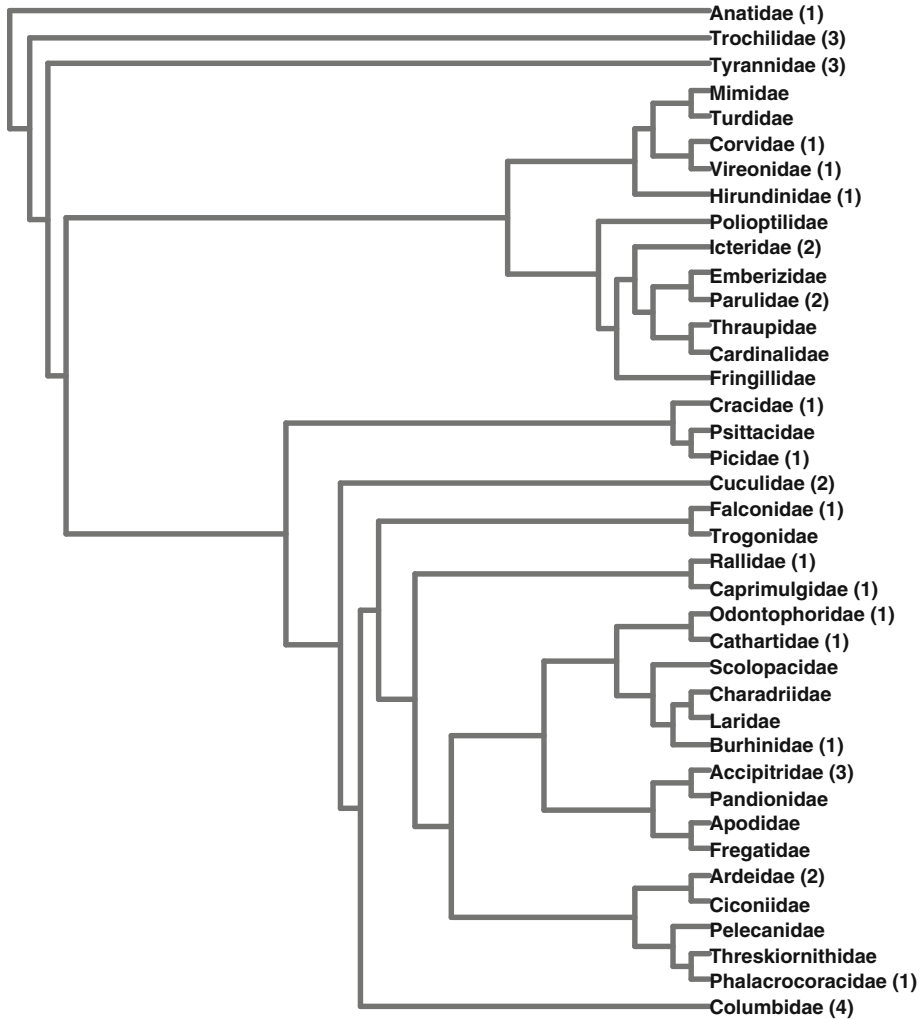
We constructed a morphospace through a principal components analysis (PCA) of the morphological variables and on this space, we measured the length of all the branches of the MST for the different sets of species. In this context, a MST is the set of lines with the minimum length that connects all species; hence, the total length of the MST is a measure of morphological dispersion (Dussert et al. 1987). In the randomization tests described above, we measured the length of the MST in each of the 10,000 simulations and constructed a frequency distribution of such values and compared the empirical value against this distribution, with $\alpha = 0.05$ in two-tailed tests.

We looked for phylogenetic conservatism of morphological traits in each set (scale) with a randomization test designed to test whether a given set of comparative data exhibit a significant tendency for related species to resemble each other (Blomberg et al. 2003). The idea is whether a given tree (topology and branch lengths) better fits a set of tip data as compared with the fit obtained for a random permutation of the data, which in theory should not preserve any phylogenetic signal that may have existed (Blomberg et al. 2003).

Results

The species pool comprised 353 species distributed in 51 families and 19 orders. For the "locality set" we encountered 112 species within the wind farm, and 71 species were seen flying in the risk zone ("risk set"; Table 3). During the searches of carcasses we found 34 species that have suffered fatal collisions ("collided set"), belonging to 21 families and 13 orders (Fig. 1).
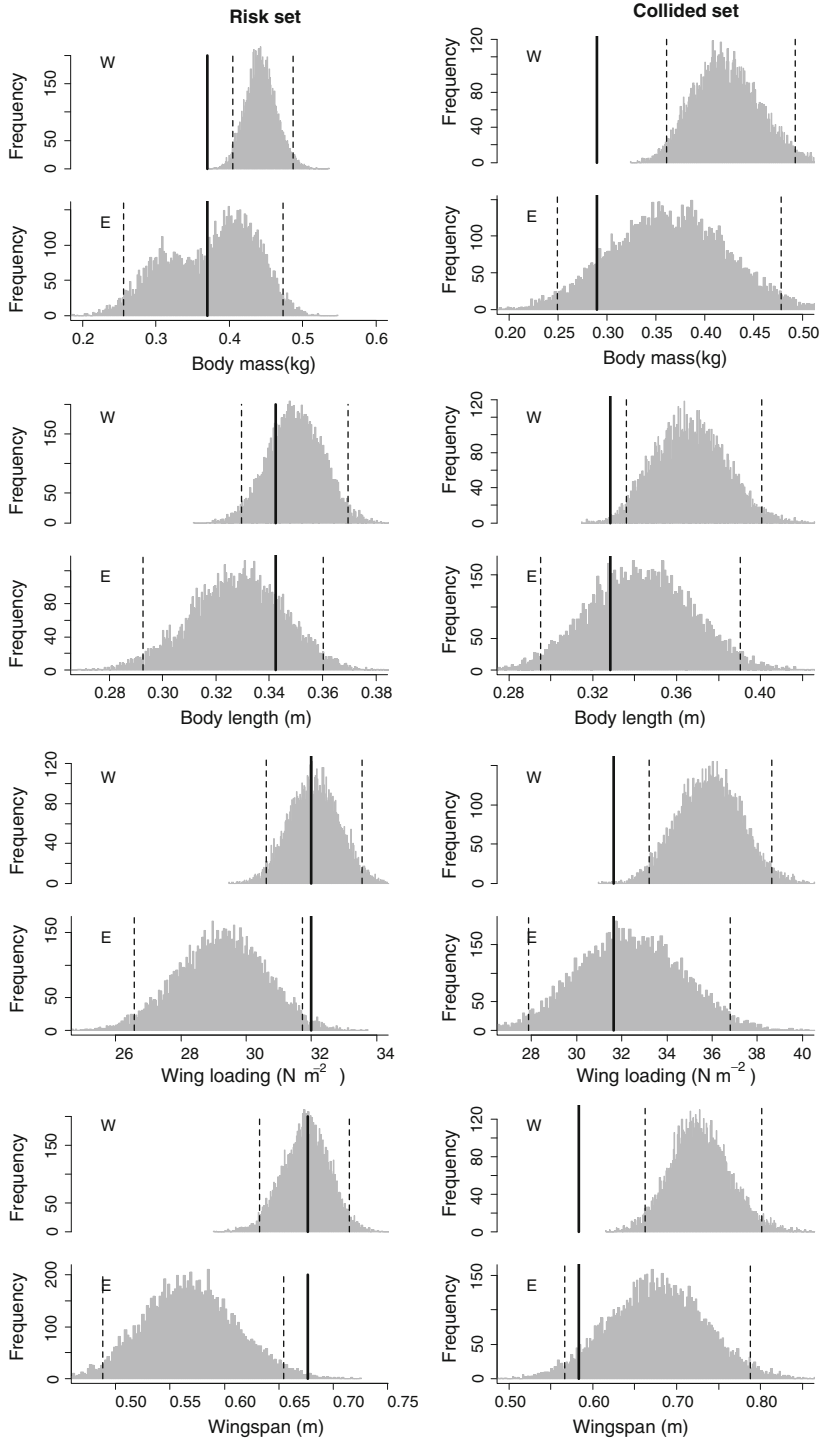
Birds flying in the risk zone had longer wings with higher loadings than expected by an equiprobable sampling from the pool ($P < 0.05$, two-tailed test; Fig. 2, left column). However, these two variables were not significantly different from a null distribution

Fig. 1 Reconstruction through maximum likelihood of a phylogeny of the species encountered in the study area, showing the number of species in the "collided" set within each family. The set of affected species is more spread across the phylogeny than expected by chance

generated with a sampling weighed by abundance. In contrast, average body mass in this set of birds was lower than expected from the weighed sampling but not from the equiprobable sampling. In the case of the collided set, the observed means for the four morphological variables were lower than expected from the weighed sampling ($P < 0.05$), but not from the equiprobable sampling (Fig. 2, right column). The weighed sampling showed, then, that birds in the collided set tended to be smaller in length (*Coccyzus minor* and

Fig. 2 Results of the null models for morphological traits associated with the probability of flying nearby ▶ and colliding with the blades of wind turbines. *Dotted lines* are 95 % confidence limits for samples based on 10,000 runs of a random sampling procedure with the equiprobable E and weighed W models described in the main text. *Black lines* indicate the observed values
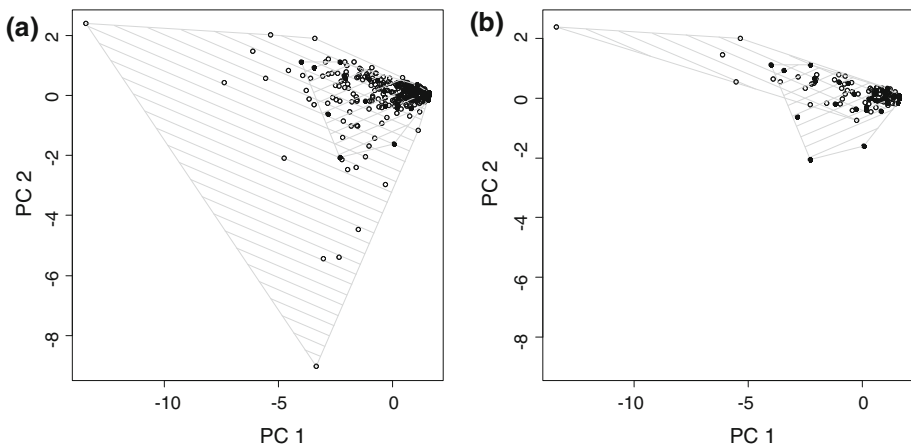
Zenaida asiatica for instance), wing span (for example, *Falco sparverius*), and body mass (around the mass of *Buteo magnirostris*), and to have lower wing loadings (wing loadings similar a *Columbina inca*). After performing the PCA analysis, we retained the first two components, which accounted for 89 % of the total variance. The first one is linked to the overall size of birds and the second one is explained mainly by wing loading (Table 1). Within this two-dimensional ecological morphospace, the distance along the MST for the species not in the collided set (i.e., the survivors set) was significantly higher than expected from a random sampling ($P < 0.05$, two-tailed test; Fig. 3).

The phylogenetic analysis yielded contrasting results. Among birds in the risk set, only the Mpd was significantly different (in this case lower) from expected in an equiprobable sampling ($P < 0.05$, two-tailed test; Fig. 4, left column). For the collided set, in contrast, both measures of phylogenetic dispersion were higher than expected under the two sampling procedures, being significantly so in three of the cases and marginally non-significant in the other one (Fig. 4, right column).

The phylogenetic signal of traits varied across the scales. When we tested in the locality and risk sets, the four morphological traits showed a phylogenetic signal, but in the collided set only wingspan and wing loading showed such a signal (Table 2). In the whole pool of species, only wingspan showed phylogenetic signal.
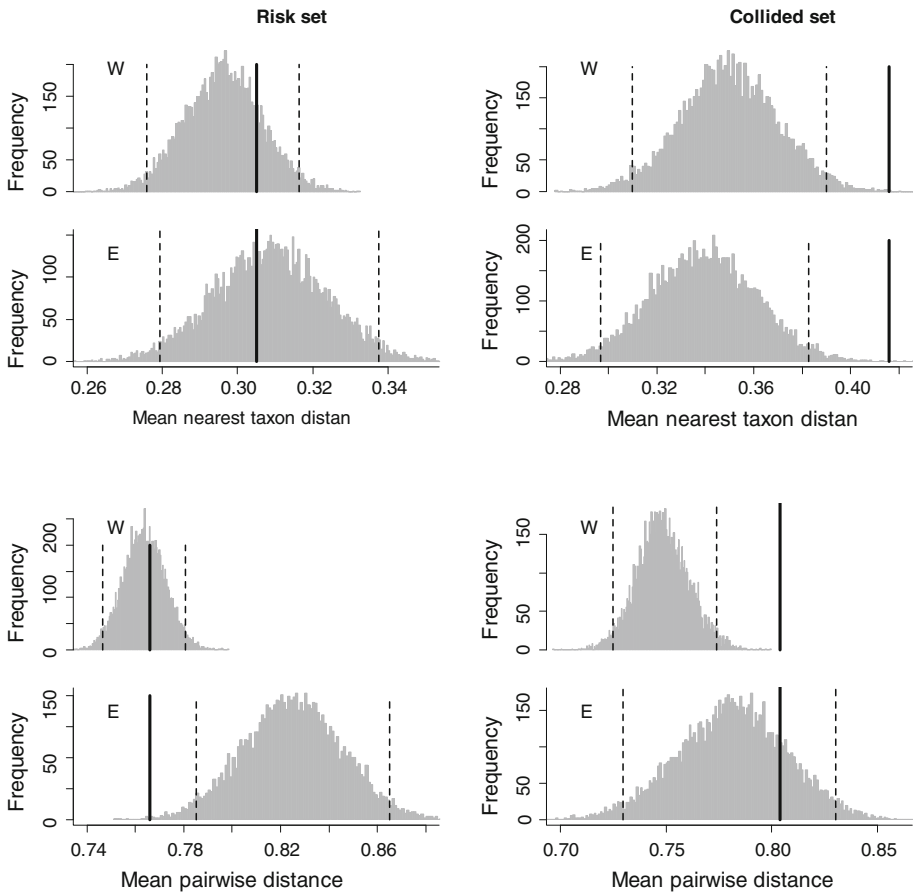
Table 1 Principal component analysis of morphological data for the birds of the Tehuantepec Isthmus of southern Mexico	PC 1	PC 2
Percentage of variance explained	70.37	19.12
Loadings		
Body mass	−0.537	0.118
Body length	−0.548	0.166
Wing loading	−0.346	−0.929
Wingspan	−0.540	0.308

Fig. 3 Ecological morphospace of species that potentially occur in the study area (**a**) and of species that actually were encountered (**b**). Collided species *filled circles* and without documented collision *open circles* are drawn alongside their convex hull

Fig. 4 Results of the null models for phylogenetic structure of species belonging to the "risk" and "collided" sets of species described in the main text. *Dotted lines* represent the 95 % confidence intervals generated by the equiprobable *E* and weighed *W* null models. *Black lines* show the observed values

Table 2 Randomization test for phylogenetic signal of morphological traits in four nested sets of bird species, as defined in the main text

	Pool	Locality set	Risk set	Collided set
Body mass	ns	PS	PS	ns
Body length	ns	PS	PS	ns
Wing loading	ns	PS	PS	PS
Wingspan	PS	PS	PS	PS

PS significant (*P* < 0.05) phylogenetic signal detected in the corresponding combination of morphological trait and subset, *ns* no significant phylogenetic signal detected

Discussion

Morphological and phylogenetic structure of subsets of species differed from expectations drawn from null models, showing that the potential and realized risks posed by wind turbines are not randomly distributed among bird groups (de Lucas et al. 2008; Ferrer et al. 2012). Our data suggest that the phenomenon of bird collision with wind turbines is a two-step process: certain birds are more likely to fly close to turbines, and a subset of these is particularly prone to colliding with the blades. Each step has different probabilities of occurring and different associated morphological variables. When compared with the species pool and using the equiprobable models, birds more likely to fly in the risk zone tend to have longer wings (higher wingspans), and to support higher wing loadings; under the weighed model, they tend to be smaller (low body mass). Among these species, and taking into account their abundances, birds more likely to come close to the blades, collide, and die are those that are smaller (in body length and body mass), have lower wingspans, and support lower wing loadings.

Because of this two-step process, conservation strategies are bound to be different at different times during the planning, development, and operation of wind farms. In a first step, all other factors being equal, recommendations for the location of wind facilities should focus on avoiding sites with higher representation of species with the phylogenetic membership and with the morphological traits that we found to be associated with probability of flying close to turbines. If that kind of choice is not feasible, then sites with representation of risk species in as many phylogenetic lines as possible should be preferred. In a second step, once the location of wind farms has been decided, specific management actions should be directed at preventing species prone to collisions to actually come close to the turbines. In the real world, these actions might represent a formidable challenge, because birds apparently do not change their behavior when turbines are active (except perhaps for some soaring birds, de Lucas et al. 2004), contrasting with responses that have been documented for European bats (Minderman et al. 2012).

Previous studies have suggested strategies for choosing the location of wind farms according to environmental variables or habitat quality (Fargione et al. 2012; Santos et al. 2013). The rationale behind these strategies is that mortality rate can be reduced by locating wind farms in sites with lower probabilities of being inhabited or visited by wildlife. Fargione et al. (2012), for example, suggested that the negative impact on wildlife can be substantially lowered simply by locating wind farms in habitats that have already been transformed. These general approaches, while adequate if information about differential impact on species is not available, are based on extrinsic factors that might or might not work in a particular case. Our proposed two-step strategy, on the other hand, incorporates intrinsic ecological and behavioral data for the species assemblage, and has the advantage of being tailored with information on the actual processes that impact the populations of birds.

Biomechanical laws determine that birds with higher wing loadings are less maneuverable (Tennekes 1996), having more difficulty in reducing flight speed and performing evading movements when faced with an obstacle (Martin 2011). It would be reasonable to expect these birds to have higher probabilities of colliding, as documented by Janss (2000) in regards to fatalities caused by power lines. A high wing load implies a relatively heavier body, small wings, or a combination of both conditions. Think, for example, of ducks flying at full speed. When faced with an obstacle, these birds have a much lower ability to reduce flight speed and to perform escape maneuvers than smaller birds with comparatively smaller wings. Our results, however, reveal a more complicated relationship between

wing morphology and risk of collision: birds with higher wing loadings are more likely to fly within the risk zone, but are less likely to collide.

This apparent contradiction can be explained by the fact that species more likely to collide tend also to be of smaller size. A combination of small size and low wing loading is associated with aerial foraging, a strategy that requires slow flight and high maneuverability (Norberg 1994; Tennekes 1996; Janss 2000). A bird with these foraging habits is more prone to colliding not because of limited flight abilities, but because its morphology is linked with foraging habits that increase the time in which the bird is airborne and, more importantly, the probability of coming close to the turbines. Horn et al. (2008) observed several species of Eastern US bats actively foraging close to wind turbines. In a similar manner, some of the bird species in our study site were observed not only passing close to turbines, but actively flying around the vicinity of moving blades. Probability of collision is also associated with relative abundance, as shown by the contrasting results of our null models using equiprobable and weighed sampling. Thus, a complex combination of morphological, behavioral, and ecological features seems to determine the rate at which different bird species come into direct contact with turbines.

Morphological differences among sets of species are reflected in the phylogenetic pattern detected by our comparisons. Our analysis of phylogenetic signal detected that some morphological traits, particularly wing loading, tend to be conserved along different clades, in a pattern consistent with the hypothesis of niche conservatism (Wiens et al. 2010). Because wing loading is associated both with the probability of flying in the risk zone and with the risk of colliding, it is reasonable to expect an effect on the degree of clustering or overdispersion of species in a phylogeny. The phylogeny of the set of species more likely to fly in the risk zone showed some degree of overall clustering (as measured by the mean phylogenetic distance), but the set prone to collisions is in fact more dispersed than expected by chance, as shown by phylogenetic distance, measured either pair-wise or between nearest neighbors.

If in fact wind farms have noticeable effects in lowering the population levels of species that collide, then the morphological and phylogenetic patterns that we found point to important impacts on the structure of the avian communities of the area. The overdispersion in the phylogeny that we have documented implies that affected species are representative of several different clades, all of them sharing morphological traits associated with increased risk from wind turbines. This finding contrasts with the worst-case scenario (extreme clustering) in which all affected birds belong to a single or a few clades. In that scenario, the impact of wind farms would put in risk whole phylogenetic lines, accelerating the process of diversity loss (Willis et al. 2008; Mouquet et al. 2012). However, the pattern that we found poses different but equally serious conservation challenges, because phylogenetic overdispersion of affected species implies that an effective strategy to mitigate the negative effect of wind farms cannot be focused on particular taxonomic groups. Instead, such a strategy should aim at reducing the risk for a phylogenetically diverse set of species, and at understanding how particular morphological traits determine the probability of collisions.

An additional perspective arises when examining the structure of the assemblage of "survivor" species, that is, the set of species not found to collide with the blades of wind turbines. This subset would be the resulting assemblage of species in the hypothetical case of an extremely drastic reduction in the population levels of birds that are in fact killed by wind turbines. In that scenario, the avian community would show an increased average distance in morphological space, which at first glance would suggest an increased level of morphological diversity (Walker et al. 1999; Heemsbergen et al. 2004). However, in the

context of this study, the increase in average distance is a reflection of the appearance of holes in different parts of the ecological morphospace, that is, the loss of species that are not extreme in morphological traits. Some species were affected by collision while others with overall similar morphology (short distances between them within the ecological morphospace) were not (Fig. 3). This variation among similar species in the outcome of collision could be linked to dissimilarities in the relative abundance of the species or to behavioral differences not reflected in the morphology. Similar holes in ecological space have been shown to foster the establishment of alien species of plants (Mwangi et al. 2007; Proches et al. 2008), but overdispersion and high taxonomic diversity is also associated with an increased resistance to invasion of non-native species (Gerhold et al. 2011). Whether these principles can be applied to the case of birds affected by wind farms remains to be studied, but as a first step our study point to non-random patterns of phylogenetic and morphological impact on assemblages that have to be taken into account in future conservation actions.

Appendix

See Table 3.

Table 3 Species encountered flying in the risk zone and species with registered collisions showing which species match their morphology with at least one trait associated with increased risk of collision

	Frequency of sightings in study area	Frequency of sightings flying at risk zone	Documented collision	Matching morphology
Dendrocygna autumnalis	108	60	X	X
Ortalis poliocephala	12	1	X	
Colinus virginianus	22	1	X	
Fregata magnificens	15	1		X
Phalacrocorax brasilianus	6	6	X	
Ardea alba	7	6	X	
Bubulcus ibis	380	162	X	X
Eudocimus albus	697	176		
Cathartes aura	258,815	17,714	X	
Coragyps atratus	645	210		
Pandion haliaetus	8	2		
Accipiter cooperii	45	15		
Accipiter striatus	25	8		X
Buteo albicaudatus	150	59	X	X
Buteo albonotatus	7	2		X
Buteo brachyurus	6	1		X
Buteo jamaicensis	30	4		
Buteo magnirostris	28	9	X	X

Table 3 continued

	Frequency of sightings in study area	Frequency of sightings flying at risk zone	Documented collision	Matching morphology
Buteo nitidus	7	4	X	
Buteo platypterus	4,631	626		X
Buteo swainsoni	188,642	1,919		X
Rostrhamus sociabilis	7	5		
Circus cyaneus	3	1		
Laterallus ruber	1	1	X	
Burhinus bistriatus	47	3	X	
Charadrius vociferus	4	1		X
Numenius phaeopus	8	6		
Leucophaeus pipixcan	22,910	5,054		X
Zenaida asiatica	1,064	380	X	X
Zenaida macroura	170	31		X
Patagioenas flavirostris	4	2		X
Columbina inca	193	1	X	X
Columbina passerina	248	3	X	
Leptotila verreauxi	14	2	X	X
Coccyzus minor	1	1	X	X
Crotophaga sulcirostris	55	2	X	X
Antrostomus vociferus	1	1	X	
Chaetura vauxi	52	42		
Streptoprocne zonaris	78	50		X
Archilochus colubris	4	1	X	
Chlorostilbon canivetii	1	1	X	
Cynanthus latirostris	2	1	X	
Melanerpes aurifrons	29	2	X	
Aratinga canicularis	50	41		X
Aratinga holochlora	46	15		X
Falco sparverius	200	74	X	X
Falco peregrinus	5	1		
Caracara cheriway	89	48		
Tyrannus forficatus	1,712	447		X
Tyrannus melancholicus	14	1	X	
Myiarchus cinerascens	1	1	X	
Vireo gilvus	1	1	X	
Calocitta formosa	100	11	X	
Corvus corax	1	1		
Hirundo rustica	930	168	X	
Petrochelidon pyrrhonota	66	33		
Progne chalybea	35	10		
Tachycineta albilinea	43	12		
Stelgidopteryx serripennis	15	7		
Polioptila albiloris	18	1		
Mimus gilvus	97	1		

Table 3 continued

	Frequency of sightings in study area	Frequency of sightings flying at risk zone	Documented collision	Matching morphology
Setophaga petechia	77	4		
Icteria virens	1	1	X	
Mniotilta varia	1	1	X	
Piranga rubra	1	1	X	
Spiza americana	522	269		
Icterus gularis	136	5		
Icterus pustulatus	32	1	X	
Molothrus aeneus	82	3		
Molothrus ater	117	2		
Quiscalus mexicanus	3,917	376	X	X

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