

Breeding birds in agro-forest habitat types (Nazzano, Tevere-Farfa Nature Reserve, central Italy): evidencing patterns following a dominance/diversity approach

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Abstract – We analysed bird assemblages breeding in three coarse-grained habitat types (cultivated lands, forests and mosaics) by following a dominance-diversity approach. Although we did not observe significant differences in mean values of both species richness and abundance among habitat types, assemblages of cultivated lands showed the lowest values of all diversity metrics. Low values of β -turnover index highlighted low heterogeneity of these anthropic and simple habitat types. The dominance/diversity diagram showed a clear difference between slopes of rank-frequency lines of mosaics and forest habitat types when they were compared to cultivated lands, indicating low species evenness resulting from the high disturbance, typical of agro-ecosystem assemblages. At this scale when we compared mosaics to forest habitats, rank-frequency lines appeared over imposed, suggesting that breeding bird assemblages did not perceive differences between these habitat types.

Key words: Whittaker plots, evenness, beta-turnover, diversity, agro-ecosystems, mosaics, forest habitats.

INTRODUCTION

In the Mediterranean area, ecosystems have been heavily modified by historical and recent human activities and disturbances (Blondel & Aronson 1999). Among them, agriculture may be considered the main driving force affecting the structural and functional patterns in landscapes (Forman & Godron 1986, Farina 2001, Bűchs 2003, Laiolo 2004). Diversity of biological assemblages in heterogeneous landscapes may be assessed by following a large number of different approaches (e.g., Moreno 2006, Magurran & McGill 2011). Among them the dominance-diversity analyses allow obtaining information on the structure, complexity and level of natural and human-induced disturbances (*sensu* Sousa 1984) of the assemblages (Magurran 2004). Such analyses have been widely used in avian ecology to explore the bird response to patchy and disturbed environments (Wiens 1976, 1989).

In central Italy, Tevere-Farfa Nature Reserve represents a heterogeneous landscape for the presence of an agro-forest mosaic with wetlands in proximity to the Tiber river (Mari 2004). Avian diversity in this reserve has been largely studied both qualitatively and quantitatively, by fo-

cus on water-related species (e.g., waders, waterfowl, rails) and their yearly cycle and phenology (Di Carlo 1976, 1983, Angelici & Brunelli 2008, Brunelli & Sorace 2008, Brunelli *et al.* 2009, Brunelli *et al.* 2011). Quantitative data on breeding bird assemblages, however, have not been investigated yet.

In the present investigation, we collected data of the community composition and structure of birds breeding on the main coarse-grained habitat types by using a standardized method. Our aim was to improve the knowledge on local breeding bird communities, also for management and conservation purposes. To reveal structural differences among breeding bird assemblages, we analysed the collected dataset by following a community ecology approach and using dominance-diversity diagrams that allowed to compare habitat types with different level of habitat heterogeneity and complexity.

METHODS

Study area

Our study area was the Nazzano, Tevere-Farfa Regional

Nature Reserve (Nazzano, central Italy), a 700-ha wide protected area developed in the 1979 and included in the Natura 2000 network as Special Area of Conservation (SIC/ZPS code IT6030012). This reserve is located along the Tiber river near the confluence of the Farfa river (approximately 40 km Northern Rome), at an altitude of 30 m a.s.l. (42°12'N - 12°37'E). The core study area was the Nazzano lake, an artificial basin originated after a dam was built in 1950s to produce hydroelectric power. Wetland areas (350 ha-wide) are largely characterized from *Phragmites australis*, *Typha latifolia* e *T. angustifolia* reedbeds. Along the river hygrophilous forests with *Alnus glutinosa*, *Populus alba* and *Salix alba* are also present. Surrounding the river, mixed termophilous oak woods with *Quercus cerris*, *Q. pubescens*, *Q. frainetto*, *Q. petrae* and *Fraxinus ornus* alternate with cultivated lands and secondary prairies (further details in Mari 2004).

Protocol and data analysis

In spring 2010, we carried out a breeding bird sampling using a quantitative point count method (IPA; Bibby *et al.* 2000). We selected 31 count points regularly located along the main longitudinal North-South axis and separated approximately 500 m to each other with the aims of both preventing potential pseudo-replication of data and representatively covering the whole nature reserve territory. In each count point, we carried out two 10 min-sampling sessions (first session in April to detect the early sedentary species; second session in May to detect the late migratory species; Bibby *et al.* 2000). During each sampling we recorded all the birds seen and heard within 100 m radius except those flying higher than 50 m over the ground. Sampling was not conducted in rainy, foggy or windy days (see Bibby *et al.* 2000). To obtain data on less detectable species, thus to collect information on the general composition of the assemblages, we carried out further not standardized samplings.

We defined each point count area (i.e., the area within 100-m radius around the count point) as a “Point Count Landscape” (PCL; i.e., a mosaic of habitat types surrounding the count point). In each PCL we quantified the percentage of three main coarse-grained habitat types, i.e.: cultivated lands, forests and mosaics. Thus we stratified the count points as following:

- I) AGR (6 count points): cultivated lands (when the land use proportion of this habitat type in the PCL was larger than 50%);
- II) FOR (13 count points): forest habitats (when the land use proportion of this habitat type in the PCL was larger than 50%);
- III) MOS (12 count points): mosaics (when no habitat type in the PCL was larger than 50% in size area).

We considered each point count dataset as related to each habitat type and belonging to the same breeding bird assemblage. We define “assemblage” as a taxonomically related assortment of species seasonally occurring in a specific habitat type (Fauth *et al.* 1996, Magurran 2004). Each assemblage dataset allowed to obtain the following parameters:

- I) total number of bird species sampled (S_{tot} ; non normalized species richness or γ -diversity);
- II) Margalef index ($D_m = S_{tot} - 1/\log N$) as a metric of normalized species richness;
- III) mean species richness (S_m ; i.e., the average number of species recorded at each count point; it may be considered a value of averaged α -diversity *sensu* Whittaker 1960, 1972);
- IV) mean total abundance (Ab_m ; i.e., the average total number of individuals in each count point);
- V) dominance (or relative species frequency, p_i ; i.e., the ratio between the number of individuals of the i^{th} -species and the total number of individuals in the assemblage); the species with a $p_i \geq 0.05$ were considered as dominant species (Turcek 1956);
- VI) Simpson diversity index ($D = 1 - S p_i^2$; Simpson 1949), a robust diversity measure less sensitive to species richness when compared to others (e.g., Shannon; Lande 1996, Magurran 2004).

To estimate the total number of species in each habitat type, we computed the Chao-1 non parametric richness estimator (Chao 1984, Colwell & Coddington 1994), as $S_{Chao1} = S_{tot} + (F_1^2/2F_2)$, where S_{tot} is the total number of bird species sampled, F_1 the number of observed species with a single individual (singletons) recorded, and F_2 the number of observed species with two individuals (doubletons) recorded.

We also quantified the β -turnover diversity index (β ; Whittaker 1960, 1972) as the ratio S_{tot}/S_{med} (i.e., ratio between the γ - and α -diversity metrics). This metric allows to obtain information on species turnover within a habitat type (or a set of sampling points), and therefore indirectly indicates the role played by the spatial heterogeneity on an assemblage (Koleff *et al.* 2003, Magurran 2004). We thus adopted a locally hierarchical approach to measure diversity: α -level (at level of point counts) and β -level to measure turnover diversity among point counts in the same habitat type, and γ -level to measure the diversity at habitat level.

Finally, we adopted a dominance/diversity approach by using Whittaker plots (Magurran 2004, Magurran & McGill 2011) where species relative frequencies (i.e., dominance) are represented as function of the species

rank. We ranked all species recorded in each habitat type (AGR, FOR, MOS), from the most to the least abundant. The most abundant species was plotted first, followed by the next more common, and so on. For each possible tendency line in dominance/diversity diagrams (linear, logarithmic, exponential) we extracted the curve with the best fit (R^2) and its equation. The curve shapes are indicative of the evenness of assemblages and suggest the presence of underlying processes that determine the revealed patterns (e.g., a stress due to a natural or an anthropogenic disturbance; Magurran 2004, Battisti *et al.* 2008, 2009). Accordingly, we also quantified the evenness metric (Simpson evenness) as: $E_{1/D} = (1/S \sum p_i^2) / S_{tot}$. This measure ranges between 0 and 1 and is not sensitive to species richness (Krebs 1999, Magurran 2004).

To test the differences among median values between habitat types, we performed the non parametric Kruskal-Wallis test by using SPSS 13.0 software for Windows. At level of single species, to test the differences in relative frequencies among the three habitat types, we performed a χ^2 test using the Primer software 4.02i for Windows only for species with more than 15 individuals totally recorded. For data reliability we followed the framework available in Battisti & Dodaro (2010).

RESULTS

By using the standard method, we recorded 1516 individual birds belonging to 70 species (Tab. 1). Nine species (*Ixobrychus minutus*, *Buteo buteo*, *Coturnix coturnix*, *Columba livia* f. *domestica*, *Tyto alba*, *Otus scops*, *Strix aluco*, *Apus apus*, *Upupa epops*) were recorded only with the use of the non standardized method.

A large number of the species with > 15 total records showed significant differences in their dominance among habitat types (χ^2 test). Among them, *Streptopelia turtur*, *Picus viridis*, *Troglodytes troglodytes*, *Turdus merula*, *Sylvia atricapilla*, *S. cantillans*, *Aegithalos caudatus*, *Cyanistes caeruleus*, *Parus major*, *Fringilla coelebs* showed among the highest dominance values in forests, *Alauda arvensis* was dominant in cultivated lands, *Corvus cornix*, *Sturnus vulgaris*, *Passer italiae*, *Passer montanus*, *Carduelis carduelis*, *C. cannabina*, *Emberiza cirrus* were dominant in both cultivated lands and mosaics, and *Emberiza calandra* in mosaics (Tab. 1).

Considering all metrics, FOR and MOS habitat types resulted richer and more diverse than AGR habitat (Tab. 2) although comparisons among their mean species richness and abundance did not reach significant values (Kruskal-

Table 1. Species composition (check-list) and relative frequencies (or dominance, p_i) in the three habitat types analysed (AGR: cultivated lands; FOR: forests; MOS: mosaics). n: number of individuals recorded in one specific habitat; N: total number of individuals recorded in all habitats; χ^2 and probability values are reported for species with > 15 total records.

species	AGR		FOR		MOS		N	χ^2	P
	n	p_i	n	p_i	n	p_i			
<i>Anas platyrhynchos</i>	2	0.006	17	0.025	14	0.026	33	4.276	0.118
<i>Phasianus colchicus</i>	6	0.019	1	0.001	8	0.015	15		
<i>Ardea cinerea</i>			5	0.007	4	0.007	9		
<i>Tachybaptus ruficollis</i>			2	0.003	1	0.002	3		
<i>Podiceps cristatus</i>			4	0.006			4		
<i>Milvus migrans</i>			2	0.003			2		
<i>Falco tinnunculus</i>	1	0.003	3	0.004	1	0.002	5		
<i>Falco subbuteo</i>			1	0.001			1		
<i>Falco peregrinus</i>			2	0.003			2		
<i>Rallus aquaticus</i>			4	0.006			4		
<i>Gallinula chloropus</i>	3	0.010	4	0.006	5	0.009	12		
<i>Fulica atra</i>	1	0.003	16	0.024	8	0.015	25	5.656	0.059
<i>Larus michaellis</i>	2	0.006	10	0.015	4	0.007	16	2.221	0.329
<i>Columba palumbus</i>					13	0.024	13		
<i>Streptopelia decaocto</i>			5	0.007			5		
<i>Streptopelia turtur</i>			20	0.030	2	0.004	22	19.504	<0.001
<i>Cuculus canorus</i>			4	0.006	2	0.004	6		
<i>Athene noctua</i>	1	0.003					1		
<i>Alcedo atthis</i>	1	0.003	3	0.004	2	0.004	6		
<i>Merops apiaster</i>	4	0.013	10	0.015	4	0.007	18	1.423	0.491

continued

species	AGR		FOR		MOS		N	χ^2	p
	n	p _i	n	p _i	n	p _i			
<i>Jynx torquilla</i>	1	0.003	1	0.001	2	0.004	4		
<i>Picus viridis</i>	2	0.006	19	0.028	7	0.013	28	6.825	<0.001
<i>Dendrocops major</i>			7	0.010	1	0.002	8		
<i>Galerida cristata</i>	7	0.022			6	0.011	13		
<i>Alauda arvensis</i>	23	0.073	8	0.012	7	0.013	38	34.615	<0.001
<i>Hirundo rustica</i>	11	0.035	30	0.045	31	0.058	72	2.240	0.326
<i>Delichon urbicum</i>			3	0.004	6	0.011	9		
<i>Motacilla flava</i>	10	0.032			5	0.009	15		
<i>Motacilla cinerea</i>	1	0.003	8	0.012	4	0.007	13		
<i>Motacilla alba</i>	6	0.019	7	0.010	8	0.015	21	1.198	0.549
<i>Troglodytes troglodytes</i>	1	0.003	20	0.030	3	0.006	24	14.869	<0.001
<i>Erithacus rubecula</i>	5	0.016	26	0.039	11	0.021	42	5.460	0.065
<i>Luscinia megarhynchos</i>			7	0.010	2	0.004	9		
<i>Phoenichurus ochruros</i>					2	0.004	2		
<i>Saxicola torquatus</i>	2	0.006			4	0.007	6		
<i>Monticola solitarius</i>			1	0.001			1		
<i>Turdus merula</i>	6	0.019	35	0.052	12	0.022	53	10.125	0.006
<i>Cettia cetti</i>	7	0.022	29	0.043	16	0.030	52	3.153	0.207
<i>Cisticola juncidis</i>	3	0.010			7	0.013	10		
<i>Acrocephalus scirpaceus</i>	3	0.010	9	0.013	7	0.013	19	0.281	0.869
<i>Acrocephalus arundinaceus</i>	1	0.003	8	0.012	5	0.009	14		
<i>Hippolais polyglotta</i>			11	0.016	2	0.004	13		
<i>Sylvia atricapilla</i>			26	0.039	13	0.024	39	12.504	0.002
<i>Sylvia cantillans</i>	2	0.006	27	0.040	6	0.011	35	15.407	<0.001
<i>Sylvia melonecephala</i>	2	0.006	7	0.010			9		
<i>Phylloscopus collybita</i>			9	0.013	2	0.004	11		
<i>Regulus ignicapilla</i>			9	0.013	1	0.002	10		
<i>Muscicapa striata</i>	4	0.013	1	0.001	4	0.007	9		
<i>Aegithalos caudatus</i>			26	0.039	6	0.011	32	18.796	<0.001
<i>Cyanistes caeruleus</i>	9	0.029	56	0.084	23	0.043	88	13.661	0.001
<i>Parus major</i>			19	0.028	4	0.007	23	14.414	<0.001
<i>Sitta europaea</i>			3	0.004	3	0.006	6		
<i>Certhia brachydactyla</i>	1	0.003	8	0.012	1	0.002	10		
<i>Remiz pendulinus</i>			2	0.003			2		
<i>Oriolus oriolus</i>			12	0.018			12		
<i>Lanius collurio</i>	1	0.003	3	0.004	6	0.011	10		
<i>Garrulus glandarius</i>			5	0.007	5	0.009	10		
<i>Pica pica</i>			2	0.003	4	0.007	6		
<i>Corvus monedula</i>	3	0.010	10	0.015	2	0.004	15		
<i>Corvus cornix</i>	34	0.108	15	0.022	41	0.077	90	28.858	<0.001
<i>Sturnus vulgaris</i>	47	0.150	6	0.009	50	0.093	103	72.664	<0.001
<i>Passer italiae</i>	21	0.067	18	0.027	27	0.050	66	8.332	0.016
<i>Passer montanus</i>	27	0.086	19	0.028	43	0.080	89	17.714	<0.001
<i>Fringilla coelebs</i>			14	0.021	2	0.004	16	12.401	0.002
<i>Serinus serinus</i>	8	0.025	20	0.030	15	0.028	43	0.152	0.927
<i>Carduelis chloris</i>			3	0.004	5	0.009	8		
<i>Carduelis carduelis</i>	14	0.045	4	0.006	18	0.034	36	16.429	<0.001
<i>Carduelis cannabina</i>	9	0.029			13	0.024	22	17.339	<0.001
<i>Emberiza cirulus</i>	18	0.057			14	0.026	32	33.165	<0.001
<i>Emberiza calandra</i>	4	0.013	1	0.001	11	0.021	16	10.288	0.006
total	314	1	667	1	535	1	1516		

Table 2. Assemblage parameters of the breeding bird assemblages in the Nazzano Tevere-Farfa Nature Reserve. AGR: cultivated lands; FOR: forests; MOS: mosaics. N: total number of breeding birds recorded in a specific habitat type; S_{tot} : total number of bird species (i.e., γ -diversity); S_{Chao1} : Chao₁ richness estimator; Dm: Margalef index; S_m : mean species richness (average α -diversity); Ab_m : mean total abundance; D: Simpson diversity index; $E_{1/D}$: Simpson evenness index; β : Whittaker β -diversity index.

parameters	AGR (N = 314)	FOR (N = 667)	MOS (N = 535)
S_{tot}	41	61	59
S_{Chao1}	47.75	65.5	64.79
Dm	16.02	21.25	21.26
S_m	16.5 (\pm 3.67)	19.69 (\pm 4.48)	17.42 (\pm 3.68)
Ab_m	52.33 (\pm 15.45)	51.31 (\pm 16.54)	44.58 (\pm 12.76)
D	0.94	0.97	0.96
$E_{1/D}$	0.38	0.53	0.43
β	2.48	3.10	3.39

Wallis test; $\chi^2 = 2.269$, $p = 0.132$ and $\chi^2 = 0.002$, $p = 0.965$, respectively; Tab. 2, Fig. 1). The highest β -turnover index was in MOS whereas the lowest was recorded in AGR habitats (Tab. 2).

Fig. 1 shows the diversity/dominance diagram fitted with exponential curves and their relative equations resulted with very high R^2 values (> 0.95). It is noteworthy that the rank-frequency lines of bird assemblages breeding in FOR and MOS overlapped and were separated from that relative to the AGR habitat because of its larger slope (higher angular coefficient; Fig. 1).

DISCUSSION

Our results showed that cultivated lands hosted poor and less diverse breeding bird assemblages when compared to

mosaics and forest habitats. Due to high habitat homogeneity and human-induced disturbances, bird assemblages in intensive agro-ecosystems showed a structural simplification with low evenness and a low species turnover among sampling points (i.e., low β -diversity index; Whittaker 1972, Magurran 2004).

When adopting a dominance/diversity approach, we observed clear differences in the slope of rank-frequency lines between mosaic and forest habitat types (small slope) when compared to cultivated lands (large slope). Since dominance/diversity diagrams are able to indicate differences in evenness among bird assemblages via the visual analysis of their line slopes, our data pointed to the low value of this parameter (Simpson evenness) in the agro-ecosystems, probably due to the anthropogenic disturbances typical of these habitat types.

We did not observe significant differences between

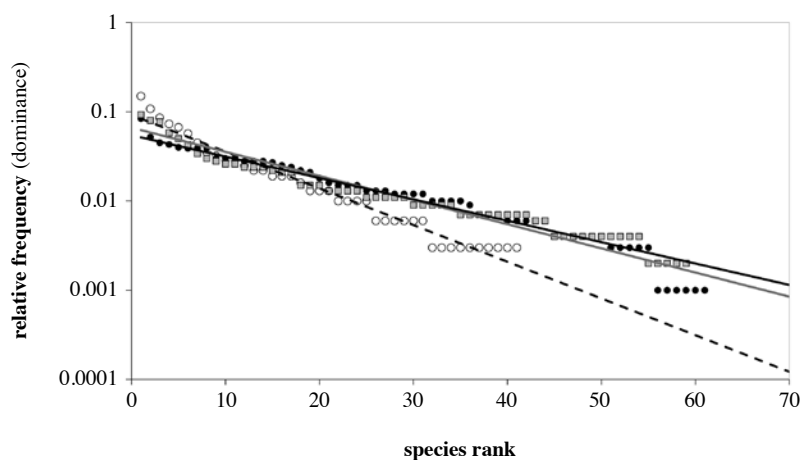


Figure 1. Dominance/diversity diagram of the breeding bird assemblages found in the three habitat types. The equation function (exponential) and the R^2 values are reported: AGR (white circles and dashed line; $y = 0.090e^{0.09x}$; $R^2 = 0.96$); FOR (black circles and gray line; $y = 0.062e^{0.058x}$; $R^2 = 0.98$); MOS (grey squares and black line; $y = 0.056e^{0.056x}$; $R^2 = 0.96$).

forest and mosaic habitat types both in values of assemblage parameters and in slope in dominance/diversity lines which were partially over imposed. When defining our point count landscapes, we conventionally defined a threshold to distinguish 'forest' (> 50% of forest cover) from 'mosaic' habitats (no habitat type larger than 50% of the area). Probably, at this spatial scale (i.e., the PCL scale), breeding birds did not perceive differences among 'forests' and 'mosaics' and therefore they should be considered belonging to a heterogeneous mosaics *sensu lato* (Tews et al. 2004), with assemblages showing similar species composition and structure. Differently than forest cover, cultivated lands were more important at this scale as a predictor to define structural differences in breeding bird assemblages.

This coarse-grained analysis should be considered a preliminary investigation, especially given the limited sample of point counts conducted in agricultural habitats. Accordingly, in Mediterranean heterogeneous landscapes, further studies are warranted to support these patterns and to discriminate thresholds between forest and mosaic covers for determining potential differences in composition and structure of breeding bird assemblages.

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