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Temporal dynamic of the phylogenetic diversity of the bird community of agricultural lands in Ukrainian steppe drylands

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This study discussed the importance of the phylogenetic components in the structure of bird communities of anthropogenically transformed ecosystems. The investigation was conducted in the landscapes of the south and south-east of Ukraine in the nesting seasons 1988–2018. The bird community in the agricultural landscape was found to be presented by 10 species. The number of species was closely correlated with its phylogenetic analogue – Faith’s index. Both indices were stationary over time, as they do not show a statistically significant time trend. The two axes were extracted as a result of the DPCOA procedure and the permutation test showed their statistical significance. The axis 1 was the most sensitive to the opposite dynamics of the abundance of *Coturnix coturnix* and *Burhinus oedicnemus* on the one hand and *Alauda arvensis* and *Melanocorypha calandra* on the other. The axis 2 is the most sensitive to the opposite dynamics of *Corvus monedula* and *Melanocorypha calandra* on the one hand and *Coturnix coturnix* and *Motacilla flava* on the other. Based on phylogenetic diversity, the years can be clustered with the extraction of four relatively homogeneous phylogenetic structures of bird communities. The indicator of the initial period of dynamics (1988–1992) was *Burhinus oedicnemus*. Sowing or mechanical weeding may be considered as a major factor of nest destruction of *Burhinus oedicnemus*. The decreasing of the abundance of the trophic recourses because of agricultural activity may have caused the monotonous negative trend over time of the *Burhinus oedicnemus* populations. The period 1993–2003 was a transitional one, for which there were no clear indicators, as a characteristic feature of this period was the processes of bird community restructuring. The period 2004–2013 was characterized by the loss of *Burhinus oedicnemus* from the community and a sharp increase in the abundance of *Corvus monedula*. These species are distinguished by their phylogenetic specificity and are located on the periphery relative to the phylogenetic core of the community. There was growing importance in the community of such species as *Alauda arvensis*, *Anthus campestris*, and *Melanocorypha calandra* between 2014 and 2018. Our results also confirm the assumption that phylogenetic overdispersion is an important requirement for the stability of the bird community in anthropogenically transformed landscapes.

Keywords: diversity; Faith’s index; Rao’s quadratic entropy; overdispersion; stability; global climate changes; agroecology.

Introduction

Bird assemblages have an amazing ecological diversity (Blinkova & Shupova, 2017). The species assemblage of a community is the result of the interaction of evolutionary and ecological mechanisms (Ricklefs, 1987) and the latter being reflected in the niche-dependent (Tilman, 1982; Weiher & Keddy, 1999; Zimaroeva et al., 2015), neutral (Bell, 2001; Hubbell, 2001) and historical (Ricklefs, 1987; Ricklefs & Schluter, 1993) processes. Information about the phylogeny is suggested to be able to decide problems with estimation of the relative role of ecological niche, neutral and historical processes in formation of community structures (Cavender-Bares et al., 2009; Dranga et al., 2016; Gorlov et al., 2016; Chaplygina et al., 2018, 2019). Species richness is the commonest approach to quantifying community taxonomic diversity. Species abundances and species richness are useful metrics but are not able to give a full information on possible consequences of the land transformation and food production on ecosystem functioning or on evolution history (Dross et al., 2017). The effect of species richness on ecosystem productivity is strongly positive in low-productivity communities and strongly negative in high-productivity communities (Wang et al., 2019). The evaluation of evolutionary distances and relationships of species may be used to measure biodiversity (Faith, 2002; Zupan et al., 2014). The bird community functional alpha and beta diversities are found to be significantly correlated with taxonomic diversities (Si et al., 2016). Variability in the number of species may contribute to both phylogenetic

clustering or overdispersion, depending on the habitat or scale studied (Sobral & Cianciaruso, 2016; Sokolov & Zhukov, 2016). Phylogenetic clustering is a situation where there is an excess of related species that coexist locally. Phylogenetic overdispersion is the situation where related species occur together less frequently than can be expected based on random assumptions (Hardy, 2008; Sokolov & Zhukov, 2017).

Conservation of bird communities with high phylogenetic diversity is essential to maintain the diversity across the tree of life (Frishkoff et al., 2014; Thuiller et al., 2011). Phylogenetic diversity was also proposed as an important component for nature conservation (Vane-Wright et al., 1991; Winter et al., 2013). The phylogenetic diversity protection was suggested to be useful for protection of the functional diversity (Mazel et al., 2018). But phylogenetic diversity as a measure of the global biodiversity values cannot be reduced only to surrogate of the functional diversity for global conservation of phylogenetic diversity embraces more than just functional diversity (Owen et al., 2019). The level of a species’ phylogenetic isolation is required to be assessed in conservation planning for choosing on which species to focus attention (Redding et al., 2014). The evolutionary distinctiveness is important because it represents uniquely divergent genomes (Faith, 2008; Jetz et al., 2014). The negative impact of urban environments on the evolutionary distinctiveness of birds was documented to be independent of eco-regions (Morelli et al., 2016). The multidimensionality of biodiversity needs to be considered to better understand the biodiversity-ecosystem multifunctionality relationship (Le Bagousse-Pinguet et al., 2019). Several

benefits of maintaining the ecosystem's stability may be provided by conservation of phylogenetic diversity as a result of the decreasing probability of loss of the unique phenotypic and ecological traits (Cadotte et al., 2012). But there is alternative evidence according to which the conservation of evolutionarily distinct species is not more effective than the conservation of species richness as a way to maintain productive and stable communities under changing environmental conditions (Venail et al., 2015). Ecological niche conservatism suggests that phylogenetically related species tend to adapt to similar habitats because they have the equivalent biological properties (Lord et al., 1995). The phylogenetic and functional diversities were applied to quantify the impact of disturbances (Bässler et al., 2016), and to investigate overall drivers of biodiversity (Gerisch et al., 2012). There are different drivers of phylogenetic and functional diversity. Phylogenetic diversity is more sensitive to environmental factors but the functional diversity is more sensitive to habitat heterogeneity (Chun & Lee, 2018). Land use intensification can reduce the functional diversity of animal communities beyond changes in species richness alone (Flynn et al., 2009; Zhukov et al., 2017). The mechanisms that influence the co-occurrence of species within the communities may be suggested to be similar along the ecological gradient due to the fact that the functional and phylogenetic evenness of the assemblages remained constant (Dehling et al., 2014).

Ecological diversity originates when climatic requirements, the feeding and breeding habitats and the food resources of the evolving lines of bird species repeatedly diverge during or between speciation events (Mayr, 1963). Species in anthropogenically transformed habitats are selectively eliminated from habitats (Si et al., 2017). Deforestation and forest fragmentation can cause species extinction, changing the phylogenetic community diversity (Arroyo-Rodriguez et al., 2012). Selective and random extinction may be discussed as alternative mechanisms to explain a biodiversity dynamic due to habitat loss and fragmentation (Terzopoulou et al., 2015; Si et al., 2016). Environmental filtering and competitive exclusion lead to selective extinction, creating community patterns that are different from random alternatives (MacArthur & Levins, 1967; Purvis et al., 2000). The phylogenetic evenness of bird communities at regional scales can be an effect of historical biogeographic processes instead of niche-based processes (Gomez et al., 2010). The local abiotic conditions may eliminate the less fit species (Webb et al., 2002). Niche differences may only be explained by combinations of traits, corresponding to differentiation between species in multiple ecological dimensions (Kraft et al., 2015). It was suggested that communities on smaller and isolated fragments appear functionally and phylogenetically clustered. However, communities on the mainland should be overdispersed if competition is important or if there is high habitat heterogeneity (Si et al., 2017). The ecological resources are more limited in the smaller landscape patches and in these conditions the coexistence of species with similar niches may be restricted by an interspecific competition (Helmus et al., 2007).

The aim of the present work is to determine the importance of the phylogenetic components in the organization of bird communities of anthropogenically transformed ecosystems.

Materials and methods

The investigation was conducted in the landscapes of the south and south-east of Ukraine in the nesting seasons 1988–2018. Agricultural land was surveyed in the area around the Molochny Estuary (46°33'00" N, 35°24'17" E). The total survey area was 1092.4 ha. Two main methods of the ornithological surveys were applied to collect data: by transect and point (Andrushenko & Zhukov, 2016; Koshelev, 2017). The width of the survey corridors with good visibility was 7–8 km, during rain – 2–4 km, in the fog – up to 500 m (in the specified boundaries it was maximum for larger species, and minimal – for small birds and individuals, which were in closed habitats with limited view). Point surveys were held during stops for scanning monotonous open areas. In all cases, the territory was examined using 12 binoculars and 60-X telescopes. Depending on the duration of the day and the quality of the illumination, counts were carried out throughout the daylight hours from 7:00–7:30 to 15:30–16:00. Counts were recorded in special cards, applied to the scale of 1:200,000 maps, and then transferred to the geographic information database created in the software ArcMap 10.0. Information about the phylogeny is applied to

assess the phylogenetic aspect of the diversity of bird communities. The Havrda & Charvat index (Havrda & Charvat, 1967) was used to measure the diversity within a community:

$$H_a(p) = (1 - \sum_{i=1}^n p_i^a) / (a - 1),$$

where $p = (p_1, \dots, p_n)$, p_i is the relative abundance of the i -th category in a community of n categories, and a is a scaling constant ($a \geq 0$) that weights the importance of rarity (Pavoine et al., 2009). When a tends to 1, then H_a tends to the Shannon (1948) index. When $a = 2$, then H_a is equal to the Simpson (1949) index (Pavoine et al., 2009). An index of phylogenetic diversity (PD) adjusted for rarity (I_a) was used (Pavoine et al., 2009):

$$I_i = \sum_{K=1}^N (t_K - t_{K-1}) H_{a,K},$$

where $H_{a,K}$ is the diversity index H_a applied to the K -th period. With $a = 0$, H_0 is the richness and I_0 is Faith's (1992) PD index minus the height of the tree. When a tends to 1, I_a is thus a generalization of the Shannon index (H_1) to account for evolutionary history. With $a = 2$, H_2 is the Simpson index and I_2 is Rao's quadratic entropy (QE) applied to phylogenetic distances between species (Pavoine et al., 2009).

Phylogenetic analysis by means of Double Principal Coordinate Analysis (DPCoA) (Pavoine et al., 2004) was conducted using library `ade4` (Dray et al., 2007) in the environment R (R Core Team, 2019). Procedure of analysis and additional scripts are described in the work of Pavoine et al. (2009). For each random permutation of the phylogenetic tree as mentioned above we calculated eigenvalues of the DPCoA-axes and with function `randtest` from the library `ade4` the Monte-Carlo test was performed. Statistical difference from the random alternative for each DPCoA-axis was assessed. This approach let us understand the degree in which phylogenetic information increases the quality of the ordination in comparison with the phylogenetic random alternative.

Statistical analysis was conducted in Statistica 10.0 (StatSoft Inc., USA). Randomization of the community matrix was done by means of the trial-swap algorithm maintaining species occurrence frequency and sample species richness (Miklos & Podani, 2004). The permutation test was done by means of the `randtest` function from the `ade4` packages (Dray & Dufour, 2007).

Results

The bird community in agricultural landscape was found to be represented by 10 species during 1988–2018 (Fig. 1).

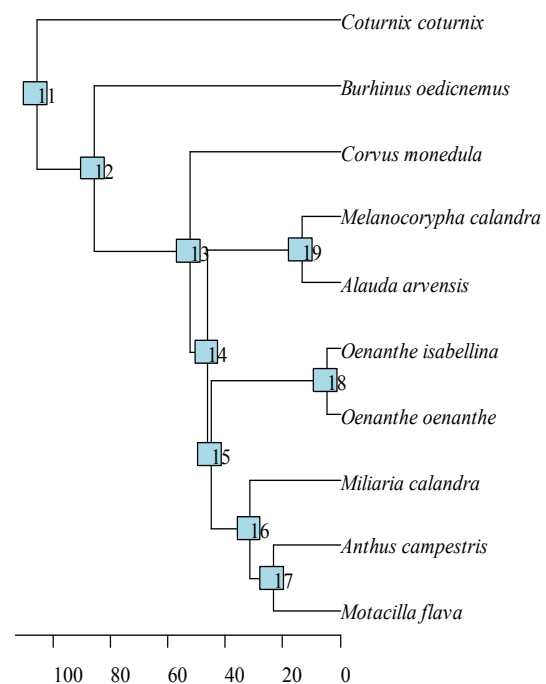


Fig. 1. Phylogenetic tree of the agroecosis bird community: the scale is a time of divergence, million years

The groups of the phylogenetically close species may be identified: *Milaria calandra* Linnaeus, 1758 and *Alauda arvensis* Linnaeus, 1758; *Oenanthe isabellina* (Temminck, 1829) and *Oenanthe oenanthe* (Linnaeus, 1758); *Melanocorypha calandra* (Linnaeus, 1766), *Anthus campestris* (Linnaeus, 1758) and *Motacilla flava* Linnaeus, 1758. *Corvus monedula* Linnaeus, 1758, *Burhinus oedicnemus* (Linnaeus, 1758) and *Coturnix coturnix* (Linnaeus, 1758) occupy an isolated position on the phylogenetic tree. The monotonous trend in population growth is typical for *A. arvensis*, *A. campestris*, *Mel. calandra*, *Mil. calandra* in the study period (Fig. 2). A monotonous decreasing trend in population dynamic is typical for *B. oedicnemus*, and *C. coturnix*. There was a maximum of the abundance of *C. monedula*, *M. flava*, and *O. isabellina* populations in the medium term of the study period. The some local max-

ima were found for *O. oenanthe*. The bird communities of agroecosystems included 6–10 species annually in the current period of study (Fig. 3). The number of species was closely correlated with its phylogenetic analogue – index I_0 ($r = 0.91$, $P < 0.001$). Both indices were stationary over time, as they do not show a statistically significant time trend. The relationship between the Shannon index and the I_1 index was less than for the previous pair of indices ($r = 0.77$, $P < 0.001$). The Shannon index was stationary in time, and the I_1 index showed a trend of increase over time (the correlation with the order of years was $r = 0.42$, $P < 0.02$). The Simpson index and I_2 index had the smallest correlation of all the pairs of indices reviewed ($r = 0.65$, $P < 0.001$). The Simpson index was stationary in time, and the I_2 index showed an upward trend (correlation with the order of years was $r = 0.63$, $P < 0.001$).

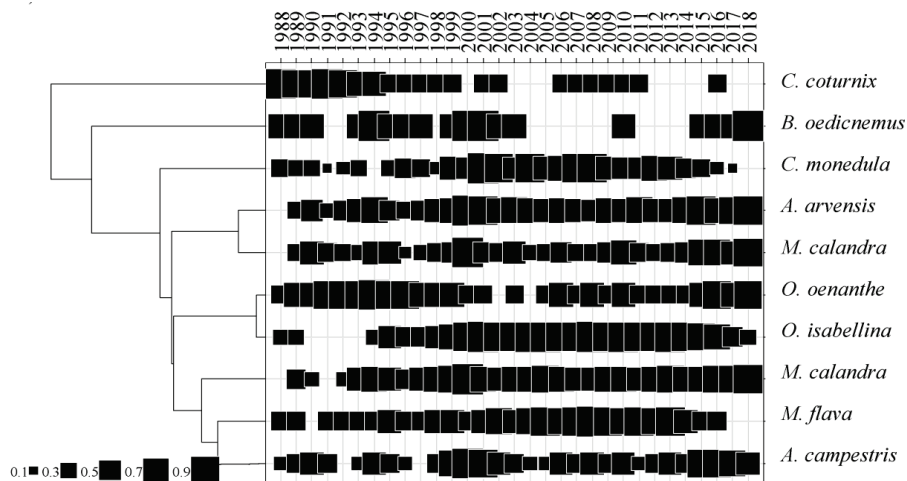


Fig. 2. Bird data set: the phylogenetic tree of the 10 bird species included in the analysis is provided; absolute abundances are measured by the number of birds detected per season (logarithm-transformed) and given by the size of black squares

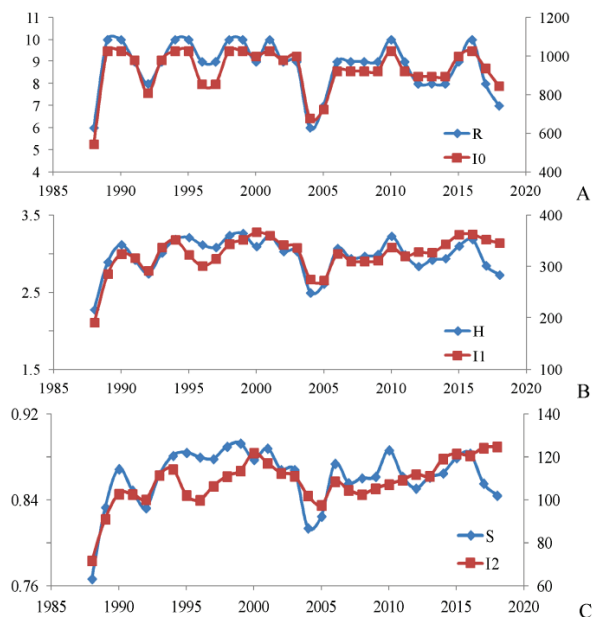


Fig. 3. The temporal dynamics of the diversity of bird communities of agroecosystems: horizontal axis is the order of years; *a* – the left y-axis is the number of species, the right y-axis is the phylogenetic diversity I_0 ; *b* – the left y-axis is the Shannon index, the right y-axis is the phylogenetic diversity I_1 ; *c* – the left y-axis is the Simpson index, the right y-axis is the phylogenetic diversity I_2

The two axes were extracted as a result of the DPCOA procedure (Fig. 4). The permutation test showed their statistical significance. The eigenvalue of the axis 1 is 1.73, which is different from the random alternative 1.29–0.05 with significance level 0.05. The eigenvalue of the axis 2 is 1.22, which is different from the random alternative 0.86.01 with signifi-

cance level 0.012. The axis 1 was the most sensitive to the opposite dynamics of the abundance of *C. coturnix* and *B. oedicnemus*, on the one hand, and *A. arvensis* and *M. calandra*, on the other. The axis 2 is the most sensitive to the opposite dynamics of *C. monedula* and *M. calandra* on the one hand and *C. coturnix* and *M. flava* on the other.

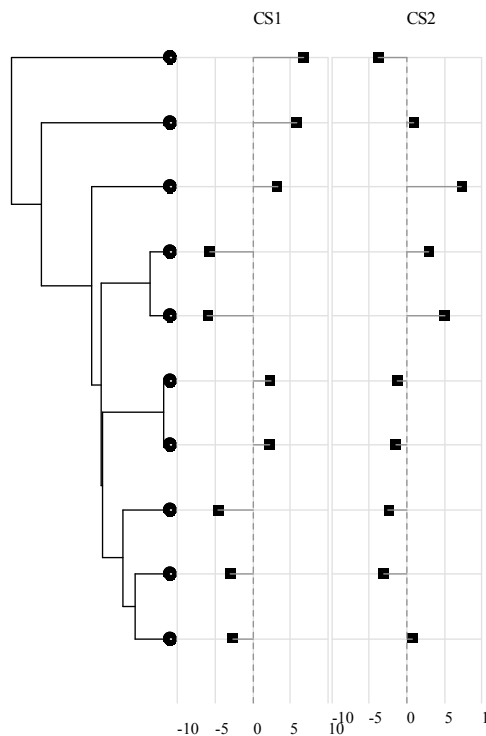


Fig. 4. Ordination of bird community by DPCoA based on phylogenetic structure

The within-year variation component of phylogenetic community structure increased together with the order of diversity index a ($a = 0, 1, 2$) (Table 2). The between-year variation component of phylogenetic diversity varied between 3.1–9.2% depending on the order of diversity index, which indicates a rather high level of the temporal stability of community phylogenetic structure. The contribution of the evolutionary period to the partitioning of the I_0 , I_1 and I_2 indices between phylogenetic periods depends on the duration of the period (Fig. 5, a). The duration of the periods between successive events of the bird species formation represented in the community was 1.96–67.3 million years. By definition, the number of lines decreased from leaves to the root of a phylogenetic tree. Accordingly, the ecological contribution of the period decreased from leaves to roots. This pattern was most prevalent for the I_0 index (Fig. 5, d), and to a slightly lesser extent for the I_1 and I_2 indices (Fig. 5, b, c). The most basal species were characterized by the least contribution to the difference of phylogenetic diversity between years.

Table 2

Overall value of I_a (total number for all phylogenetic periods, $a = 0, 1, 2$) and its share within and between years (% indicate the proportion of total diversity attributable to the components of diversity within and between years)

Diversity components	I_0 (% from total)		I_1		I_2	
Within-year diversity	931.1	90.8%	329.7	93.0%	110.1	96.9%
Between-year diversity	94.7	9.2%	24.8	7.0%	3.5	3.1%
Total diversity	1025.8	100.0%	354.4	100.0%	113.6	100.0%

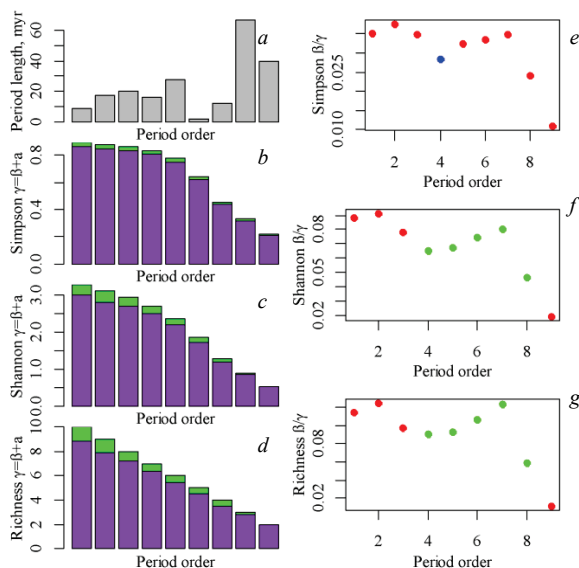


Fig. 5. Hierarchical partitioning of phylogenetic diversity across years and evolutionary periods: application to the bird data set. Periods are ordered from tips to root: (a) provides the length of the periods in million years; (b) gives the decomposition of Simpson diversity into α^* (purple bars), β^* (green bars) components and across evolutionary periods (the height of the whole purple and green bar is γ^*); (c) and (d) are equivalent bar plots for the Shannon (c) and richness (d) indices; in (e), the difference between the years (measured β^*/γ^* with the Simpson index) is partitioned between the evolutionary periods; red circles highlight insignificant tests; green circles highlight significant tests revealing the overdispersion and blue circles highlight significant tests revealing the clusterisation; (f) and (g) are equivalent graphs for the Shannon (f) and richness (g) indices

The difference in phylogenetic diversity between years was estimated to increase using all indices between evolutionary period 2 (dichotomy 12 in Fig. 1) and 7 (dichotomy 17 in Fig. 1). The phylogenetic origin of the differences between the years (low value of the β^*/γ^* ratio, phylogenetic overdispersion) was statistically significant for periods of 4 to 8 (dichotomy 16 to 12 in Fig. 1) based on the I_0 and I_1 indices. This indicates that a greater number of the phylogenetic lines was formed during these periods than can be expected from a random alternative, and the I_1 index also indicates that the abundance of representatives of these lines in community

is even. For the I_2 index, a statistically significant phylogenetic clustering was revealed for period 4 (the ratio β^*/γ^* was higher than can be expected based on a random alternative). This means that the abundance of the representatives of phylogenetic lines, which were below the specified significant period, varied considerably between years.

Based on phylogenetic diversity, the years can be clustered with the extraction of four relatively homogeneous phylogenetic structures of bird communities (Fig. 6).

As a rule, each cluster is contained in a series of years, allowing them to be considered as temporal periods. The homogeneous period was A (1988–1992). The cluster B mainly included the years 2004–2013, with the exception of 2010, which was a part of the cluster D. In turn, the cluster D corresponded to the period 1993–2003, with the exception of 2000, which was a part of the cluster C. The cluster C embraced the period 2014–2018. It is obvious that the trajectory of the bird community development was not monotonous, which was due to some heterogeneity of the allocated periods.

The most sensitive to the phylogenetic structure was the period 4 and the corresponding monophyletic groups allowed us to interpret meaningfully the established periodization of the stages of development of the bird community. In the initial research period (cluster A) the community was associated with a relatively high frequency of occurrence of *Burhinus oedicnemus*. The transition to the next period (D) was due to the successive changes of the local maximum of abundance of the *Oenanthe oenanthe* (local maximum occurred in 1993–1994), *Oenanthe isabellina* (2001–2014), *Motacilla flava* (2008–2010). The next time period (B) was associated with a return of the community structural characteristics to initial state (similar to cluster A). The next period C was marked by an increase in the role of phylogenetically different species *Alauda arvensis*, *Anthus campestris* and the complex *Melanocorypha calandra* and *Miliaria calandra*.

Discussion

The study of community species composition is a key ecological problem (Pavoine et al., 2004). Human impact significantly reduces the diversity of biotic communities (Kunah & Papka, 2016, a,b). Farmlands with high crop production can lead to a loss of avian phylogenetic diversity (Frishkoff et al., 2014; Morelli et al., 2017). It has been suggested that agriculture reduces the functional diversity of bird communities more than their taxonomic diversity (Dross et al., 2017). The effect of canopy density in temperate forests on taxonomic diversity of bird assemblages was generally bell-shaped, whereas the relationship was U-shaped for functional and phylogenetic diversity (Bae et al., 2018). This generalization was reflected in our results.

The modern agrolandscape in the south of Ukraine is a mosaic of various biotopes: arable fields, gardens, field-protective forest belts, irrigation canals and ponds, a network of roads, various buildings, inclusions of the remains of natural biotopes (steppes, meadows, solonchaks, rivers, etc.). According to our data, 56 bird species nest in agrolandscapes of Southern Ukraine. Only 10 species were found in the bird community in the agroecosystems which we monitored over 30 years of research, which, except for *C. monedula*, belong to the ecological group of campophiles. These species nest on the ground and collect food from the ground surface. *C. monedula* nests in hollow concrete poles among open woodless fields, but they also collect food from the ground, so they were included in this list. In this community 6–10 species were present annually. This raises the question of the nature of the mechanisms of formation and functioning of bird communities with low diversity level. Two alternative hypotheses can be offered. First, extreme environment regimes in the anthropogenically transformed landscapes offer relatively homogeneous conditions, which lead to a functional and phylogenetic homogenization of the communities. Another is that the intense competition between species in the extreme conditions should lead to phylogenetic overdispersion.

Information on phylogenesis is considered to be useful to decide some problems about the importance of the ecological niche, neutral and historical processes of the community, and some mechanisms of community structure formation (Cavender-Bares et al., 2009). Functional diversity explains resource-use patterns better than species diversity (Petchev & Gaston, 2006). A lot of traits demonstrate a phylogenetic signal, suggest-

ing that phylogenetic diversity can reveal the functional trait space of a community, and thus ecosystem functioning (Srivastava et al., 2012). The traditional diversity indices were found to be stationary, while the phylogenetic diversity indices indicated an increase in diversity over the study period. The reasons for this can be of different nature. During this period a rise in crop yields occurred (Kunah et al., 2018; Zymarioeva et al., 2019a, 2019b) that could affect the phylogenetic diversity of bird communities. The response of species richness and diversity to habitat complexity can

be controlled by productivity, as species richness and diversity respond to productivity and increased resources in complex habitats (Hulbert, 2004). Also during this time period critical climate changes were observed, which have a mixed impact on the community of living organisms and in some cases can stimulate an increase in the diversity of some groups of animals or plants. Therefore, the trend of increasing of the phylogenetic diversity can be also linked to global climate change.

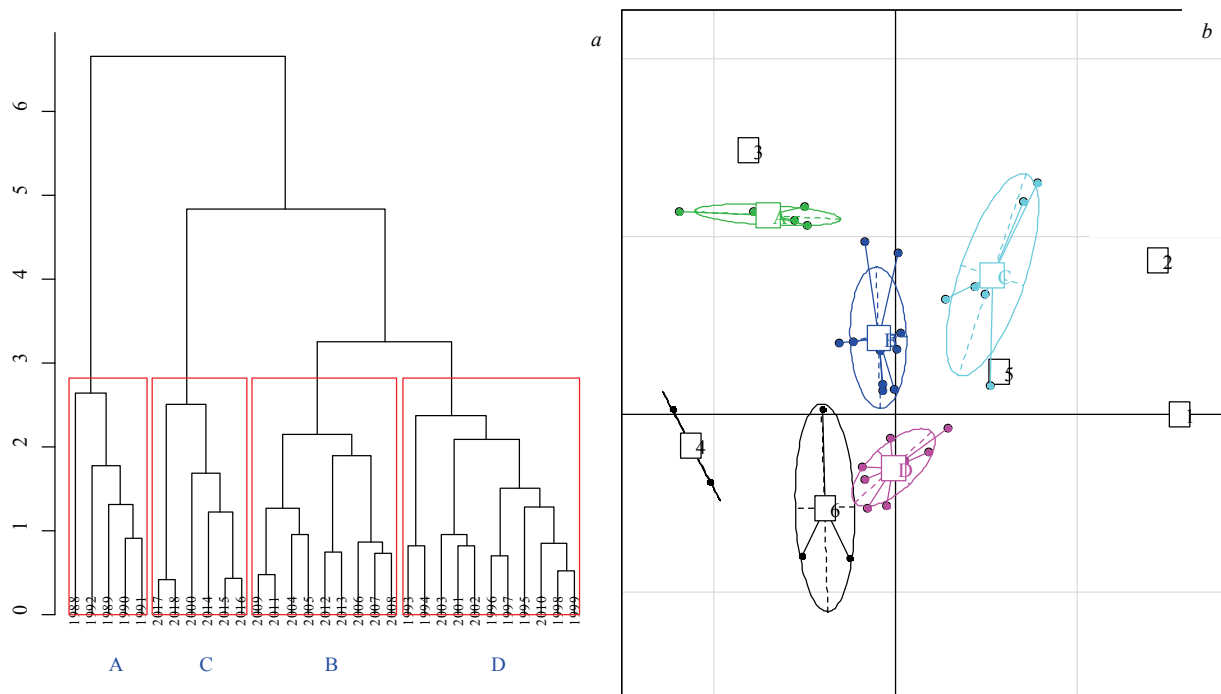


Fig. 6. Cluster analysis of the phylogenetic diversity of bird communities in different years based on the Rao metric (a) and the results of a double analysis of the principal coordinates of the bird community with a phylogenetic matrix as a distance measure (b): the clusters of years on A (rectangles) are corresponded to clusters on B (ellipse); clusters of birds (monophyletic groups) are allocated for evolution period 4 (48 million years ago): 1 – *Alauda arvensis*; 2 – *Anthus campestris*; 3 – *Burhinus oedicnemus*; 4 – *Coturnix coturnix*, *Corvus monedula*; 5 – *Melanocorypha calandra*, *Miliaria calandra*; 6 – *Oenanthe oenanthe*, *Oenanthe isabellina*, *Motacilla flava*

Phylogenetic diversity can reflect the diversity of unknown traits, which is why it was used as a proxy for functional diversity (Webb et al., 2002). Phylogenetic diversity is a key biodiversity attribute when it effectively encompasses unmeasured biological traits that are relevant for ecosystem functioning (Le Bagousse-Pinguet et al., 2019). The quantitative trend of phylogenetic diversity was associated with successive transformations of the bird community, which have a qualitative nature. These qualitative modifications are the basis for the typification of time series. The indicator of the initial period of dynamics (1988–1992) was *Burhinus oedicnemus*. This species is phylogenetically isolated. At present it is listed in the Red Book of Ukraine. Grazing, the disturbance factor, increase in number of feral dogs and crows are considered as the reasons for its population decrease. The demographic parameters of the *Burhinus oedicnemus* demonstrated a total negative trend over time. Sowing or mechanical weeding may be considered as a major factor in the nest destruction of *Burhinus oedicnemus* (Gaget et al., 2019). The decline in bird populations is proportional to the agricultural intensity, and cereal yield alone is able to explain over 30% of the variation in population trends across Europe in the last quarter of the twentieth century (Donald et al., 2001). The decrease of diversity and abundance of insects as a food resource may be one of the possible mechanisms of the effect of agriculture on the habitat quality for birds (Johnson, 2007; Hallmann et al., 2014; Gilburn et al., 2015) and is due to the widespread application of pesticides (Geiger et al., 2010; Mineau & Whiteside, 2013). The diet of the *Burhinus oedicnemus* is known to be based on mollusca, insecta, amphibia, and birds (Amat, 1986) or earthworms, soil-surface arthropods and mollusca (Green et al., 2000). The decrease in the abundance of these animals because of agricultural activity may have caused the monotonous negative trend over time for the *Burhinus oedicnemus* population. The period 1993–2003 was a transitional

one, for which there were no clear indicators, as a characteristic feature of this period was the processes of bird community restructuring. These processes affect events related to the monophyletic group *Oenanthe oenanthe*, *Oenanthe isabellina*, *Motacilla flava*. The increase in abundance of *Oenanthe isabellina*, *Motacilla flava* and substitution of *Oenanthe oenanthe* by the phylogenetically close species *Oenanthe isabellina* should be noted. The peculiarity of the period was a sharp drop in agricultural production and subsequent growth after the stabilization of the socio-economic situation in the country (Zimaroeva et al., 2015, 2019a, 2019b). Obviously, the rapid dynamics of the ecological processes is the reason why there was no clear indicator of this period.

The period 2004–2013 was characterized by the loss of *Burhinus oedicnemus* from the community and a sharp increase in the abundance of *Corvus monedula*. These species are distinguished by their phylogenetic specificity and are located on the periphery relative to the phylogenetic core of the community. This indicates the importance of maintaining the phylogenetic overdispersion of the community as a condition for its sustainable functioning. A higher degree of functional and phylogenetic dispersion in fragmented areas may occur due to the competitive exclusion of closely related species with similar features or resource requirements (Sobral & Cianciaruso, 2016). The phylogenetic overdispersion can be a consequence of a) exclusion due to competition between two closely related species with similar ecological requirements; b) mortality that is determined by the density of closely related species; c) ecological species formation that is affected by habitat differentiation between related species (Cavender-Bares et al., 2004, 2006; Gilbert & Webb, 2007). The rate of evolutionary changes is much lower than the rate of anthropogenic transformation of ecosystems, so the actual causes of phylogenetic overdispersion should be considered as variants a and b.

There was growing importance in the community of such species as *Alauda arvensis*, *Anthus campestris*, and *Melanocorypha calandra* between 2014 and 2018. The species *Alauda arvensis* and *Melanocorypha calandra* are phylogenetically close, while *Anthus campestris* is at a significant phylogenetic distance from them. Such a result also confirms the assumption that phylogenetic overdispersion is an important requirement for the stability of the bird community in anthropogenically transformed landscapes.

Conclusion

After long term research the bird community in agricultural areas was shown to be represented by a very small number of species. The species composition indicates that this community is a derivative of steppe zonal ecosystems. The low diversity of the community leaves an opportunity to maintain its sustainability and to respond to the intensity of dynamics of human pressure and the changing global climate situation. The phylogenetic aspect is an important source of information for assessing the diversity of the bird community of anthropogenically transformed biotopes. The phylogenetic diversity of the bird community demonstrates the presence of trends in both clusterization and overdispersion. The phylogenetic clusterization is found for the dominant bird species, which indicates the ecological homogeneity of the community component, which plays a key role in its functioning. The phylogenetic overdispersion is subject to indicators of diversity that are more sensitive to the number of species than to their abundance. It is this aspect of diversity that reflects a community's ability to adapt to changing environmental conditions. This result underlines the importance of efforts to protect endangered bird species in anthropogenically transformed areas.

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