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INVOLVEMENT OF LOCAL AND NON-LOCAL HUNTERS IN THE TASKS OF THE HUNTING CLUB AS EXEMPLIFIED BY WKŁ 294 HUBERTUS IN BYDGOSZCZ IN THE PERIOD OF TIME BEFORE AND DURING THE COVID-19 PANDEMIC

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Abstract

In Poland, hunting can be practiced only by a member of the Polish Hunting Association (PZŁ). Hunting club (basic unit of PZŁ) members include people residing on the club's premises, as well as non-local hunters. An analysis of hunter involvement in the club's tasks was carried out, on example of the Military Hunting Association no. 294 and covering hunting seasons from the 2018/2019 to the 2021/2022. The research was based on the data available in the PZŁ club system and the club's documentation. Local hunters show greater interest and efficiency during individual hunts. Membership in more than one club does not reduce involvement in the club's activities. Hunters prefer to pay the contribution for the development of the club rather than work it off. Local hunters engage in conducting the animal inventory. The impact of the COVID-19 social restrictions on the increase in hunting activity was ambiguous.

Introduction

In Poland, hunting can be practiced only by members of the Polish Hunting Association (PZŁ). The Association was founded in 1923 and is one of the older ones in Europe (DZIEDZIC 2014). As of 2021, there were 2761 hunting clubs and 127 897 hunters in Poland, including 107 779 (84.27%) hunters who were members of a hunting club and 20 118 (15.73%)

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unaffiliated hunters (CODROW et al. 2021). The number of hunters in Poland has been growing steadily since the founding of the Second Polish Republic (DZIEDZIC 2014, KOŚCIELNIAK-MARSZAŁ 2020, KOZŁOWSKI et al. 2018). Despite this fact, Poland is a country with a small number of hunters compared to other European countries. Hunters constitute 0,4% of the Polish society, whereas the European average is 1% (KROKOWSKA-PALUSZAK et al. 2020).

The basic organizational units within the Polish Hunting Association as well as economic entities of the hunting industry in Poland are hunting clubs. This constitutes one of the most essential features of the Polish hunting model. The hunting clubs have legal personality and are economically independent. Every year, the clubs allocate large sums of money for game management. The members of hunting clubs are natural persons and the clubs are the basic organizational units of the PZŁ implementing hunting objectives and tasks (KOZŁOWSKI et al. 2018). Hunting clubs operate within one or more hunting districts. The supreme authority of the club is the general meeting and day-to-day work is managed by the club's board. All field activities regarding game management, including hunting, are carried out in hunting districts. The districts are leased out for a period of ten years, for which an annual lease fee is charged (DZIEDZIC 2014, Law 1995). Annual hunting plans serve as the basis for game management in the districts. The basic information included in the plan is game species abundance, the acquisition plan for the following management year and a game harvest report for the last management year. The plan is drawn up by the board of the hunting club and then approved by the local forest district. The culled game is the property of the leaseholder or the manager of the hunting district, but the hunter has the right to purchase the carcass of the culled game by paying a fixed amount to the leaseholder or the manager (DZIEDZIC 2014).

RUDY (2020) found that in most hunting clubs, 30–35% of the members hunt systematically. It has not been examined how this involvement is distributed among hunters living on the premises of the leased districts or in their vicinity and those living further away from them. Apart from the hunts, social ties between the hunters are very important in hunting clubs (DANIŁOWICZ 2014), culture, music, painting, collecting and trophy hunting all play an important role in hunting itself (DZIEDZIC 2014). It can thus be assumed that membership in a hunting club goes beyond the implementation of game acquisition plans and involves the social life in the club's community – canoeing, carnival balls, practicing together at the shooting range.

The results of a study by Baranowska et al. (2021) suggest that, especially during a pandemic, the forest may be a particularly popular place for strolls due to the need to avoid crowded places. On 11 March 2020, the World Health Organization declared the SARS-Cov-2 virus outbreak a pandemic. The COVID-related restrictions led to substantial changes in people's lives in all areas, making their situation difficult. According to Talarowska et al. (2020), higher levels of experienced stress were caused by the inability to achieve one's social, cognitive, emotional and spiritual goals. Furthermore, the lower frequency of social contact during this period promoted feelings of loneliness and reduced life satisfaction (Kosowski and Mróz 2020). The COVID-19 pandemic may have temporarily disrupted or blocked the fulfilment of some of the developmental needs and the accomplishment of short-term goals, causing frustration, fear and uncertainty, which may lead to increased emotional stress reflected in depressive and anxiety symptoms. Different age groups perceived these disruptions to a different extent. According to the researchers, people in middle (45–59 years) and late adulthood (over 60 years), who have typically achieved economic, professional and personal stability, may experience fewer changes and less frustration regarding meeting their needs during a pandemic than those in younger age groups. Moreover, these age groups may have more resources and experience in dealing with crises and change. Finally, another factor which varies across age groups and may influence the level of anxiety and depressive symptoms, is the risk to life and health posed by COVID-19, which increases at older age (Applegate and Ouslander 2020, Gambin et al. 2021). As the hunters are of different ages (Codrow et al. 2021, Kowalewski 2011, Potapiuk 2010), their approach to hunting during a pandemic may differ. Stressed, frustrated, lonely and anxious people seek different ways to cope with the tension they experience. Many people seek solace in nature, by fishing or hunting (Karpiński 2022).

Therefore, we decided to examine the involvement of local and non-local hunters in the activity of a hunting club before and during the pandemic, as exemplified by a hunting club which leases two hunting districts located far away from each other and differing significantly in terms of forest cover. Research questions: (1) Which group (local ver. non-local) of hunters participate in hunting more often? (2) How pandemic changed hunters involvement in hunting activities? (3) Is type of hunting district (forest, fields) factor influencing involvement of hunters? (4) Is belonging to more than one hunting club affecting hunter involvement?

Materials and Methods

An analysis of the hunters' involvement was carried out taking as an example the Military Hunting Club (WKŁ) no. 294 Hubertus in Bydgoszcz. The analysis covered four hunting seasons from the 2018/2019 to the 2021/2022. The hunting club holds a lease on two hunting districts, numbered 22/BY "Zalesie" and 210/BY "Świątkowo" and located in the Kujawsko-Pomorskie Voivodeship, which fall under the management of the Regional Board of the Polish Hunting Association in Bydgoszcz (ZO PZŁ). For the purpose of the study, club members residing on the premises of the leased hunting districts and within 30 km from their borders were defined as local hunters. Hunters living further than 30 km from borders of hunting districts are define as non-local hunters.

The analysis was based on data available in the system of the Hunting Clubs of the Polish Hunting Association, including the Electronic Book of Hunting Records, as well as the club's documentation. As engagement or involvement we understand: participation in individual hunts, the number of game animals culled during these hunts, the participation in maintenance work. The hunters' involvement was analyzed with respect to the following areas: participation in individual hunts (number of outings per district per year), implementation of acquisition plans during individual hunts (number of animals per district per year), participation in group hunts (battue) (number of hunters per one hunt). Maintenance work was generally made by outsourcing and hunters pay contribution for it so we skip it in analysis. Local hunters for one district were classified as non-local hunters for the other district. A year-by-year analysis was carried out to examine the impact of COVID-19 restrictions on the hunting activity. As of 31 March 2022, the club has 42 members, including: 6 hunters (14.3%) who reside outside the territory under the management of the Regional Board of the Polish Hunting Association in Bydgoszcz and 9 hunters (21.4%) who reside in Bydgoszcz, amounting to a total of 15 non-local hunters. 19 hunters (45.2%) reside on the premises of the hunting district no. 22 and within 30 km of its borders and 8 hunters (19.0%) reside on the premises of the hunting district no. 210 and within 30 km of its borders. A total of 27 hunters resides on the premises of and around the hunting districts up to 30 km from their borders, which accounts for 61.9% of the total number. 13 hunters are also members of other hunting clubs. Six hunters joined the club during the period of analysis: four local hunters, all from district no. 22, two of whom are members of another club, and two non-local hunters residing on territories under the management of a regional board other than the ZO PZŁ in Bydgoszcz, one of whom is also a member of another club. In the same period, two hunters left the club. One of them, resident on the premises of district no. 22, left in 2018 and was not a member of another club, the other one, a non-local hunter who was also a member of another club, left in 2019. Furthermore, two hunters have gone on three-year leave, one from district no. 22 in 2021 and one from district no. 210 in 2022. Both are not members of other clubs (PZŁ EKEP).

The obtained data was analyzed based on descriptive statistics and statistical inference (ŁOMNICKI 2010, STANISZ 2006; 2007). Basic statistical descriptors included means and standard deviations (±SD). The normality of the distribution of features was tested with the Kolmogorow-Smirnov test, and the equality of variances in different groups with the Levene test. Multivariate analysis of variance and Tukey's post-hoc test were used to determine significant differences in activities taken by local and non-local hunters in general, comparing time before and during pandemic, and comparing hunting districts. The level of statistical significance for all analyzes was assumed to be the minimum $\alpha = 0.05$. Statistical calculations were performed using MS Excel 2019 software (MICROSOFT, REDMOND, WA, USA), STATISTICA 13.3 package (Dell, Round Rock, TX, USA, 2021).

Study site

The hunting district no. 22 is located around 60 km north of Bydgoszcz. It has an area of 9486.00 ha, including the woodland area of 6086.00 ha, its area after exclusions referred to in Article 26 of the Act of 13 October 1995 – Hunting Law amounts to 8392.00 ha (*Bank Danych o Lasach* 2023). During the period of analysis, the club harvested an average of 31.75 red deer; 32.75 roe deer; 64.50 wild boar; 35.50 predators (foxes, raccoon dogs and badgers – two ind. per four seasons) and 17.75 game birds (mallards, green-winged teal and wood pigeons) yearly in this district. Compensation for game and hunting damage averaged 14 356.44 PLN per year (PZŁ EKEP).

The hunting district no. 210 is located around 60 km to the south-west of Bydgoszcz. It has a total area of 4485.00 ha, with woodlands covering an area of 41.00 ha. The area after exclusions is 4185.00 ha (*Bank Danych o Lasach* 2023). During the period of the analysis, the hunters killed, on average, 5.00 red deer; 31.25 roe deer; 11.25 wild boar; 25.25 predators (foxes and raccoon dogs) and 6.50 game birds (mallards, graylag geese and male common pheasants) in the district per year. Compensation for game and hunting damage averaged PLN 1450.00 per year (PZŁ EKEP). In the period of analysis, hares were not hunted in either district despite the presence of this species in both districts. The distance between the districts is about 120 km.

Results

Local hunters participate more frequently in individual hunts and culled more animals than non-local hunters, the results are statistically significant. At the same time, the attendance of non-local hunters at group hunts is higher, but statistically insignificant (Table 1).

Table 1

Number of participants in group hunting, number of individual hunts, number of animals culled during individual hunts, divided into: local hunters and non-local hunters

Hunters	Attendance on group hunts (no. of hunters per one hunt)		Number of individual hunting (per hunting district per hunting season)		Number of animals killed during individual hunting (per hunting district per hunting season)	
	$\bar{x}$	SD	$\bar{x}$	SD	$\bar{x}$	SD
Local hunters	11.4a*	12.5**	322.4*a*	247.3	33.6*a*	21.6
Non-local hunters	13.8*a*	12.1	90.9*b*	63.2	10.7*b*	8.9
F	0.3		13.2		15.4	
p	0.590		0.001		<0.001	

*, **Mean values ± standard deviation (SD) in the columns, followed by different letters indicating significant differences between hunters at $p \leq 0.05$

Comparing time before and during pandemic we can observe significantly higher attendance in group hunts in years 2018–2020 for both groups. Number of individual hunts was higher during pandemic but difference is not significant (Table 2). Comparing involvement of local and non-local hunters in two periods of time we can observe as follow: before pandemic of COVID-19 attendance on group hunts was almost the same, and local hunters were almost four times more often on individual hunts and culled four times more animals. For second period of time (years 2020–2022) non-local hunters were more active for group hunts but difference is not statistically significant. Involvement in individual hunts of non-local hunters incised but still local hunters were more often on individual hunt and culled much more animals (Table 3). To answer research question no. 3 we compared activities of two hunters groups in hunting districts.

Table 2

Activity of individual groups of hunters in collective and individual hunting in the years before and during the pandemic

Hunting season	Hunters type	Attendance on group hunts (no. of hunters per one hunt)		Number of individual hunting (per hunting district per hunting season)		Number of animals killed during individual hunting (per hunting district per hunting season)	
		$\bar{x}$	SD	$\bar{x}$	SD	$\bar{x}$	SD
PP_2018–2020	local hunters	$17.4a^{*}$	13.6^{**}	305.9*a*	252.2	38.5*a*	24.5
P_2020–2022		5.5*b*	8.5	338.9*a*	258.4	28.6*a*	18.6
	F	4.39		0.07		0.83	
	p	0.014		0.799		0.379	
PP_2018–2020	non-local hunters	18.3*a*	11.8	81.5*a*	63.8	10.9*a*	8.8
P_2020-2022		9.4*b*	11.5	100.4*a*	65.4	10.5*a*	9.5
	F	2.32		0.34		0.01	
	p	0.044		0.568		0.935	

[*, **] Mean values ± standard deviation (SD) in the columns, followed by different letters indicating significant differences between hunters at $p \leq 0.0$

Table 3

Activity of individual groups of hunters in collective and individual hunting in the years before and during the pandemic according to time periods

Hunting season	Hunters type	Attendance on group hunts (no. of hunters per one hunt)		Number of individual hunting (per hunting district per hunting season)		Number of animals killed during individual hunting (per hunting district per hunting season)	
		$\bar{x}$	SD	$\bar{x}$	SD	$\bar{x}$	SD
PP_2018–2020	local hunters	$17.4a^{*}$	13.6^{**}	305.9*a*	252.2	38.5*a*	24.5
	non-local hunters	18.3*a*	11.8	81.5*b*	63.8	10.9*b*	8.8
	F	0.02		5.95		9.01	
	p	0.892		0.028		0.009	
P_2020–2022	local hunters	5.5*a*	8.5	338.9*a*	258.4	28.6*a*	18.6
	non-local hunters	9.4*a*	11.5	100.4*b*	65.4	10.5*b*	9.5
	F	0.59		6.40		6.05	
	p	0.457		0.024		0.028	

[*, **] Mean values ± standard deviation (SD) in the columns. followed by different letters indicating significant differences between hunters at $p \leq 0.05$

In field district (no. 210) local hunters were more often on individual hunt and culled more animals, when non-local hunters were more often participated in group hunts but differences were not significant. In forest hunting district (no. 22) attendance on group hunts was almost the same for both groups of hunters, local hunters were significantly more often on individual hunt and culled significantly more animals (Table 4).

Table 4

Activities of local and non-local hunters within hunting districts

Hunting district	Hunters type	Attendance on group hunts (no. of hunters per one hunt)		Number of individual hunting (per hunting district per hunting season)		Number of animals killed during individual hunting (per hunting district per hunting season)	
		$\overline{x}$	SD	$\overline{x}$	SD	$\overline{x}$	SD
O_22	local hunters	$17.0a^{*}$	14.2^{**}	519.3*a*	166.3	48.9*a*	15.0
	non-local hunters	16.3*a*	15.5	139.8*b*	35.4	12.9*b*	7.3
F		0.01		39.8		37.5	
p		0.921		<0.001		<0.001	
O_210	local hunters	5.9*a*	8.1	125.5*a*	121.6	18.3*a*	15.5
	non-local hunters	11.4*a*	8.0	42.1*a*	43.1	8.5*a*	10.2
F		1.9		3.3		2.2	
p		0.191		0.089		0.159	

$^{*,\,**}$Mean values ± standard deviation (SD) in the columns. followed by different letters indicating significant differences between hunters at $p \leq 0.05$

To answer to the question: is belonging to more than one hunting club affecting hunter involvement? We divided previous two groups to two more: (1) member of one hunting club, (2) member of two hunting clubs. Non-local hunters hunting in only one club showed the highest attendance at group hunts (19.6 ±14.4) but difference was non-significant in comparison to three other groups. On other hand local hunters hunting in one hunting club were significantly more often on individual hunts (430.9 ±230.2, $F = 9.34$, $p < 0.001$). In both districts, local hunters hunting in only one club constituted the group with the highest number of individual hunts, the difference being statistically significant ($F = 40.25$, $p < 0.001$). In district no. 22, local hunters hunting in more than one club constituted the second most active group with respect to individual hunting activity, while in district no. 210, non-local hunters hunting in more than one club participated in the hunts more frequently. The highest number of animals in district no. 210 was culled by local hunters hunting in one club. This number was higher, however not statistically significant, than in the remaining three research groups.

Discussion

Studies on the efficiency of recreational hunters have been carried out by, DZIĘCIOŁOWSKI (1992, 2010), KOWALEWSKI (2011), MATTSON (1990a, b), POTAPIUK (2010) and WILL (1973), among others. POTAPIUK (2010) analyzed the data of 862 hunters from east-central Poland, who went on 16 290 individual hunts in the 2006/2007 season. The typical hunter averaged 18.8 outings per year. DZIĘCIOŁOWSKI and MIKOŁAJCZYK (1993) report an average of 50 trips per year for the region of Kielce. ROGERS (1996) reports that in 1991, the average hunter in the USA spent 17 days hunting, and 18 days in 1986. According to MATTSON (1990a), the average Swedish hunter spends 20 days per year hunting. In a study carried out in the region of the Great Masurian Lakes, hunting efficiency was examined over a three-year period (2004–2006). The average number of hunting club members at the study site is 63 and the district area per hunter amounts to 268 ha. The study found that hunters with 31–40 years' hunting experience hunt most frequently, they go on a hunt 28 times a year on average. On the other hand, hunters with more than 50 years of experience go hunting only 9 times a year on average (KOWALEWSKI 2011). In most cases, a recreational hunter spends between 17 and 20 days per year hunting (DZIĘCIOŁOWSKI 2013). The study of hunters from WKŁ 294 Hubertus found that the average number of outings in district no. 22 was 31.4, which corresponds with the values reported in the literature, while in district no. 210 it was 8.0 outings, much less than the numbers reported in the literature.

In addition, POTAPIUK (2010) found that hunter activity, as measured by the number of outings per year, declines with age. Hunters aged 20–29 averaged 21 individual hunting outings per year, three of which were successful. By contrast, hunters over 70 averaged 16 outings per year, of which only one was successful. Hunters with a maximum of 9 years of experience, thus relatively young hunters, were the most efficient group, as two out of their 20 outings were successful. As for species preferences, according to the study by POTAPIUK (2010), wild boar hunts were the most popular (52% of all hunts), followed by roe bucks (13%), foxes (9%), does (8%) and wild ducks (7%). Such preferences were not studied among hunters hunting in the districts leased by WKŁ 294 Hubertus, however, given the greater (at a statistically significant level) hunting participation of hunters in district no. 22, which has a much larger wild boar population than district no. 210, species preferences similar to those of the hunters from east-central Poland may be assumed.

In the study by POTAPIUK (2010), the average distance travelled by a hunter for a single hunt was 58 km, with local hunters travelling 17 km and non-local hunters travelling 102 km. In the case of WKŁ 294 Hubertus, the study showed statistically lower participation in individual hunts among non-local hunters compared to local hunters. This results from the difference in the distance that non-local hunters are required to travel for hunting. At the same time, the analysis showed that non-local hunters participate more frequently in group hunts and that the hunting district no. 22 (with the Tuchola Forest, a large hunting lodge, high forest cover and bigger acquisition plans) is visited more frequently than district no. 210 (with farming monocultures, low acquisition plans, very low forest cover, an area unattractive to tourists and a small hunting lodge). The possible reasons for this include the hunters' desire to socialize and to hunt in more attractive areas, both in terms of hunting and nature, as well as better accommodation. The study also corroborates the conclusions reached by other researchers, which is the fact that recreational hunting is generally inefficient in terms of game acquisition, as game acquisition is not its goal. The goal is to provide recreation to the participants (DZIĘCIOŁOWSKI 2010). In addition, recreational hunting is understood as a long-term use of a natural resource such as wildlife and it goes hand in hand with nature conservation (PALUCH 2006). During the period of the study, non-local hunters constituted a statistically significant proportion of the participants in group hunts which underlines the social aspect of this type of hunting. No difference in hunting involvement was found between members of one or more hunting clubs. Local hunters were found to hunt less frequently during the COVID-19 pandemic and the period of COVID-related social restrictions, and non-local hunters hunted more frequently. This confirms the findings of other studies indicating that the forest is an important site of leisure for people in times of a pandemic (BARANOWSKA et al. 2021, KIKULSKI 2021), as some non-local hunters live in big cities. The activity of local hunters may, on the other hand, support the claims of researchers who believe that the COVID-19 pandemic did not have as much impact on mental health as initially assumed, and that most people experienced a low intensity of anxiety and depressive symptoms in response to it (KIMHI et al. 2021, SAUNDERS et al. 2021, SHEVLIN et al. 2021). However, the study did not examine whether hunters used the forest in other ways during the period of analysis.

Conclusion

Local hunters show greater interest and efficiency when hunting individually than non-local hunters, for whom group hunts seem more attractive. Membership in more than one club does not lead to a decrease in the involvement in the tasks of a club compared to membership in only one club. The hunters show little interest in working off the fee for hunting ground management in the form of maintenance work, they prefer to bear the financial costs instead. Mainly local hunters, engage in keeping the animal inventory, making them a group of people who can help with large-scale monitoring of game populations. The impact of the COVID-19 social restrictions on the increase in hunting activity was ambiguous. The presented study is a pilot study and more detailed analysis of the hunters' activities is needed especially taking into consideration the time and financial requirements for catching one piece of cloven-hoofed game.

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BIOMASS, STEM VOLUME, AND CARBON SEQUESTRATION BASED ON ALLOMETRIC EQUATIONS FOR *POPULUS DELTOIDES* W. BARTRAM EX MARSHALL. PLANTATIONS (A STUDY OF GUILAN, IRAN)

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Key words: allometric equation, correlation, annual increment, regression analysis.

Abstract

Populus deltoides W. Bartram ex Marshall is one of the most important economically (wood production), environmentally (biomass production and carbon sequestration), and fast-growing species in plantations. Therefore, this study aimed to investigate biomass, volume, and carbon sequestration models according to age by using the stem analysis method in poplar plantations in five regions of Guilan province. Measurement features included DBH and the total height of all trees in two plots with one hectare area in each region. 30 trees were randomly selected in different diameter classes and cut down and the discs were obtained in order to stem analysis. The annual rings of discs were counted, ages at different tree heights were obtained, and the diameter of the annual rings was measured to determine the annual diameter and volume increments. Carbon measurement, volume measurement of wood, and volume conversion to weight ratio were calculated. Finally, regression analysis was performed by the relationship between volume and biomass growth by age based on the highest coefficient of determination and minimum standard error. The results showed that the nonlinear models were able to show the highest coefficient of determination (R^2 = 0.93–0.99) and the least standard error of the relationship between these characteristics. These models can be applied for the annual growth assessment of poplar plantations in carbon sequestration and optimal management for achieving sustainable development of the various plantations.

Introduction

Tree allometry is the study of the relationships between tree's stem size, physiology, behavior in biology-associated, and differences in the

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growth rates of the various parts of a tree stem. This allometry represented by equations in the form of regression models. Models could reflect the empirical relationship between biomass and easily measured dendrometrical variables of trees. Therefore, Efficient and accurate models for growth and yield are fundamental tools in forest sciences and play a key role in forest management, planning, and ecological studies. Forests compensate for the urgent need to reduce carbon dioxide at the atmosphere by increasing biomass storage. This solution achieved by increasing forest cover and plantation. Among the tree species, poplar has remarkable characteristics that make it suitable for plantation. Hence, It has become one of the most abundant species used in the world's forests for environmental and economic purposes (FANG et al. 2007). Among the fast-growing tree species, poplar becomes a good option for villagers, wood producers, and owners of the wood industries due to its fast growth, widespread distribution, ability to settle in different conditions, produce timber in the short harvest period, not produce large branches and leaves, rapid capital return investment, high biomass production mainly in stem, the possibility of hybridization, and ease of propagation, the feasibility of simultaneous cultivation with crops, abundant use and extensive in advanced woodworking industries as well as rural and traditional uses such as leaf edibility in animal husbandry (GUO and ZHANG 2010, MOUSAVI KOPAR et al. 2011, ESLAMDOUST and SOHRABI 2017).

The world's forest ecosystems influence carbon dioxide absorption and provide suitable carbon spin and storage conditions (NOBAKHT et al. 2011). Tree growth is important for storing atmospheric carbon in plants and producing biomass. Numerous biomass data and allometric equations have recently been collected to predict above-ground carbon in forest trees and the need to assess carbon stocks for national greenhouse gas balance estimating. It is consequential that accurate allometric equations are available to estimate carbon stocks from field inventory data (ARORA et al. 2014).

Growth means increasing the value of the characteristics (the diameter, height, biomass, and volume) of a living tree over a given period of time. It is one of the main biological components of plants, and the stem analysis method is a way to study the increment that can accurately evaluate the growth characteristics of trees. The principal purpose of this method is to calculate species growth in terms of forest management effects, competition, insect attack, and air pollution (ELAMDOUST et al. 2015). In this method, the tree is cut, split, dried, and weighed to calculate biomass accurately. Although it is a complex and high-cost process method in the operational phase, its integration into the allometric equations could lead to credible results. These equations are the functions that can compute dependent variables through the independent variables, thereby converting direct measurements of trees (diameter and height) into other variables such as biomass (PARSAPOUR et al. 2013). Regression-based approaches are used to construct allometric equations from the generated dataset (MALAKINI et al. 2020).

Many studies have been done on the growth behavior of woody species, especially poplar (PARSAPOUR et al. 2013, ESLAMDOUST and SOHRABI 2017, ESLAMDOUST 2022).

Using the regression analysis to find the relationships between biomass production and poplar characteristics to develop different allometric models between various parts of trees and their carbon sequestration ability showed significant correlations to predict biomass for the whole tree's organs (PARSAPOUR et al. 2013).

Predicting aboveground biomass (AGB) and carbon pools in Hyrcanian mixed-beech forests of Iran was measured by destructive sampling method (weighing 174 fallen trees and recording diameter at breast height (DBH), total height (H), and basic wood density (r) as explanatory variables). Developing allometric equations in ANN (Artificial Neural Network) models showed that the best-designed model for aboveground biomass predicted in the ANN method had higher accuracy than other allometric equations (VAHEDI 2016).

The potential of three fast-growing tree species' carbon storage in biomass, litter, and soil in south Caspian Sea plantations revealed that *P. deltoides* reached the highest biomass and carbon (81%) into the stem (ESLAMDOUST and SOHRABI 2017).

Allometric power equations were fitted based on the bark of *P. deltoides* in Iran and concluded that R^2 ranged from 0.89 to 0.90. These allometric equations provided the best fitted for relationships between total stem dry biomass, dry bark biomass, and DBH (ESLAMDOUST 2022).

An individual-tree diameter growth model was developed using the mixed effects regression method for managed uneven-aged stands of *Quercus* spp. and *Pinus echinata* Mill. in Highlands of Missouri. The model efficiency (R^2) was calculated from 0.26 to 0.57 (LHOTKA and LOEWENSTEIN 2011).

The potential of biomass production and carbon sequestration in the poplar plantations in China showed that biomass production did not differ significantly from seven to ten years, and trees had the highest biomass in the stem and lowest in the leaves. In addition, evaluating and comparing the percentage of diameter increment, basal area, height, and volume of poplar and swamp cypress by stem analysis method showed that the highest current diameter increment of poplar was obtained at four years (5.1 cm), the highest height growth at six years (3.1 m) and the greatest volume of poplar (0.094 m^3) was at the age of eight and concluded that this species to be suitable for economic and environmental plantations (Fang et al. 2007).

The diameter increment, biomass, volume, and carbon sequestration were reported by age in a poplar plantation in India. According to the allometric models, Carbon sequestration rates were calculated from 0.5 to 90.1 mg/ha at the age of 11 by the highest coefficient of determination. In consequence, the poplar was introduced as a suitable solution for sustainable carbon production and global carbon reduction (Arora et al. 2014)

It was evaluated that the general or site-specific allometric equations, using diameter at breast height (as a predictor) are more accurate for estimating stem volume, stem biomass, branch biomass, aboveground woody biomass, and coarse root biomass in 14-year-old poplar plantations. Allometric model selection depended on the objective (yield evaluation, nutrient budget, carbon stocks), tree size, and plantation environmental condition (Fortier et al. 2020)

According to reports, Iran ranks 10th in the world in terms of the area under plantation (1 001 000 hectares (FAO 2020)). The northern Iran is a specific region due to its geographical location in terms of environmental and economic capabilities, and *P. deltoides* plantation has been popular in this region in recent decades (Eslamdoust 2022). But there is no specific model to estimate biomass and carbon in poplar plantations in Guilan province (one of the northern provinces of Iran). Consequently, the present study aims to investigate allometric equations of the biomass, volume, and carbon sequestration of *Populus deltoides* by stem analysis, to provide the best-fitted models for estimating these characteristics by age and supply information based on local condition of poplar plantations in Guilan province.

Materials and Methods

Study area

Five district plantations of *Populus deltoides* W. Bartram ex Marshall. located in Guilan Province, in the north of Iran are considered in this study (Figure 1). The characteristics of the plantations show in Table 1.

Table 1

Characteristics of study areas

District	Age	Site altitude [m.a.s.l]	Area [ha]
1	37	13	89
2	38	70	66
3	37	70	43
4	29	60	48
5	32	-20	38.9

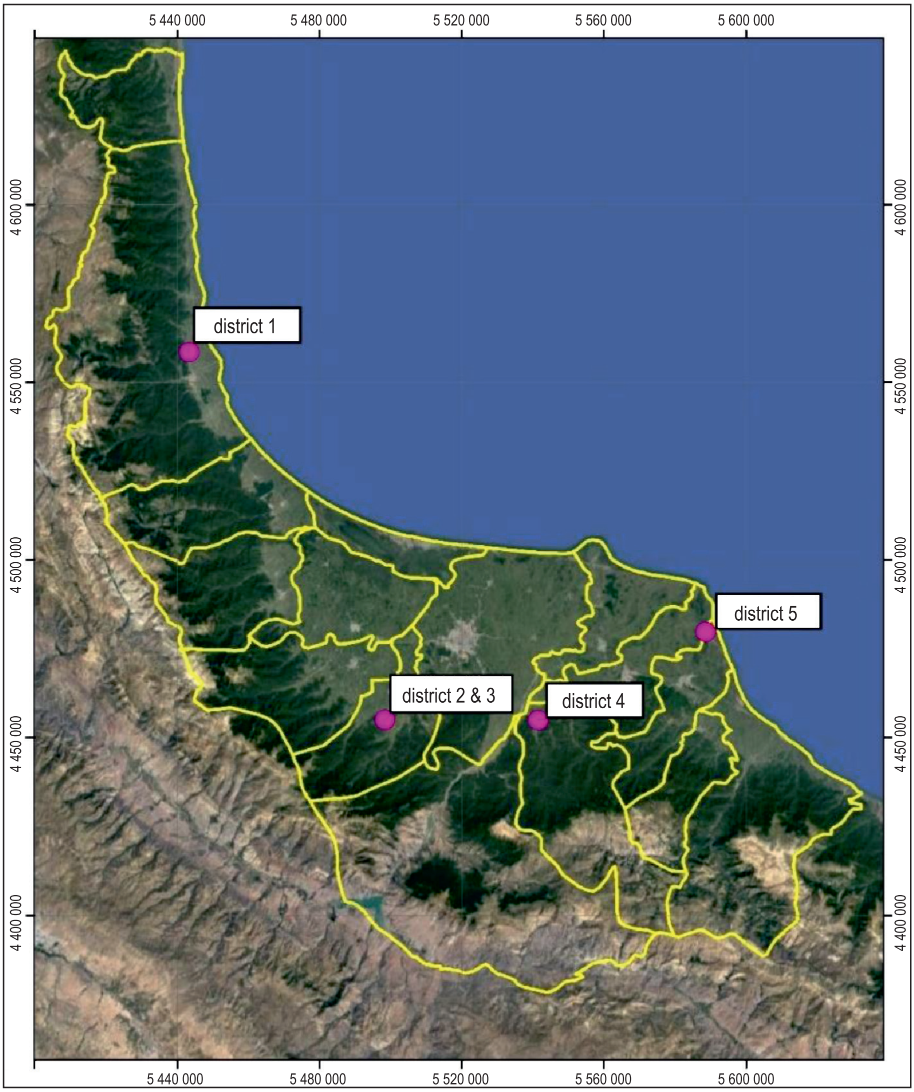

Fig. 1. Geographic location of study areas

Volume estimation

A single sample plot with one hectare area (100 m ×100 m) was sampled in each district of plantation (Arora et al. 2014, Mohammadi et al. 2017). The location of these plots was determined randomly inside the districts because the every district had homogenous stand condition (such as the same DBH classes, height, age and etc.). The diameter at breast height (DBH) and height of all trees were measured in each plot. The estimation of stem volume and compartment biomass at the plantation-scale often requires that trees of various sizes be felled, dissected into components, and weighed or measured. In total, 30 trees were destructively sampled, with regular distribution in diameter classes (Wang 2006, Segura et al. 2006). Data of stem analysis from these trees in different diameter classes across various site types and conditions were combined with plot sample data to calibrate the volume-age, volume increment- age and carbon storage- age equations in the whole stand model (Tian et al. 2020). The biomass and volume data obtained from these destructive sampling procedures are then used to develop allometric equations between a predictor variable that is easily measurable in the field, is usually diameter at breast height (DBH), and response variables, such as stem volume or the biomass of a given tree compartment. Then, these relationships are used to scale compartment biomass and volume at the plantation level using DBH values directly measured on each tree, or on a representative subset of trees of the plantation. Thus, the allometric equations selected have a direct effect on the volume or biomass estimated at the plantation level.

The cut-down trees were stratified into two biomass compartments: stem and branches (with DBH of greater than 10 cm) (Beets et al. 2012, Turner et al. 2012). In order to estimate the stem volume, discs are chosen from a different height of each tree's stems. Stems were cut at a height of 0.3 m from the ground. The trees were felled and cut into logs of acceptable merchantable lengths (2.3 m). At the end of each stem section, a disc with 8 cm thickness was cut and taken to the laboratory for stem analysis. The surface of each disc was sanded smoothly in order to reveal the growth rings. The rings were analyzed for annual increments (Metsaranta and Bhatti 2016). Annual diameter increment of tree-ring data is used to estimate the annual increment of a tree. Tree ring widths were measured by Digimizer graphical program and using dendrochronological methods analysis.

Tree volume is determined based on the tree's diameter and length. The stem is subdivided into sections of which length (L) and basal area (g) are measured; the basal area is either taken at the lower end (g_l) or the upper (g_u) end. Then, the following Smalian's formula is used for volume calculation (Zobeiry 1994):

$$V = \frac{g_l + g_u}{2} \cdot L \tag{1}$$

where:
V – the volume of logs [m^3],
g_l – the basal area at the lower end of trunk [m^2],
g_u – the basal area at the upper end of trunk [m^2],
L – trunk length [m].

Stand volume or stock is calculated by the multiplying volume of each age class by the number of trees per hectare.

The sampled discs were weighed and taken to the laboratory where square sub-samples of 4 cm × 4 cm × 4 cm were oven-dried at 100°C to constant biomass and the dry mass was determined with an electronic balance (Henry et al. 2010). The volume and the dry mass measurements were used to calculate the wood density as below:

$$D_C = \frac{W_0}{V_w} \tag{2}$$

where:
D_c – critical density [gr/cm^3],
W_0 – the dry mass of wood [gr],
V_w – the wet volume [cm^3].

The percentage of organic carbon in 30 stems and branches disc samples was determined by combustion in an electric oven (Arora et al. 2014). This study considered the carbon stored in live biomass as the stem. The amount of carbon sequestrated was obtained when the biomass increased by one unit per age. Finally, the conversion factor of volume to weight per ton of wood was obtained.

Carbon estimation

To measure carbon from 30 felled trees, some stem and branch discs were randomly selected in the diameter classes and transferred to the laboratory for carbon measurement and carbon stored in the tree biomass by combustion in the electric oven (Arora et al. 2014, Haidari et al. 2016). To measure the percentage of organic carbon, the wood was dried in the oven at 105°C for 24 hours (Forouzeh et al. 2008, Ghasemi Nejad Raeini and Sadeghi 2018, Naghdi et al. 2021). The discs that were completely dried were milled by an electric mill and after weighing the samples with digital scales, the samples were placed in the oven and burned for 4 hours at 600°C (Ghasemi Nejad Raeini and Sadeghi 2018). The burned samples were then weighed in the desiccator. By determining the ash weight, initial weight, and organic carbon/ organic matter ratios (eq. 3), the amount of organic carbon in each part was calculated separately (Ghasemi Nejad Raeini and Sadeghi 2018, Forouzeh et al. 2008).

$$OC\% = 0.56OM \tag{3}$$

where:
OC – organic carbon,
OM – organic material.

Results

The quantitative characteristics of the stands including the mean values of diameter, basal area, height, and volume are given in Table 2.

Table 2

Quantitative characteristics of the study areas

District	DBH ±se [cm]	Basal area ±se [m^2/ha]	Height ±se [m]	Volume [m^3/ha]
1	35.04 ± 7.06	19.04 ± 0.04	26.74 ± 5.85	285.33
2	26.59 ± 6.84	19.29 ± 0.03	19.10 ± 4.10	212.29
3	35.67 ± 6.28	7.50 ± 4.9	23.22 ± 3.36	179.36
4	27.59 ± 4.67	13.27 ± 0.02	21.68 ± 1.98	155.58
5	30.68 ± 7.54	10.10 ± 0.04	22.93 ± 4.61	132.48

It was needed coefficients to convert volume to weight in carbon and biomass calculations in this study. The derived coefficients are shown in Table 3.

Table 3

Coefficients used in the analysis

Factor	Value
Wood density [g/cm^3] The conversion factor of volume and total carbon (*t* carbon/m^3)	0.32 $V = 0.1792C$ $R^2 = 0.99$

The diameter at the breast height relative to the age is shown in Figure 2. The relationship between age and diameter is an exponential relationship that is always increasing.

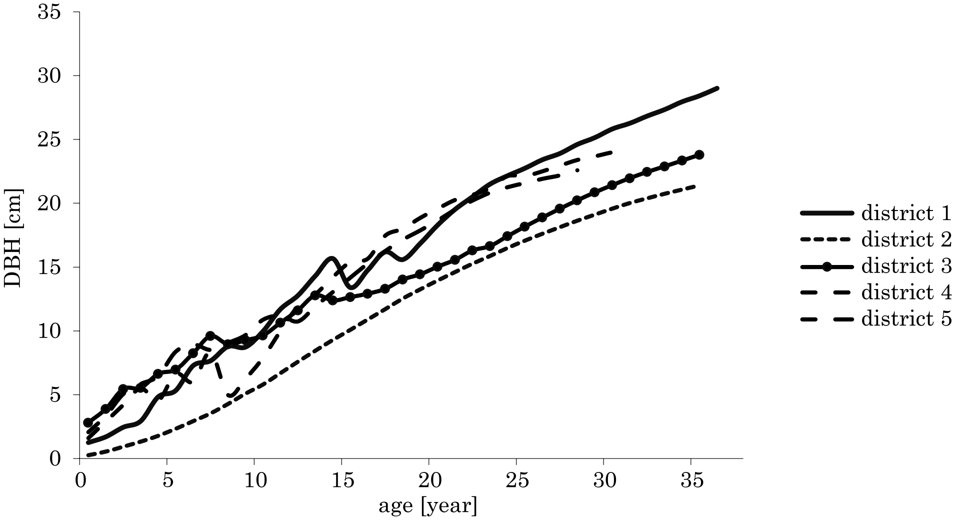

Fig 2. DBH relative to the age in plantations (district 1, district 2, district 3, district 4 and district 5)

The regression analysis of the DBH (*D*) and the stand age (*A*) of the *P. deltoides* plantations is shown in Table 4. This regression equations are very important because DBH is the most easily measurable parameter in the forest that can be obtained by determining its relation to other growth parameters. In these equations, after the formation of the points of DBH equal to age, the equations that have a higher determination coefficient of determination (R^2) and lower standard error (SE) are selected as the most appropriate equations because they show a better pattern of relationship between *D*-*A*. Therefore, according to the results, R^2 had high values with a range from 0.98 to 0.99, and SE was from 0.61 to 0.92. Therefore, the achieved models have sufficient high accuracy to show the relationship between DBH and Age in the studied stands.

Table 4

Dependence of DBH (*D*) and stand age (*A*) in *P. deltoides* plantations

District	Equation	R^2	SE	Kind of distribution
1	$D = 0.12 + \frac{76.05A^{1.13}}{56.43^{1.13} + A^{1.13}}$	0.99	0.67	Dr-Hill
2	$D = \frac{A}{(0.47 + 0.06A - 0.0007A^2)}$	0.99	0.38	resiprocal-quadratic-YD
3	$D = \frac{3.42 + 1.04A}{1 + 0.04A - 0.0003A^2}$	0.99	0.31	Hoerl
4	$D = \frac{2.98 + 0.71A - 1.74}{A^2}$	0.98	0.69	heat capacity
5	$D = \frac{24.24}{(1 + e^{4.07-0.23A})^{0.56}}$	0.98	0.92	Richards

Explanations: *D* – DBH [cm]; *A* – stand age [year]

Stand stock volume in plantations is shown in Figure 3. The volume relation to age showed that the highest volume per hectare is 272.7 m^3 per hectare in district 1 216.2 m^3 per hectare in district 2 247.3 m^3 per hectare in district 3 167.8 m^3 per hectare in district 4, and 91.2 m^3 per hectare in district 5. These volume values occurred at 31, 29, 29, 24 and 21 years, respectively. And according to the principle of diminishing marginal returns, it has been decreasing since these ages.

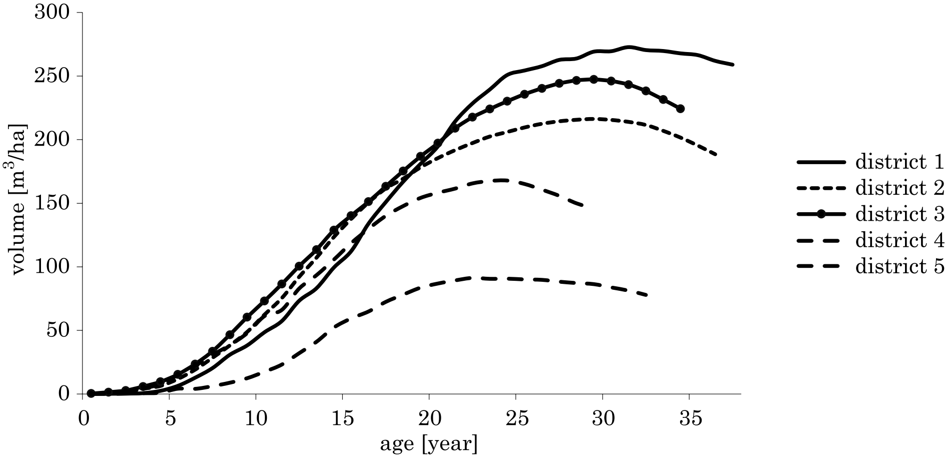

Fig 3. Stand stock volume in study areas (district 1, district 2, district 3, district 4 and district 5)

Volume (V) and age (A) regression analysis of *P. deltoides* plantations are shown in Table 5. Regression analysis of the relationship between volume and age based on the maximum coefficient of determination (R^2) and minimum standard error (SE) for plantations showed that R^2 was 0.99 in all districts and SE ranged from 1.83 (in district 5) to 4.06 (in district 3). Equations that have higher R^2 are more important because they show a better pattern of relationship between volume and age. However, all district's V-A aquations showed the same and high amount coefficient. The resulting regression models had sufficient accuracy and were able to fit the relationship between these two variables (V-A) with acceptable accuracy.

Table 5

Relationship between volume (V) and age (A) in *P. deltoides* plantations

District	Equation	R^2	SE	Kind of distribution
1	$V = 0.017(0.87)^A A^{3.96}$	0.99	3.49	Hoerl
2	$V = 0.13(0.89)^A A^{0.13}$	0.99	2.59	Hoerl
3	$V = \frac{-9.4 + 5.33A}{1 - 0.05A + 0.001A^2}$	0.99	4.06	rational model
4	$V = \frac{-6.39 + 3.57A}{1 - 0.07 + 0.002A^2}$	0.99	1.84	rational model
5	$V = e^{18.30 + \frac{-78.89}{A} - 3.30\ln(A)}$	0.99	1.83	vapor pressure model

Explanations: V – volume [m^3/ha]; A – stand age [year]

The volume increment curve shows the annual volume increment in the plantations in Figure 4. The volume increment was 3.04 m^3/ha/year at the age of 16 years in district 1. The volume increment was 3.9 m^3/ha/year at the age of 9 in district 2. The annual volume increment has the highest amount in this area. Volume increment was 3.07 m^3/ha/year at age 9 in district 3, and it was 2.43 m^3/ha/year at age 10 in district 4. volume has 2.4 m^3/ha/year at age 14 in district 5.

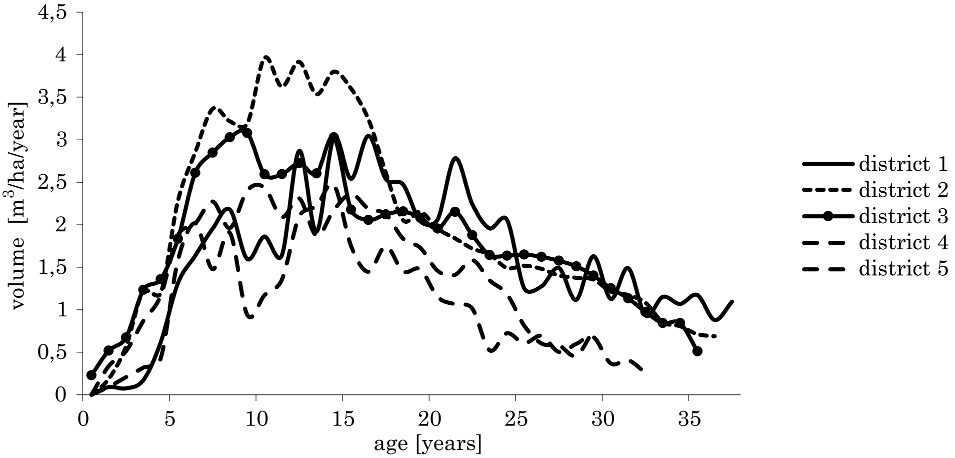

Fig 4. Above-ground volume increment [m^3/ha/year] of study areas (district 1, district 2, district 3, district 4, district 5)

Regression analysis between Annual Volume Increment (AVI) and age (*A*) of *P. deltoides* plantations are shown in Table 6. Equation's coefficient of determination (R^2) ranged from 0.86 to 0.94 in districts and Equation's standard error (SE) ranged from 0.19 to 0.34. The highest equation coefficient of determination was calculated for districts 1 and 2 ($R^2 = 0.94$; SE = 0.25) followed by district 3 ($R^2 = 0.93$; SE = 0.25), district 4 ($R^2 = 0.92$; SE = 0.19), and the lowest for district 5 ($R^2 = 0.86$; SE = 0.34). However, all districts had a high coefficient of determination and all the models in the regression between these two variables (AVI-*A*) were fitted with sufficient accuracy.

Table 6

Relationship between annual volume increment (AVI) and stand age (*A*) in *P. deltoides* plantations

District	Equation	R^2	SE	Kind of distribution
1	$\mathrm{AVI} = 0.83(0.87)^A A^{2.01}$	0.94	0.25	Hoerl
2	$\mathrm{AVI} = \dfrac{0.21 + 0.16A}{1 - 0.13A + 0.008A^2}$	0.94	0.25	rational model
3	$\mathrm{AVI} = \dfrac{0.09 + 0.29A}{1 - 0.09A + 0.01A^2}$	0.93	0.25	rational model
4	$\mathrm{AVI} = 5.09 - 5.60(0.85)^A - 5.60A$	0.92	0.19	exponential plus linear
5	$\mathrm{AVI} = 0.08(0.82)^A A^{2.18}$	0.86	0.34	Hoerl

Explanations: AVI – annual volume increment [m^3/ha/year]; *A* – stand age [year]

The results of the carbon change values by age in the study areas are shown in Figure 5. The process of carbon change is dependent on volume. The amount of carbon increases with volume. Therefore, the pattern of carbon sequestration is similar to the stand volume.

Results showed that carbon values related to age had the highest value of 49.7 tons per hectare in district 1, followed by 46.9 tons per hectare in district 2 45.1 tons per hectare in district 3 30.6 tons per hectare in district 4 and 16.6 tons per hectare in district 5. These carbon values occurred at 31, 32, 29, 24, and 22 years, respectively. These ages were similar to the amounts of the stand volume in relation to age (Figure 3).

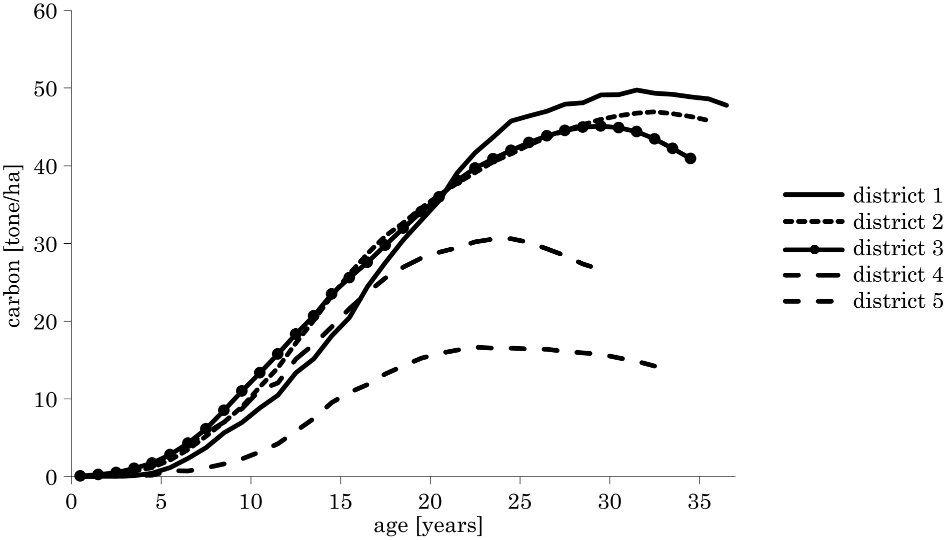

Fig 5. Carbon storage in stand stock in study areas (district 1, district 2, district 3, district 4, district 5)

The results of the regression analysis of carbon dependence (*C*) and the age (*A*) in the study areas are shown in Table 7. The equations show the nonlinear pattern between carbon storage and age in all districts. The best equations are the higher coefficients of determination (R^2) and lower standard errors (SE). All districts had a high coefficient of determination ($R^2 = 0.99$). Equation's standard error (SE) ranged from 0.33 (district 4 and 5 equations) to 0.63 (district 1 equation). Therefore, all the models in the regression between these two variables (*C*-*A*) were fitted with sufficient accuracy.

Table 7

Dependence of carbon [ton/ha] and stand age [year] in *P. deltoides* plantations

District	Equation	R^2	SE	Kind of distribution
1	$C = 0.003 \cdot 0.879^{A} \cdot A^{3.96}$	0.99	0.63	Hoerl
2	$C = 0.024 \cdot 0.891^{A} \cdot A^{3.17}$	0.99	0.46	Hoerl
3	$C = 0.37 \cdot (0.9)^{A} A^{2.97}$	0.99	0.54	Hoerl
4	$C = \frac{-1.16 + 0.65A}{1 - 0.07A + 0.002A^{2}}$	0.99	0.33	rational model
5	$C = e^{16.59 - \frac{78.89}{A} - 3.30\ln(A)}$	0.99	0.33	vapor pressure model

Explanations: C – carbon sequestration [ton/ha]; A – stand age [year]

Discussion and Conclusions

In the study of ESLAMODOUST et al. (2014), the highest volume increment was reported for poplar at the age of eight, while the highest volume increment was nine to ten years old in the present study (Figure 4). This can be attributed to site conditions, planting distance, density, and silvicultural operations on the plantation. In a study by FANG et al. (2007), biomass analysis showed that higher densities have more biomass.

Volume increment variations by age appear due to thinning over the past years, and data on the thinning rate of the study areas are not available. Therefore, the thinning operation effects were not considered in calculations of optimal operating age in the present study.

The allometric equations of biomass estimation for four poplar species demonstrated that the tree stems as a dependent variable produced more accurate models than other variables. Other features such as DBH, height, and bark thickness presented moderate to poor accuracy (PARSAPOUR et al. 2013). In the present study, stem biomass was computed by the stem analysis method. Consequently, highly accurate models have been obtained with a coefficient of determination greater than 0.99 (Tables 4 to 7). Fang et al. (2007) also reported the most accurate models in calculating carbon sequestration from stem biomass analysis.

According to Figure 2, the diameter growth based on age has a sine shape diagram. The diameter growth was fit using inventory data from the growth of 29–38 years in the study areas. Diameter growth was developed using stem analysis by a destructive method.

Allometric relationships are often applied in tree biomass model fitting and described by power-high equations. In the present study, power functions provided a strong fit (R^2 values in the range of 0.93–0.99 and the low value of SE) for biomass estimation of P. deltoides. Moreover, the relationships between stem volume, volume increment, and carbon biomass were in specific age to each stand. Therefore, allometric equations that ignore stand age may lead to inaccurate estimations of tree biomass. Consistent with this finding, PEICHL and ARAIN (2007) found a relationship between allometric equations of aboveground biomass and stand age in other tree species.

Carbon sequestration in plantations is directly related to age (Figure 5). Furthermore, the influence of different factors such as types of species, stand age, and management activities may have made different results from the effect of plantation on carbon (KARAMI-KORDALIVAND et al. 2015). mortality caused a loss in the carbon of the standing budget (Figure 4) (METSARANTA and BHATTI 2016). The modeling of the annual carbon uptake by poplar seedlings explained that the linear logarithmic model in terms of seedling collar diameter had the highest accuracy (VAHEDI et al. 2015). It was in accordance with the results of the present research that all the factors including volume – age, volume increment – age, and carbon – age obtained the high coefficient of determination ($R^2 = 0.99$) and low standard error in the top models. It means that the presented models have a high accuracy and indicate a very high correlation between the parameters in the modeling process and the high accuracy of the computations. Therefore, it can conclude that these models can be used as allometric models and indicators to predict volume, volume increment, and especially carbon sequestration values to save time, cost, and non-destructive sampling in future studies. Even, the models can be applied for the annual assessment of carbon sequestration of poplar plantations for optimal management and achieving sustainable development of the plantations.

In this context, ALEMI et al. (1977) have emphasized that the assessment of forest stands over time depending on the accuracy and type of used models. Therefore, the presentation of highly accurate models would be validated. PARSAPOUR et al. (2013) and ALI et al. (2019) explicated that stem biomass provides a high accuracy for modeling this parameter. On the other hand, it seems that the incorporation of the stem analysis method and allometric equations will lead to the development of high-accuracy models that can be easily documented from their results. It can be used in annual management decisions such as thinning at different ages of plantations to reach the optimum rotation age. Although the stem analysis method is a time-consuming and costly destructive method, its results will be highly documented and reliable. Furthermore, this method is performed for a specific species or a site for one time, and its results can be usable many times. Comparison between destructive and non-destructive carbon sequestration measurement methods showed that the destructive methods had more acceptable accuracy for carbon sequestration evaluation than the non-destructive, and the outputs of all optimized destructive allometric equations have high reliability (VAHEDI et al. 2016). These results can be easily and accurately available for optimal management and operation of plantations.

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NATURAL VALUES OF THE HORBACHYKHA TRACT (KYIV, UKRAINE)

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Key words: Kyiv left-bank floodplane, flora and vegetation, fish, birds, rare species, biotopes.

Abstract

In this article we examined the complex value of Horbachykha floodplain tract of Dnipro River in Kyiv. Its history, flora, vegetation, animal species composition and peculiarities of distribution of rare animal species were studied. Horbachykha tract have natural island origin, and in result of Dnipro regulation in beginning of 20th century finally was formed as left bank flood tract, that in 1960–1970s lost original flood regime. Flora of Horbachykha tract consist of 161 species of vascular plants; 7 rare species of plants and 8 rare vegetation communities were registered. This clearly indicate its natural origin and current semi-natural state. Currently this is the biggest Kyiv left-bank alluvial forest fragment and very significant part of ecological corridor along the Dnipro floodplain. We also registered the presence of rare fauna: 158 species of vertebrate animals, including: 14 fish species, 7 amphibians, 3 reptiles, 132 birds, and 3 mammal species. One of the most important values – complex of rheophilic fish species that still exist according conservated hydrological regime here. A total of 62 bird species were found nesting. The registration of nesting *Otus scops* is only one current and very important registration for whole Kyiv area. This tract area is very important for most of birds migrated along Dnipro River corridor. The settlement of *Castor fiber* (melanistic) – species with high indicator significance was registered in the wetlands of Horbachykha tract. Taking into account the limited transformation of tract area and the presence of rare biodiversity, area of Horbachykha together with the adjacent water area of the Desenka distributary need to be protected initially by landscape reserve of local significance creation. After this including of this tract in National Park “Dnipro Island” strongly recommended.

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Introduction

Most of the Dnipro valley has been transformed by the construction of big reservoirs. On the Middle Dnipro River in the near-natural state of, only separate fragments remained, in particular in Kyiv (KUTSOKON and KOBZAR 2017). In addition, the ecosystems of the Dnipro floodplain are very important for the conservation of the landscape and biological values of the capital of Ukraine. The landscape of Kyiv has changed dramatically over the past 20 years due to development of the city (ROMANENKO et al 2015). Business projects aimed at the development of coastal areas without proper environmental impact assessment and/or its neglect are especially destructive. This leads to the reduction of natural areas in the city. Together with global climate change, this affects the structure and distribution of flora and fauna (PIMM et al 2014). Changes in the typical natural landscape have led to a reduction in the populations and extinction of certain representatives of the flora and fauna of Dnipro River system – islands and floodplain tracts in Kyiv. The remaining ones were included in local, national and international red lists of threatened species (HRYHYK 2019, Red Book of Ukraine, Order of the Ministry of Environmental... No. 29 of January 19, 2021, GODLEVSKA et al 2010). That is why the problem of conservation the original floodplain landscapes now is critically actual. One of the main problems is that most of them are either poorly studied or practically not studied. Some regions of the Antarctic are better studied than most tracts of Kyiv (PARNIKOZA et al 2020). Moreover, some Kyiv tracts and floodplain objects, such as the area of Telbin Lake, Zapisochcha Pivdenne tract, the Gatne Island of, etc., were destroyed and never studied. Studying the nature of Kyiv is important both for its science and conservation. Horbachykha is the left bank tract with the area of 88.0 ha belongs to such areas, is a good example of such a tract, which can be destroyed. At the same time, information about its natural value is very important both for studying the question of how the nature of Kyiv initially looked and for assessing the need and form of protection of this object. The aim of the research is to characterize the history, flora, vegetation and fauna for special attention to protected species of the Horbachykha tract. We also prepared nearest measures for this tract protection.

Materials and Methods

The research was carried out in 2013–2022. The areas of research are shown in Figure 1. The boundaries of the potential landscape reserve of local significance are shown in Figure 2.

Fig. 1. Areas of research: *1* – Northern Bay; *2* – Bobrove Lake; *3* – Rusanivske Lake (upper part); *4* – Rusanivske Lake (lower part); *5* – the Chapline Lake; *6–8* – Desenka distributary

Source: own elaboration based on Google Maps

Fig. 2. Boundaries of the potential landscape reserve of local significance

Source: own elaboration based on Google Maps

The objects of research were the Horbachykha tract history, rare plants, vegetation types as well as vertebrates: fish, amphibians, reptiles, birds and mammals.

The Horbachykha tract history were studied on base of archive of Kyiv Dnipro River system maps collected by I. Parnikoza.

Rare plants and vegetation types were recognized according to following documents: Decision of the Kyiv City Council № 219/940 from 29.06.2000 (List of plants and animals.., 2023), European Red List, 1991 (European… 1992), Green Book of Ukraine (Green Book.., 2009), EU Habitats Directive (Interpretation manual.., 2007), Annex 1 of Resolution No. 4 of Bern Convention, 1996 (Interpretation manual.., 2019). Rare animal species were recognized according to following documents: Red Book of Ukraine (Order of the Ministry of Environmental... No. 29 of January 19, 2021), Appendices II and III of the Bern Convention, Resolution 6 of the Bern Convention, the Habitats and Birds Directive, and the Bonn Convention (GODLEVSKA et al 2010).

Flora and vegetation investigation of Horbachykha tract were realized in the frame of project “List of flora of vascular plants of the islands and floodplain tracts of the Dnipro River, Kyiv (2018)”. All species of vascular plants were collected and determined, why Latin name of the species was presented according to the Plants of the World Online (https://powo.science.kew.org/). Vegetation was described on the basis (TSKUKANOVA 2005, MATUSZKIEWICZ 2008, WYSOCKI and SIKORSKI 2009).

For fauna investigations 8 locations located in different biotope components (lakes, bays, main river stream, coastal strip, shrubs, floodplain forest) were established. Fish were caught with a fry drift net (permit No. 76 dated 22.03.2019, issued by the State Agency of Fisheries), as well as with ichthyological nets and hook-and-line fishing gear. The taxonomy and nomenclature of fish is given according to were carried out according to the official ichthyological website fishbase (FishBase org.). After identification the fish were returned to their natural environment.

Bird counting was carried out by the route-point method. We spent 20 minutes to 1 hour at the selected points 12 x 5 “Arsenal” binoculars and a Nikon P 900, 83x digital camera were used for species identification. The ecological status of birds was determined according to key (FESENKO and BOKOTEY 2002). The probability of nesting was evaluated according to the criteria recommended by the European Ornithological Atlas Committee (EOAC) (*European Breeding...* 1992, *The EBCC Atlas... 1997*). Observations of migratory birds of prey were carried out on September 5 and 30 as well as October 7, 2022. Systematics and nomenclature of birds in the article are given according to (FESENKO and BOKOTEY 2007). The presence of other rare animals: amphibians, reptiles and mammals are determined by tracks on the ground (mammals).

Results and Discussion

Horbachykha tract history

The Horbachykha tract is located within the Dnipro district of the city of Kyiv (Figure 1–2). The tract is a typical example of the Middle Dnipro floodplain tract, which passed from an actively functioning part of the active floodplain to a left-bank tract connected to the mainland coast. In the 19th century, the Horbachykha tract was a part of the river floodplain (once an island, once a left-bank tract) with sand dunes (in Ukrainian "horby") parallel to the Desenka distributary, which stretched from the village of Vygurivshchyna to Mykilska Slobidka. This is where the name of this tract probably comes from.

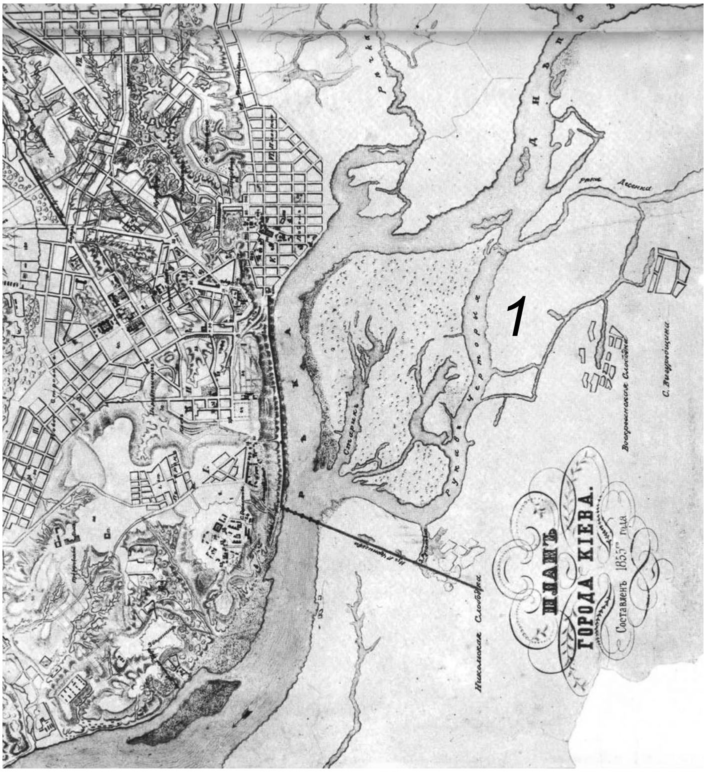

Fig. 3. The nowadays Horbachykha tract (*1*) on the Kyiv map of 1855
Source: own elaboration based on Parnikoza and Prychepa (2022)

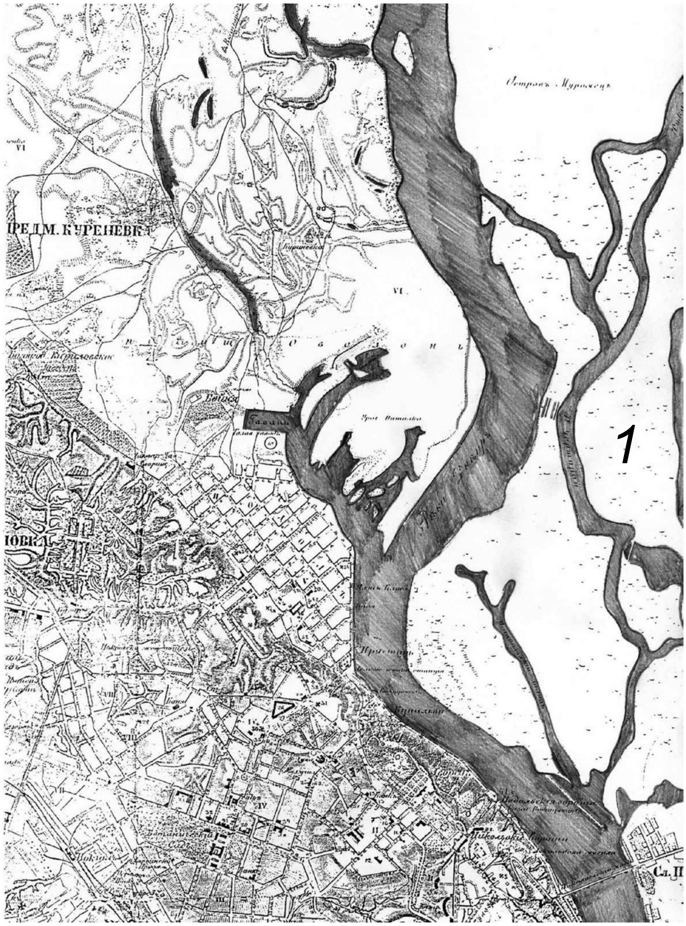

Fig. 4. Nowadays Horbachykha tract (*1*) on the Kyiv map of 1871–1873
Source: own elaboration based on Parnikoza and Prychepa (2022)

According to cartographic data of the middle of the 19th century, around 1855, Horbachykha was an island separated from the left bank coastal floodplain by the branch of Desenka distributary (Figure 3). Thus in 1871–1873, Horbachykha was a coastal tract separated from the mainland's left bank only by a relict bay (currently – Rusanivske Lake). So Horbachykha turned into an island only during regular spring floods (Figure 4). At that time, the tract probably was used by local residents for mowing of local meadows.

The status of the left-bank tract in the case of Horbachykha was fixed by the regulation of the Dnipro in connection with the construction of the Chain Bridge. In the course of this, in 1884, the entrance to the strait separating Horbachykha tract from the left bank was closed. This is how the tract appears on the map of the 1896, 1903, 1910 and 1914 (Figure 5). Instead, some very interesting 1940s details have been preserved on the German map of Kyiv of 1943. Here we can find the local name of Horbachykha at that time – Kodachek (Figure 6). According to VAKULISHYN (2014), the name of the Horbachykha was established at the turn of the 1940s and 1950s.

The construction of the Kyiv and Kaniv hydropower plants led to the slowing of the current and rising of the Dnipro River level. This provides a certain fixation of the current borders of the Dnipro islands and tracts. The limitation of original regular flooding caused a change in vegetation. Most of the Horbachykha is covered by alluvial forest.

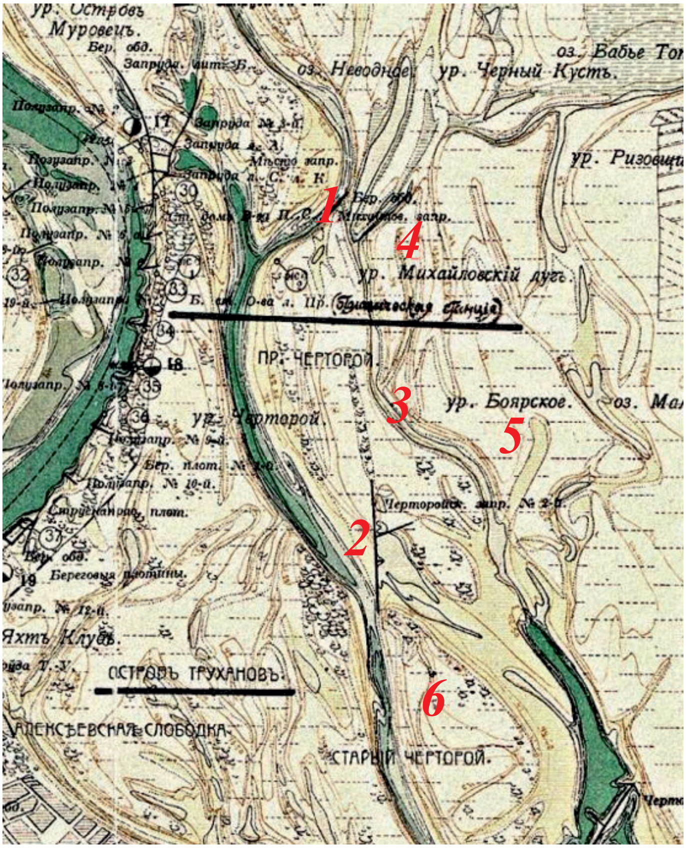

Fig. 5. The nowadays Horbachykha tract on the map of the Dnipro valley in 1914:
1 – Mykhailiv dam; *2* – Chortoriy dam No. 2b; *3* – the former tributary – Rusanivske Lake;
4 – Mykhailivsky Lug tract; *5* – Boyarske tract; *6* – northern part of Dolobetsky Island
Source: own elaboration based on Parnikoza and Prychepa (2022)

Fig. 6. Kodachek tract – the nowadays Horbachykha tract (*1*) on the German map of 1943. An interesting detail that is clearly visible on the map of 1943 is the longer than current length of the Northern Bay of Horbachykha. After all, its long southern corner shown on the map is currently probably flooded after the water level rose when the Kaniv Reservoir was filled
Source: own elaboration based on Parnikoza and Prychepa (2022)

On the Sailing Directions of 1982, for the first time, we meet the hydronym – *Horbachev distributary*, from which the modern name of the tract probably came (Figure 7). From the cartographic materials available to us, the name – *Horbachykha tract* appears for the first time on the scheme of Kyiv in 1989 (Figure 8).

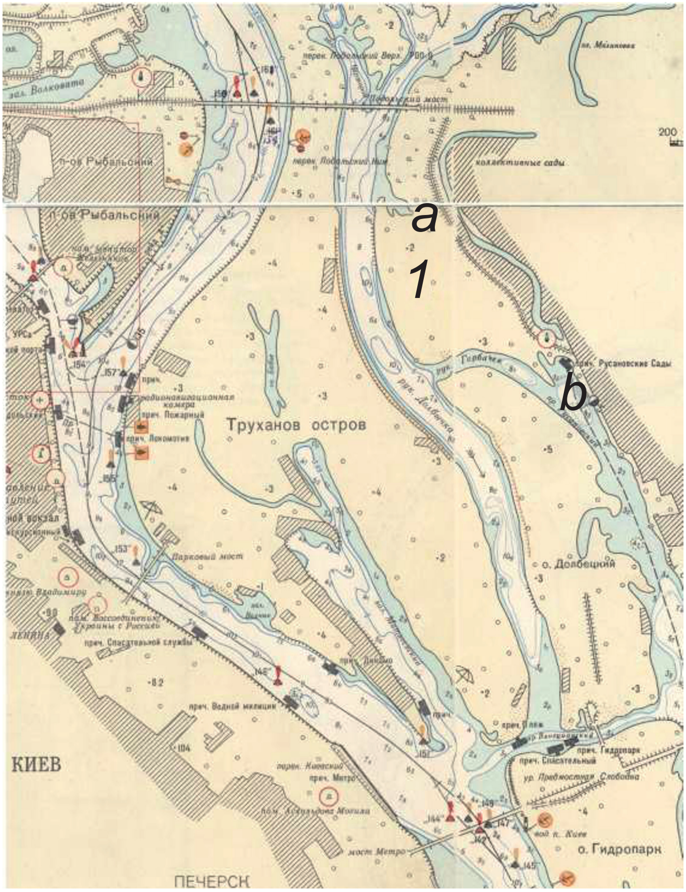

Fig. 7. Horbachykha tract on the 1982 map. The Northern (*a*) and Southern Bays (*b*) are clearly visible, the development of which was probably caused by the rise of the water level with the construction of the Kaniv Reservoir

Source: own elaboration based on Parnikoza and Prychepa (2022)

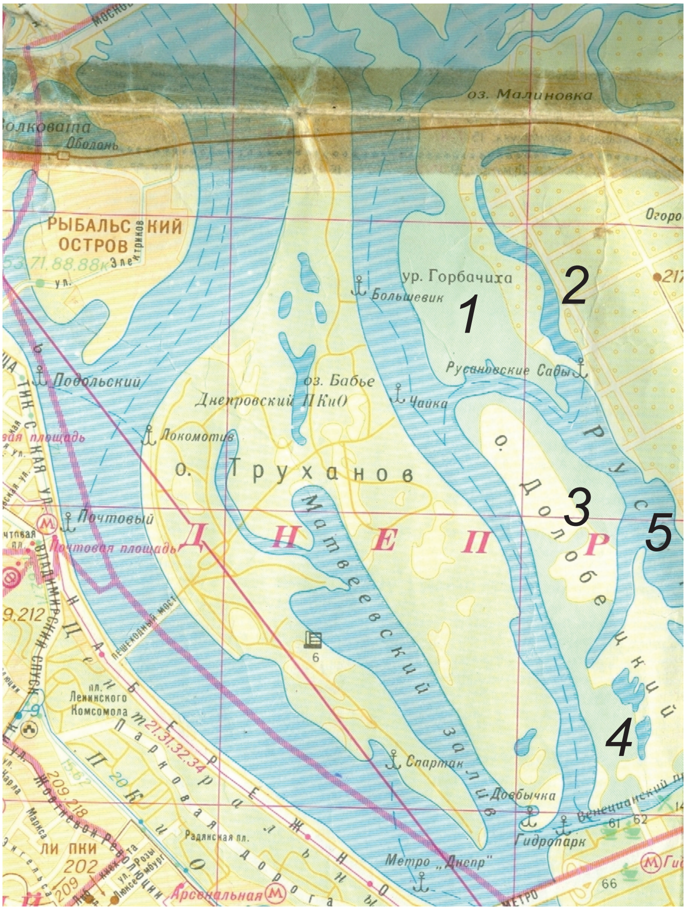

Fig. 8. Horbachykha tract (*1*), Dolobetsky Island (*2*) on the scheme of 1989, Rusanivska Strait (*3*) and the pier *Rusanivski Sady*
Source: own elaboration based on Parnikoza and Prychepa (2022)

Flora and vegetation

In the flora of the tract, 161 species of vascular plants were found, including 1 species of horsetails (Equisetophyta), 2 species of ferns (Polypodiophyta), 1 species of gymnosperms (Pynophyta), and 157 species of flowering plants (Magnoliophyta). For comparison, the flora of the Dnipro Islands and adjacent tracts in Kyiv, according to G. Tsukanova (2005), totals 717 species. So, flora of Horbachykha tract is 22% of total Kyiv`s Dnipro floodplain flora. For the northern Kyiv islands, 267 species of vascular plants were discovered for the “Ptashyny Raj” Regional Landscape Park with area 466.8 ha (KOLOMIICHUK and ONYSHENKO 2018). All rare species are present in the flora of the tract, listed in Table 1.

Table 1

Rare plants species (7 species in total) of Horbachykha tract, Kyiv

Species	Biotope	Base of protection
Nymphaea alba L.	Inner bays of the tract, Chapline Lake	Decision of the Kyiv City Council № 219/940 from 29.06.2000 (List of plants and animals… 2023)
Nuphar lutea (L.) Sm.	Desenka distributary	Decision of the Kyiv City Council № 880/2029 from 23.12.2004 (List of plants and animals… 2023)
Sparganium emersum Rehmann	Riparian vegetation	Decision of the Kyiv City Council № 880/2290 from 23.12.2004 (List of plants and animals… 2023)
Iris pseudacorus L.	Riparian vegetation	Decision of the Kyiv City Council № 880/2290 from 23.12.2004 (List of plants and animals… 2023)
Tragopogon ucrainicus Artemczuk	Xeric sand vegetation	European Red List, 1991 (European… 1992)
Ophioglossum vulgatum L.	Alluvial forest	Decision of the Kyiv City Council № 219/940 from 29.06.2000 (List of plants and animals… 2023)
Teucrium scordium L.	Riparian vegetation	Currently not protected, but as a rare species recommended by us for inclusion in the list of plants protected in the city of Kyiv

As part of the vegetation of the Horbachykha tract, transformed alluvial forests occupy the largest part of the area. They are also the main value of this tract (PARNIKOZA et al 2020). As evidenced by the analysis of archival materials dating from the time before the regulation of the Dnipro River, most of the tract was probably covered with xeric sand meadows, combined with fragments of *Populus-Salix* forests. Currently, in the absence of periodic and long-term flooding, most of the tract is covered with a forest biotope. This is the largest fragment of the alluvial forest on the floodplain of the left bank of the Dnipro within Kyiv. In other near-main channel left-bank floodplain from Vygurivshchyna to Osokorki, such complexes are much smaller (Zapisochcha Pivnichne tract) or very fragmentary (the coast of Berkovshchyna Bay) or irreversibly anthropogenically transformed (Rusanivska and Bereznyakivska embankments). The basis of Horbachykha forests is relic stands of *Populus nigra* Mill. and *Populus alba* L. on more elevated sites, and *Salix alba* L. near inland bays and on low-lying areas that are still subject to flooding in the spring. At the same time, there are very old specimens of these trees (Figures 9 and 10).

Fig. 9. Chapline Lake is surrounded by a stand of alluvial forest created by *Salix alba*, its water area is developed with aquatic vegetation, and along the coast riparian vegetation
Source: photo by I. Parnikoza

Fig. 10. Fragment of xeric sand calcareous grasslands on sand dunes. In the background are the remnants of an alluvial *Populus nigra* forest
Source: photo by I. Parnikoza

Both native and introduced species are present in the local tree-stands: *Ulmus laevis* Pall., *Salix triandra* L., *Pinus sylvestris* L., *Fraxinus excelsior* L., *Quercus robur* L., *Acer negundo* L., *Acer saccharinum* L., *Acer platanoides* L., *Acer tataricum* L., *Sorbus aucuparia* L., *Betula pendula* Roth, *Morus alba* L., *Prunus cerasus* L., *Prunus padus* L., *Prunus tomentosa* Thunb. In the shrub layer the following species were found: *Ribes spicatum* E. Robson, *Sambucus nigra* L., *Viburnum opulus* L., *Cornus alba* L., *Cornus sanguinea* L., *Amorpha fruticosa* L., *Genista tinctoria* L., *Ligustrum vulgare* L., *Physocarpus opulifolius* (L.) Maxim., *Frangula alnus* Mill., *Rosa canina* L., *Rubus caesius* L. Such a diverse composition of species indicates the advance of species not characteristic of the natural floodplain as a result of the loss of the floodplain regime. In the deciduous forests of Horbachykha tract, lianas introduced on the Dnipro floodplain are widespread: *Parthenocissus inserta* (A. Kern.) Fritsch and wild *Vitis vinifera* L. *Viscum album* L., which is important for wintering birds, develops on old specimens of trees.

The herbaceous plants flora of forest biotopes is more diverse in comparison with areas with a water regime close to natural (Ptashyny Island or fragment of alluvial forest near the right-bank abutments of the Northern Bridge). After all, in addition to species that could withstand regular flooding with its cessation, a number of other species spread to the tract spontaneously or through human impact. Currently the following species found where: *Equisetum arvense* L., *Ophioglossum vulgatum* L., *Poa nemoralis* L., *Poa trivialis* L., *Urtica dioica* L., *Geum urbanum* A. Gray, *Geum rivale* L., *Fragaria vesca* L., *Filipendula vulgaris* Moench, *Barbarea stricta* Andrz. ex Besser, *Anthriscus sylvestris* (L.) Hoffm., *Daucus carota* L., *Heracleum sibiricum* L., *Torilis japonica* (Houtt.) DC., *Aristolochia clematitis* L., *Vincetoxicum hirundinaria* Medik., *Achillea millefolium* L., *Achillea setacea* Waldst. & Kit., *Artemisia abrotanum* L., *Mycelis muralis* (L.) Dumort., *Petasites spurius* Miq., *Taraxacum officinale aggr.*, *Impatiens parviflora* DC., *Silene vulgaris* (Moench) Garcke, *Betonica officinalis* L., *Glechoma hederacea* L., *Epilobium montanum* Boiss., *Chelidonium majus* L., *Plantago lanceolata* L., *Plantago major* L., *Rumex crispus* L., *Lysimachia nummularia* L., *Lysimachia vulgaris* L., *Odontites vulgaris* Moench, *Scrophularia nodosa* L., *Asparagus officinalis* L., *Carex hirta* L. and *Brachypodium sylvaticum* (Huds.) P.Beauv. A diverse composition of stands, developed shrubs are important for the existence of a rich fauna here, in particular birds, which will be described in the next section.

In the conditions of Horbachykha tract, the sand dunes are overgrown by *Salix acutifolia* Willd. Fragments of xeric sand communities *of Festuco-Koelerietum glaucae* association with *Festuca beckeri* (Hack.) Trautv. and *Koeleria glauca* DC. (Spreng.) are common on these dunes. *Secale sylvestre* Host, *Eryngium planum* Lapeyr., *Artemisia campestris* Scop. ex Steud., *Centaurea borysthenica* Gruner, *Chondrilla juncea* L., *Tanacetum vulgare* L., *Tragopogon major* Jacq., *Tragopogon ucrainicus* Artemczuk, *Silene tatarica* (L.) Pers., *Hylotelephium maximum* (L.) Holub, *Sedum acre* L., *Sedum sexangulare* L., *Oenothera biennis* L., *Rumex acetosella* Fingerh, *Rumex confertus* Willd., *Rumex thyrsiflorus* Fingerh., *Potentilla* *argentea* L.*, Carex colchica* J. Gay and *Agrostis vinealis* Honck are spread here. In some places there are fragments of the Calamogrostitetum epigeji association formed by *Calamagrostis epigejos* (L.) Roth.

The Desenka distributary area adjacent to the Horbachykha tract is the habitat of well-preserved complexes of riparian and aquatic vegetation. These original vegetation types are characterized by a significant diversity of species: *Ranunculus repens* L.*, Calystegia sepium* (L.) R. Br., *Symphytum officinale* L.*, Myosotis scorpioides* L.*, Berula erecta* (Huds.) Coville*, Bidens tripartita* L.*, Achillea salicifolia* Besser*, Sonchus palustris* L.*, Lycopus europaeus* L.*, Lycopus exaltatus* L.f.*, Mentha pulegium* L.*, Scutellaria galericulata* L.*, Stachys palustris* L.*, Teucrium scordium* L.*, Lythrum virgatum* L.*, Persicaria hydropiper* (L.) Delarbre*, Rumex hydrolapathum* Huds.*, Galium palustre* M. Bieb.*, Valeriana officinalis* L.*, Carex riparia* (R. Br.) Poir.*, Eleocharis palustris* (L.) Roem. & Schult.*, Iris pseudacorus* L.*, Juncus articulatus* L.*, Calamagrostis arundinacea* (L.) Roth, *Catabrosa aquatica* (L.) P.Beauv.*, Glyceria maxima* (Hartm.) Holmb., *Typha angustifolia* L.*, Typha latifolia* L.*, Sparganium emersum* Rehmann*, Butomus umbellatus* L.*, Alisma plantago-aquatica* L. and *Sagittaria sagittifolia* L.

The coast, bays and inland reservoirs of the Horbachykha tract have a rich aquatic vegetation. The following hydrophytes were found here: *Trapa natans* L.*, Stratiotes aloides* L.*, Ceratophyllum demersum* L.*, Myriophyllum spicatum* L.*, Lemna minor* L.*, Lemna trisulca* L.*, Spirodela polyrhiza* (L.) Schleid.*, Najas major* All.*, Potamogeton perfoliatus* L.*, Nymphaea alba* L. and *Nuphar lutea* (L.) Sm.

The trace of the human impact on the ecosystems of the tract is the presence of fragments of ruderal communities and certain species connected with human impact: *Bromus tectorum* L., *Oxalis stricta* L., *Geranium robertianum* L., *Erysimum cinereum* Moench, *Silene baccifera* (L.) Durande L., *Stellaria media* (L.) Vill., *Lepidium densiflorum* Schrad., *Sisymbrium officinale* (L.) Scop. (L.) Scop., *Chelidonium majus* L., *Berteroa incana* (L.) DC., *Phalacroloma annuum* (L.) Dumort. ex F. Mull., *Artemisia vulgaris* L., *Amaranthus retroflexus* L., *Salsola tragus* L., *Artemisia absinthium* L., *Ambrosia artemisiifolia* L., *Helianthus tuberosus* L., *Chenopodium album* L., *Solidago canadensis* L., *Polygonum aviculare* L., *Portulaca oleracea* L., *Linaria vulgaris* Mill., *Echinochloa crus-galli* (L.) P. Beauv. and *Setaria viridis* (L.) P. Beauv. A number of Horbachykha`s plant communities are under protection (Table 2).

Table 2

Protected Values of the communities (8 communities in total) of Horbachykha tract, Kyiv

Biotope	Base for protection	Reference
Community of Salvinieta natantis	Green Book of Ukraine	Green Book… 2009
Community of Nymphaeeta albae (in complex with *Salvinia nutans* and *Trapa natans*)	Green Book of Ukraine	Green Book… 2009
Community of *Nuphareta luteae* (in complex with *Salvinia nutans* and *Trapa natans*)	Green Book of Ukraine	Green Book… 2009
Community of *Trapeta natantis*	Green Book of Ukraine	Green Book… 2009
Natural eutrophic lakes with Magnopotamion or Hydrocharition	EU Habitats Directive or as separate hydrophyte biotopes according to the Annex 1 of Resolution No. 4 of Bern Convention, 1996	Interpretation manual... 2007; Interpretation manual… 2019
Community of arborescent galleries of tall *Salix alba* and *Populus nigra*, 91E0	EU Habitats Directive and Annex 1 of Resolution No. 4 of Bern Convention, 1996	Interpretation manual... 2007; Interpretation manual… 2019
F9.1 Riverine scrub	Annex 1 of Resolution No. 4 of Bern Convention, 1996	Interpretation manual... 2019
Xeric sand calcareous grasslands (6120)	EU Habitats Directive	Interpretation manual… 2007

Vertebrates fauna

Fishes

Presence of 36 fish species belonging to 9 families was recorded over the research period. The ichthyofauna is represented by species native and typical of the Middle Dnipro. In general, 60% of the fish species composition of Kyiv is concentrated here in the water area of the Desenka distributary and internal reservoirs: *Leuciscus leuciscus* Linnaeus, 1758, *Squalius cephalus* Linnaeus, 1758, *Leuciscus idus* Linnaeus, 1758, *Rutilus rutilus* Linnaeus, 1758, *Scardinius erythrophthalmus* Linnaeus, 1758, *Alburnus alburnus* Linnaeus, 1758, *Leucaspius delineatus* Heckel, 1843, *Blicca bjoerkna* Linnaeus, 1758, *Abramis brama* Linnaeus, 1758, *Ballerus sapa* Pallas, 1814, *Ballerus ballerus* Linnaeus, 1758, *Leuciscus aspius* Linnaeus, 1758, *Pelecus cultratus* Linnaeus, 1758, *Rhodeus amarus* Bloch,1782, *Pseudorasbora parva* Temminck & Schlegel, 1846, *Carassius carassius* Linnaeus, 1758, *Carassius auratus* 1758, *Tinca tinca* Linnaeus,1758, *Cobitis taenia* Linnaeus, 1758, *Misgurnus fossilis* Linnaeus, 1758, *Silurus glanis* Linnaeus, 1758, *Esox lucius* Linnaeus, 1758, *Pungitius platygaster* Kessler, 1859, *Syngnathus abaster* Risso, 1827, *Lepomis gibbosus* Linnaeus, 1758, *Sander lucioperca* Linnaeus, 1758, *Perca fluviatilis*, Linnaeus, 1758, *Gymnocephalus cernua* Linnaeus, 1758, *Gymnocephalus baloni* Holcik & Hensel, 1974, *Gymnocephalus acerina* Gmelin, 1789, *Perccottus glenii* Dybowski, 1877, *Neogobius melanostomus* Pallas, 1814, *Ponticola kessleri* Gunther, 1861, *Neogobius fluviatilis* Pallas, 1814, *Babka gymnotrachelus* Kessler, 1857, *Mesogobius batrachocephalus* Pallas, 1814, *Proterorhinus semilunaris* Hockel, 1837. The presence of rare rheophilic (*Leuciscus aspius*, *Leuciscus idus*, *Leuciscus leuciscus, Ballerus sapa*) and limnophilic complexes (*Misgurnus fossilis, Carassius carassius*), is a valuable feature of the reservoirs and streams of the Horbachykha tract. This is evidence of the conservation of key landscape-biotope characteristics for lithophilic (21.6%) and psamophilic (16.2%) ecological groups of fish. The geographical location of the tract near Desenka branching between two islands creates hydrological conditions favourable for the existence of rheophilic fish (whose share in the ichthyofauna is 33.3%) on Desenka. To a large extent, in most watercourses in Kyiv, as a result of a significant transformation, the evolutionarily formed hydroecological conditions of rivers (changes in the flow velocity, deformation and siltation of the channel, the creation of hydraulic structures) were disturbed, which affected the abundance of rheophilic species (ROMANENKO et al. 2015). Such processes are observed on the Pochaina, Vita, Darnytsia, and Sovka rivers. In addition, most small rivers are chained in concrete chutes and collectors like Lybid river (ROMANENKO and MEDOVNYK 2017). Among the representatives of ichthyofauna 14 are rarities; 4 species are included in the Red Book of Ukraine 10 are protected by the Bern Convention (VASYLYUK et al 2019). One of the most abundant fish species in the coastal areas of the Desenka distributary is the *Rhodeus amarus*, the proportion of which reaches 59.8 %. *Rhodeus amarus* occupies the largest percentage (83.2%) among rare fish species. This is due to favourable topographic conditions: a sufficient population of *Bivalvia*, which serve as a spawning substrate for its population. It is a common species that forms a significant percentage of ichthyocenosis in Kyiv's water bodies (KUTSOKON and KOBZAR 2017). The presence of rheophilic fish in the river channel section indicates the natural conservation of the hydrological regime of the ecosystem of Horbachykha tract. Today, due to the regulation of river flow, disturbed hydrological regime and pollution of watercourses with toxic compounds, a significant number of these species have reduced the boundaries of their ranges (DEMCHENKO 2011, TKACHENKO et al 2019). They have ceased to occur at all in some reservoirs and watercourses. That is why the places of their reproduction need to be protected. Because of this, the water area of the Desenka distributary, is an important area as place for reproduction and fattening of young fish of commercially valuable species of the middle Dnipro River.

The little-disturbed hydrological regime provides ecological conditions for fish that actively move along the *Pelecus cultratus, Leuciscus leuciscus* (Figure 11) and *Leuciscus idus* are recorded in the flocks of coastal juveniles in the clean water areas. *Pelecus cultratus* is found during spring migration. In recent years, the number of populations of *Leuciscus leuciscus* and *Leuciscus idus* in the water bodies of Kyiv has significantly decreased. In particular, the species were found in the mouth of the Desna River (TYMOSHENKO et al 2019), as well as Lybid and Syrets Rivers (ROMANENKO and MEDOVNYK 2017). *Leuciscus leuciscus* is characterized by special requirements to habitat conditions – these are areas of watercourses with undisturbed migration routes. It should be noted that in the bays and areas of Desenka distributary adjacent to Horbachykha tract there are wintering holes, which also require protection.

Gymnocephalus acerina is the other protected fish species recorded on Horbachykha tract in deep pits (Figure 12). *Gymnocephalus acerina* and *Leuciscus leuciscus* require stable ecological conditions for reproduction, the change of which leads to a drop in their numbers and impaired reproductive capacity (MOVCHAN 2011). In the past years, *Lota lota* Linnaeus, 1758 was recorded in the Desenka distributary (TKACHENKO et al. 2008). Its presence cannot be excluded near Horbachykha tract. Another important finding is a specimen of *Gymnocephalus baloni* near Dolobetskyi Island (PARNIKOZA et al. 2020). This species is poorly studied, but is included in the list of fish protected by the Bern Convention. It is a river bottom fish that lives in clean, well aerated, fast flowing river sections, mainly near steep banks. *Carassius carassius* Linnaeus, 1758 and *Misgurnus fossilis* were found in Chapline Lake (Table 3). These species live in additional river systems, such as old rivers and floodplain lakes, overgrown with submerged vegetation. Currently, most of what such water bodies in Kyiv have been destroyed as a result of city development.

Cobitis taenia, Linnaeus, 1758 (Figure 13) was found in the researched locations of the Desenka distributary and Rusanivske Lake. It prefers coastal areas of water bodies with moderate current and sandy or muddy-sandy substrate. Its characteristic feature is the ability to exist in lotic and lentic biocenoses, i.e. the species is plastic to different habitats. However, the *Misgurnus fossilis* suffers from the biotic influence of invasive fish species, in particular representatives of the Ponto-Caspian faunal complexes and *Perccottus glenii* Dubowsky, 1877 (KUTSOKON et al. 2021).

Fig. 11. *Leuciscus leuciscus* – a representative of the rheophilic group of fish (listed in the Red Book of Ukraine), which inhabits parts of the Desenka distributary near to sandy beaches, where there is a current

Source: photo by M. Prychepa

Specimens of *Aspius aspius* of different ages are regularly recorded in places with a current.

Fig. 12. *Gymnocephalus acerinus*, a representative of the rheophilic group of fish (included in the Red Book of Ukraine), which inhabits the deep parts of the Desenka distributary

Source: photo by M. Prychepa

Fig. 13. *Cobitis taenia*, representative of limnophilic-rheophilic fish complex (included in Resolution 6 of the Bern Convention)

Source: photo by M. Prychepa

One of the main factors limiting the number of native rheophilic species is the regulation of rivers and disruption of the normal functioning of spawning grounds, in particular, their destruction during the transformation littoral zone. Due to the geographical location of Dolobetsky Island, two arms are formed near Horbachykha tract (Vishnevsky 2021). This creates favourable biotope conditions for the existence and reproduction of rheophilic species. In most water bodies, populations of rheophilic species of the Dnipro floodplain were significantly affected by natural regime transformation. 63.2% of total fauna of rheophiles of Kyiv's water bodies are concentrated in the water area of Desenka within Horbachykha tract. Among them, most have a protected status (included in Appendices II and III of the Bern Convention, Resolution 6 and the Red Book of Ukraine) and form the core of rare species.

Among the studied rare species, the largest fraction has the *Rhodeus amarus* (86.6%) (Table 3). The least represented species are *Carassius carassius*, *Cobitis taenia* and *Misgurnus fossilis*, whose proportion ranged from 0.3 to 0.8%.

Table 3

Species that have the status of protection (14 species in total) in the reservoirs and watercourses of Horbachykha tract, Kyiv

Species	Biotops	Conservation status	Proportion [%]
1	2	3	4
Leucaspius delineatus	Desenka water area	Appendix III of the Bern Convention*	3.3
Leuciscus leuciscus	Desenka water area	The Red Book of Ukraine***	2.3
Idus idus	Desenka water area	The Red Book of Ukraine***	2.5
Aspius aspius	Desenka water area	Appendix III of the Bern Convention* Resolution 6 of the Bern Convention**	1.5
Ballerus ballerus	Desenka water area	Appendix III of the Bern Convention**	0.5
Ballerus sapa	Desenka water area	Appendix III of the Bern Convention*	0.3
Pelecus cultratus	Desenka water area	Appendix III of the Bern Convention*, Resolution 6 of the Bern Convention**	3.1
Rhodeus amarus	Riparian vegetation of Chapline Lake, inner bays of the tract	Appendix III of the Bern Convention*, Resolution 6 of the Bern Convention**	83.2
Carassius carassius	Riparian vegetation of Chapline Lake	The Red Book of Ukraine***	0.3

cont. Table 3

1	2	3	4
Cobitis taenia	Desenka water area	Appendix 3 of the Bern Convention*, Resolution 6 of the Bern Convention**	0.5
Misgurnus fossilis	Riparian vegetation of Chapline Lake	Resolution 6 of the Bern Convention**	0.8
Silurus glanis	Desenka water area	Appendix III of the Bern Convention*	0.5
Gymnocephalus acerinus	Desenka water area	The Red Book of Ukraine***	1.0
Gymnocephalus baloni	Desenka water area	Resolution 6 of the Bern Convention**	0,3

Explanations: *Godlevska et al (2010); **Vasylyuk et al (2010); ***Order of the Ministry of Environmental... No. 29 of January 19, 2021

Based on the results of ichthyofauna research, the distribution of species in relation to the current was analysed. It was established that the majority of rare species are rheophiles (61.5%). Limnophiles and indifferent accounted for 15.4 and 23.1% (Figure 14).

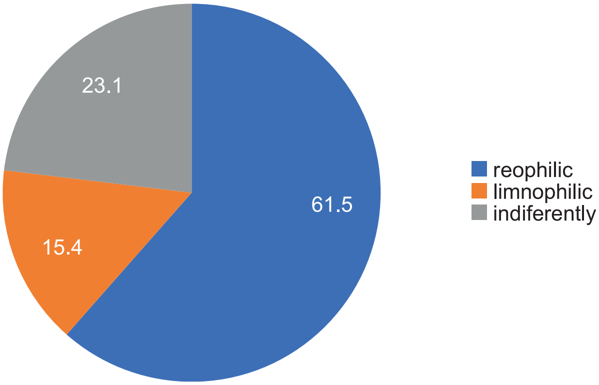

Fig. 14. Fractions [%] of rare fish species depending on biotope in the reservoirs and watercourses of Horbachykha tract, Kyiv

Amphibians and reptiles

According to data (Nekrasova 2008, Nekrasova 2010), 10 species of amphibians have been registered within the Dnipro floodplain in Kyiv. Amphibians and reptiles are a group of animals sensitive to environmental conditions. This is evidenced by the decline in the number of certain species in river floodplains since the 1940s in European countries (Gonçalves et al. 2016, Shulse et al. 2010). This is due to the reduction of biotopes suitable for breeding as a result of habitat destruction. It's true for the *Bombina bombina* Linnaeus, 1758 (Bern Convention), which is reducing its range as a result of a decrease in the number of biotopes typical for the species, such as old rivers and temporary reservoirs (Pupina et al 2018).

Batrachofauna of studied tract includes 7 species: *Lissortiton vulgaris* Linnaeus, 1758, *Bombina bombina, Pelobates fuscus* Laurenti, 1768*, Bufo bufo* Linnaeus, 1758*, Rana arvalis* Nilsson, 1842*, Pelophylax ridibundus* Pallas, 1771*, Hyla arborea* Linnaeus, 1758. The registered species are distributed in water and forest biotopes. For comparison, 5–7 species were found in similar biocenoses located on the Zhukiv, Muromets, and Trukhaniv islands (Parnikoza, 2020). Herpetofauna is represented by 3 species: *Lacerta agilis* Linnaeus, 1758, *Emys orbicularis* Linnaeus, 1758*, Natrix natrix* Linnaeus, 1758. The most typical representative of the reptile taxon in the tract is *Emys orbicularis*. Different age groups of this species were found in significant numbers in Chaplyne Lake. Currently, this species is vulnerable, especially at the borders of its range, since, in addition to changing climatic conditions (Nekrasova et al. 2021). All species of amphibians and reptiles are subject to protection and are included in Appendixes II and III of the Bern Convention.

Avifauna

227 species have been registered in the avifauna of the Dnipro floodplain (Parnikoza et al 2020). We recorded a significant species diversity of rare or endangered birds. The avifauna of Horbachykha tract is represented by 144 species belonging to 40 families (37.6% of total avifauna of Kyiv). Most species of avifauna are representatives of forest biotopes. The presence of floodplain forests on the area of the tract has a significant impact on the formation of the ornithocomplex and its structure. In general, these are typical representatives of the Dnipro floodplain: *Columbia polumbus* Linnaeus, 1758*, Streptopelia turtur* Linnaeus, 1758, *Corvus corax* Linnaeus, 1758, *Certhia familiaris* Linnaeus, 1758, *Aegithalos caudatus* Linnaeus, 1758, *Parus palustris* Linnaeus, 1758, *Coccothraustes coccothraustes* Linnaeus, 1758, *Fringila coelebs* Linnaeus, 1758, *Turdus philomelos* C.L. Brehm, 1831, *Oriolus oriolus* Linnaeus, 1758, *Sylvia atricapilla* Linnaeus, 1758, *Erithacus rubecula*, Linnaeus, 1758, *Troglodytes troglodytes*, Linnaeus, 1758, *Phylloscopus sibilatrix* Bechstein, 1793, *Ficedula albicollis* Temminck, 1815, *Muscicapa striata* Pallas, 1764. To a large extent, the avifaunistic complex of the Horbachykha tract is similar to the

rest of the Dnipro islands, in particular Muromets, Trukhaniv, Zhukiv Islands, and Hydropark (connected Dolobecky and Venetian Islands) (KOSTUSHYN 1994). That is why an important stage in the formation of an eco-network is the creation of local protected tracts with a protective status in order to preserve typical and rare representatives of the bird fauna. Given the total pressure of the city on various components of the biota, this disrupts migration processes and fragments biotopes (construction of roads, houses, entertainment centres). A small participance of meadow birds compared to the Muromets Island is related to the peculiarities of the local vegetation. In general, there are nesting groups of campophile birds in open areas: *Emberiza citrinella* Linnaeus, 1758, *Saxicola rubetra* Linnaeus, 1758, *Motacilla flava* Linnaeus, 1758, *Lanius collurio* Linnaeus 1758. As for wetland species, the Desenka water area is visited by many representatives of Charadriformes during trophic migrations, which increases the general biodiversity of the tract compared to Trukhaniv Island or the Hydropark, where, as a result of excessive recreation and construction of a large part of the coastal strip, this species stopped relatively rarely. It should be noted that the dominance of alluvial forests in the landscape-biotope structure of the Horbachykha tract creates favourable conditions for migrating and wintering of forest birds. In the future, a detailed description of the rare avifauna of the Horbachykha tract will be carried out, in particular connections with the landscapes and biotopes.

The fraction of Horbachykha`s rare species is 24.8% In the researched biotopes of the tract, 67 species are nesting, which is slightly higher than the faunal indicators of the avifauna of Veliky (Pivnichny) Island, Muromets, Trukhaniv, Hydropark, where 36-55 bird species are concentrated (KOSTUSHYN 1994). It should be noted that a significant fraction of nesting species is hollow nesting birds, which is 13.2% (19 species). Piciformes made up 10.4% (7 species) Especially important are the findings of nesting settlements of the *Picus canus* Gmelin, 1788 and the *Dryocopus martius* Linnaeus, 1758 (Resolution 6 of the Bern Convention). These species for nesting use alluvial poplar and willow forests (Table 4).

On the Desenka distributary and Chaplyne Lake, there are species that are biotopically adapted to aquatic and coastal biotopes, in particular, ichthyophages (Ardeidae and Laridae), which used them during foraging migrations (Table 4). During the winter period, representatives of the Anatidae family can be found on open water: *Anas crecca* Linnaeus, 1758, *Bucephala clangula* Linnaeus, 1758, *Aythya fuligula* Linnaeus, 1758, *Mergus albellus* Linnaeus, 1758, *Mergus serrator* Linnaeus, 1758, *Mergus merganser* Linnaeus, 1758.

It should be noted about the nesting colonies (10–15 pairs) of the *Chlidonias hybrida* Pallas, 1811 located on a *Trapa natans* cover south of the Horbachykha tract. Every year, the *Haematopus ostralegus* Linnaeus, 1758 (The Red Book of Ukraine) is observed on flooded stumps along the Desenka distributary. There are conditions allowing us to believe that the species periodically nests within the floodplain.

Table 4

Species that have the status of protection (132 birds' species in total) registered on Horbachykha tract, Kyiv

Species	Biotope	Conservation status
1	2	3
Gavia arctica Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bonn Convention*, Resolution 6 of the Bern Convention**
Podiceps nigricollis C.L. Brehm, 1831	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Podiceps cristatus Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Podiceps ruficollis Pallas, 1764	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Phalacrocorax carbo Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention*
Ardea cinerea Linnaeus, 1758	riparian vegetation	Appendix II of the Bern Convention*
Egretta alba Linnaeus, 1758	riparian vegetation	Appendix II of the Bern Convention, Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bonn Convention*, Resolution 6 of the Bern Convention**
Nycticorax nycticorax Linnaeus, 1758	wetland shrubs	Appendix II of the Bern Convention*, Resolution 6 of the Bern Convention**
Ixobrychus minutus Linnaeus, 1766	riparian vegetation	Appendix II of the Bern Convention, Appendix II of the Bonn Convention, Council Directive 2009/147/EC on the conservation of wild birds* Resolution 6 of the Bern Convention**
Ciconia ciconia Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention
Anser anser Linnaeus, 1758	riparian vegetation	Appendix II of the Bern Convention, Appendix I and II of the Bonn Convention*
Anser albifrons Scopoli, 1769	channel part of the river	Appendix II of the Bern Convention, Appendix I and II of the Bonn Convention*
Cygnus olor Gmelin, 1789	channel part of the river	Appendix III 3 of the Bern Convention, Appendix II of the Bonn Convention*

cont. Table 4

1	2	3
Anas platyrhynchos Linnaeus, 1758	riparian vegetation	Appendix III of the Bern Convention, Appendix II of the Bonn Convention*
Anas crecca Linnaeus, 1758	riparian vegetation	Appendix III of the Bern Convention, Appendix II of the Bonn Convention*
Anas querquedula Linnaeus, 1758	riparian vegetation	Appendix III of the Bern Convention, Appendix II of the Bonn Convention*
Anas penelope Linnaeus, 1758	channel part of the river	Appendix III of the Bern Convention, Appendix II of the Bonn Convention*
Aythya fuligula Linnaeus, 1758	channel part of the river	Appendix III of the Bern Convention, Appendix II of the Bonn Convention*
Bucephala clangula Linnaeus, 1758	channel part of the river	The Red Book of Ukraine***, Appendix III of the Bern Convention, Appendix II of the Bonn Convention*
Mergus albellus Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention*
Mergus merganser Linnaeus, 1758	channel part of the river	Appendix III of the Bern Convention, Appendix I, II of the Bonn Convention*
Mergus serrator Linnaeus, 1758	channel part of the river	The Red Book of Ukraine***, Appendix III of the Bern Convention, Appendix I, II of the Bonn Convention*
Pandion haliaetus Linnaeus, 1758	channel part of the river	The Red Book of Ukraine***, Appendix II of the Bern Convention, Appendix II of the Bonn Convention *
Pernis apivorus Linnaeus, 1758	alluvial forests	Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention* Resolution 6 of the Bern Convention**
Milvus migrans Bodaert, 1783	alluvial forests	The Red Book of Ukraine***, European Red List*, Appendix 2 of the Bern Convention, Appendix I, II of the Bonn Convention*
Circus cyaneus Linnaeus, 1758	open habitats	Council Directive 2009/147/EC on the conservation of wild birds, The Red Book of Ukraine***, Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention*
Circus pygargus Linnaeus, 1758	open habitats	The Red Book of Ukraine*** Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Circus aeruginosus Linnaeus, 1758	open habitats	Council Directive 2009/147/EC on the conservation of wild birds, Appendix II 2 of the Bern Convention*, Appendix II of the Bonn Convention*, Resolution 6 of the Bern Convention**

cont. Table 4

1	2	3
Accipiter gentilis Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Accipiter nisus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Buteo buteo Linnaeus, 1758	open habitats	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Buteo lagopus Pontoppidan, 1763	open habitats	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Circaetus gallicus Gmelin, 1788	open habitats	Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bern Convention, Appendix II of the Bonn Convention*, The Red Book of Ukraine***
Aquila pomarina C.L.Brehm, 1831	open habitats	Council Directive 2009/147/EC on the conservation of wild birds, The Red Book of Ukraine, Appendix II of the Bern Convention, Appendix II of the Bonn Convention* Resolution 6 of the Bern Convention**
Haliaeetus albicilla Linnaeus, 1758	channel part of the river	Council Directive 2009/147/EC on the conservation of wild birds, The Red Book of Ukraine, Appendix II of the Bern Convention, Appendix II of the Bonn Convention*, Resolution 6 of the Bern Convention**
Falco subbuteo Linnaeus, 1758	open habitats	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Falco tinnunculus Linnaeus, 1758	open habitats	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Falco vespertinus Linnaeus, 1766	open habitats	Council Directive 2009/147/EC on the conservation of wild birds, IUCN, European Red List, Appendix II of the Bern Convention, Appendix II of the Bonn Convention*, Resolution 6 of the Bern Convention**
Porzana porzana (Linnaeus, 1758)	riparian vegetation	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Fulica atra Linnaeus, 1758	riparian vegetation	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Gallinula chloropus Linnaeus, 1758	riparian vegetation	Appendix III of the Bern Convention*
Grus grus Linnaeus, 1758	open habitats	Appendix II of the Bern Convention* The Red Book of Ukraine***, Appendix II of the Bonn Convention*
Charadrius dubius Scopoli, 1786	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*

cont. Table 4

1	2	3
Tringa ochropus Linnaeus, 1758	channel part of the river, chaplyne lake	Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention
Tringa glareola Linnaeus, 1758	channel part of the river, chaplyne lake	Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention
Tringa nebularia Gunnerus, 1767	channel part of the river	Appendix III of the Bern Convention, Appendix I, II of the Bonn Convention*
Actitis hypoleucos Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention*
Philomachus pugnax Linnaeus, 1758	channel part of the river	Appendix III of the Bern Convention, Appendix I, II of the Bonn Convention, Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Calidris alpina Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention, Appendix I, II of the Bonn Convention*
Calidris ferruginea Pontoppidan, 1763	channel part of the river	Appendix II of the Bern Convention, Appendix 1, 2 of the Bonn Convention*
Scolopax rusticola Linnaeus, 1758	alluvial forests	Appendix III of the Bern Convention, Appendix I, II of the Bonn Convention*
Larus minutus Pallas, 1776	channel part of the river	Appendix II of the Bern Convention*
Larus ridibundus Linnaeus, 1758	channel part of the river	Appendix III of the Bern Convention*
Larus canus Linnaeus, 1758	channel part of the river	Appendix III of the Bern Convention*
Chlidonias hybrida Pallas, 1811	channel part of the river	Appendix III of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Chlidonias leucopterus Temminck, 1815	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Chlidonias niger Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention, Appendix II of the Bonn Convention Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Hydroprogne caspia Pallas, 1779	channel part of the river	Appendix II of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bonn Convention*, The Red Book of Ukraine***, Resolution 6 of the Bern Convention**,

cont. Table 4

1	2	3
Sterna albifrons Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bonn Convention*, The Red Book of Ukraine***, Resolution 6 of the Bern Convention**
Sterna hirundo Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds, Appendix II of the Bonn Convention*, Resolution 6 of the Bern Convention**
Streptopelia decaocto Frivaldsky, 1838	alluvial forests	Appendix III of the Bern Convention*
Streptopelia turtur Linnaeus, 1758	alluvial forests	Appendix III of the Bern Convention*
Cuculus canorus Linnaeus, 1758	riparian vegetation	Appendix III of the Bern Convention*
Asio otus Linnaeus, 1758	alluvial forests	Appendix III of the Bern Convention*
Strix aluco Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Otus scops Linnaeus, 1758	open habitats	The Red Book of Ukraine***, Appendix II of the Bern Convention*
Apus apus Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Alcedo athis Linnaeus, 1758	channel part of the river, chaplyne lake	Appendix II of the Bern Convention, Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Merops apiaster Linnaeus, 1758	open habitats	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Upupa epops Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Junx torquilla Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Dryocopus martius Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention, Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Picus canus Gmelin, 1788	alluvial forests	Appendix II of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Dendrocopos major Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Dendrocopos minor Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*

cont. Table 4

1	2	3
Dendrocopos syriacus Hemprich et Ehrenberg, 1833)	alluvial forests	Appendix II of the Bern Convention Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Dendrocopos medius Linnaeus, 1758	alluvial forests	Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Riparia riparia Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention*
Hirundo rustica Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Delichon urbica Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Motacilla flava Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Motacilla alba Linnaeus, 1758	channel part of the river	Appendix II of the Bern Convention*
Lanius collurio Linnaeus, 1758	open habitats	Appendix II of the Bern Convention, Council Directive 2009/147/EC on the conservation of wild birds*, Resolution 6 of the Bern Convention**
Lanius excubitor Linnaeus 1758	open habitats	Appendix II of the Bern Convention, The Red Book of Ukraine***, Resolution 6 of the Bern Convention**
Oriolus oriolus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Corvus corax Linnaeus, 1758	alluvial forests	Appendix III of the Bern Convention*
Bombucilla garrulus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Troglodytes troglodytes Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Acrocephalus scirpaceus Hermann, 1804	riparian vegetation	Appendix II of the Bern Convention*
Acrocephalus arundinaceus Linnaeus, 1754	riparian vegetation	Appendix II of the Bern Convention*
Hippolais icterina Vieillot, 1817	alluvial forests	Appendix II of the Bern Convention*
Sylvia atricapilla Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Sylvia borin Boddaert, 1783	alluvial forests	Appendix II of the Bern Convention*

cont. Table 4

1	2	3
Sylvia communis Latham, 1787	open habitats	Appendix II of the Bern Convention*
Phylloscopus trochilus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Phylloscopus sibilatrix Bechstein, 1793	alluvial forests	Appendix II of the Bern Convention*
Phylloscopus collubita Vieillot, 1817	alluvial forests	Appendix II of the Bern Convention*
Regulus regulus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Ficedula albicollis Temminck, 1815	alluvial forests	Appendix II of the Bern Convention*
Ficedula hupoleuca Pallas, 1764	alluvial forests	Appendix II of the Bern Convention*
Muscicapa striata Pallas, 1764	alluvial forests	Appendix II of the Bern Convention*
Saxicola rubecula Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Oenathe oenathe Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Phoenicurus phoenicurus Linnaeus, 1758	sparse forest in floodplain	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Luscinia luscinia Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention, Appendix II of the Bonn Convention*
Luscinia svecica Linnaeus, 1758	wetland shrubs	Appendix II of the Bern Convention, Appendix II of the Bonn Convention, Council Directive 2009/147/EC on the conservation of wild birds, * Resolution 6 of the Bern Convention**
Turdus iliacus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Turdus merula Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Turdus pilaris Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Turdus philomelos C.I.Brehm, 1831	alluvial forests	Appendix II of the Bern Convention*
Turdus viscivorus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Aegithalos caudatus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*

cont. Table 4

1	2	3
Parus palustris Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Parus cristatus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Parus ater Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Parus caeruleus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Parus major Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Sitta europaea Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Certhia familiaris Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Passer montanus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Fringilla coelebs Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Fringilla montifringilla Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Chloris chloris Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Spinus spinus Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Carduelis carduelis Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Acanthis cannabina Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Pyrrhyla pyrrhyla Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Coccothraustes coccothraustes Linnaeus, 1758	alluvial forests	Appendix II of the Bern Convention*
Emberiza citrinella Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Emberiza schoeniclus Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*
Emberiza calandra Linnaeus, 1758	open habitats	Appendix II of the Bern Convention*

Notes: *Godlevska et al 2010, **Vasylyuk et al (2019), ***Order of the Ministry of Environmental... No. 29 of January 19, 2021.

The distribution of rare bird species analysis shown that the largest number of bird species was recorded in two biotopes – alluvial forests and open habitats, with a fraction of 71.0 % and 12.9 %, respectively (Figure 15).

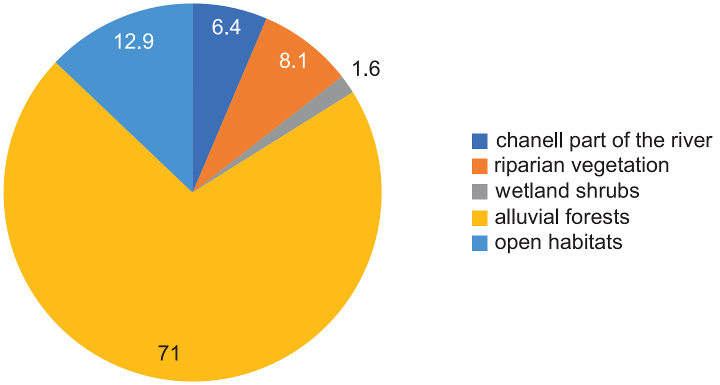

Fig. 15. Fractions [%] of bird's species in different biotopes of Horbachykha tract, Kyiv

Nesting of 44 species of birds was recorded in Horbachykha`s forest biotopes. The nesting of the *Dendrocopos syriacus* Hemprich et Ehrenberg, 1833 and the *Dendrocopos medius* Linnaeus, 1758 also has been recorded in gallery forests along the Desenka distributary. The habitats of *D. medius* Linnaeus, 1758 are mostly associated with very important ill and died trees. The species often inhabits alluvial forests with shrubs of *Populus nigra* and *Salix* sp.

During 2021, nesting of the *Otus scops* Linnaeus, 1758 (The Red Book of Ukraine, Order of the Ministry of Environmental… № 29 of January 19, 2021) was observed. It is a rare bird found in small numbers in the Kyiv region. It is mainly an inhabitant of southern Ukraine (FESENKO BOKOTEY 2002). The birds used to nest on sparse poplar forest edges. Until 1982, it was widespread within Kyiv as a breeding bird (LOPAREV 1996), but according to (ATAMAS et al 2012), it was recorded only on Kozachyi Island as of the late 90s. For a long time, the species has not been observed on the Dnipro floodplain. This may be due to the intensive cutting down of green zones for buildings and the transformation of biotopes typical for the bird.

Some rare birds of prey are represented by the *Circus aeruginosus* Linnaeus, 1758 (Bern Convention) and the *Milvus migrans* Boddaert, 1783 (The Red Book of Ukraine, Order of the Ministry of Environmental... No. 29 of January 19, 2021) have been observed several times on foraging migration, in particular along the Desenka distributary.

The Horbachykha tract, like the other islands (Zhukiv Island, Trukhaniv Island and Kozachyi Island) and tracts of the Dnipro River, is a key element of the Dnipro Ecological Corridor, through which birds of prey make their annual migrations (DOMASHEVSKY and DEMIDENKO 2009, DUBROVSKYI et al. 2008). 14 migratory species of prey birds were detected at one of the stations over the period of September-October 2022 (Table 5). 12 of it belonged to the Accipitridae and 2 to the Falconidae. The dominant species among transit migrants was the *Buteo buteo* Linnaeus, 1758 with a share of 72.1%. The percentage of the *Pernis apivorus* Linnaeus, 1758, the *Accipiter nisus* Linnaeus, 1758, the *Circus cyaneus* Linnaeus, 1766 and the *Falco subbuteo* Linnaeus, 1758 was 4.1–5.1 % (Table 5).

Table 5

Migrating birds of prey (14 species of total) on Horbachykha tract, Kyiv (2022)

Species	Number of specimens	Fraction of each species [%]
Aquila pomarina**	5	2.57
Haliaeetus albicilla**+	2	1.03
Circaetus gallicus**+	2	1.03
Pernis apivorus+	8	4.12
_Buteo buteo_*	140	72.16
Buteo lagopus+	2	1.03
Accipiter nisus+	8	4.12
_Accipiter gentilis_*	1	0.51
Circus aeruginosus+	4	2.06
Circus pygargus**+	1	0.52
Circus cyaneus**·+	10	5.15
Milvus migrans**	2	1.03
Falco vespertinus ///	1	0.51
Falco subbuteo+	8	4.12
Total	194	100

Explanations: Table 5 shows species protected by the Bonn Convention (protection of migratory animals) – +; species listed in the IUCN – ///; species listed in the Red Book of Ukraine Order of the Ministry of Environmental... No. 29 of January 19, 2021**

The survey identified 53 species of birds protected by the Bonn Convention. To ensure the reliability of the migratory corridor for migratory birds, which have adapted to certain landmarks of the Desenka distributary floodplain in the process of phylogenesis, it is necessary to secure a reliable transit route.

According to the bird's species status, we recorded 62 breeding, 21 summering, and 3 probably breeding and 46 migrating species. The rest are passing and migratory and were recorded in varying numbers during the observation periods (Figure 16). Among the migratory and nesting species which were recorded in the Horbachykha tract biotopes, 32–34 were wintering.

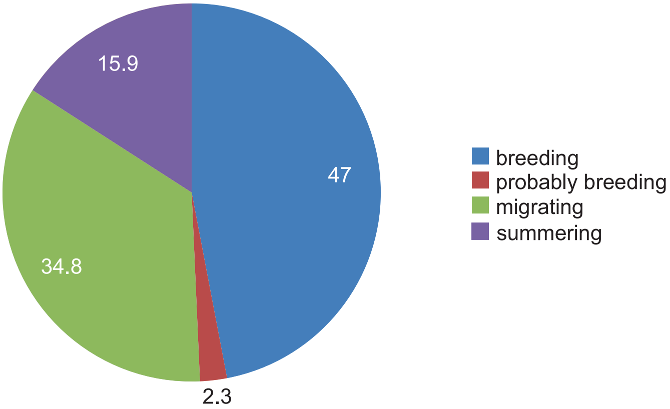

Fig. 16. Fractions [%] of rare bird species by status recorded on Horbachykha tract, Kyiv

Mammals

In the floodplain biotopes of Horbachykha tract, there is also a characteristic mammal fauna. Currently, it is poorly and in particular, following animals were recorded: *Castor fiber* Linnaeus, 1758*; *Erinaceus roumanicus* Barrett Hamilton, 1900; *Sorex araneus* Linnaeus, 1758;* *Lepus europaeus* Pallas, 1778;* *Neogale vison* Schreber, 1777; *Vulpes vulpes* Linnaeus, 1758 (PARNIKOZA and ZAGORODNIUK 2021). Species marked with an asterisk are protected by Appendix III to the Bern Convention (GODLEVSKA et al 2010).

Among the mammals, a settlement of *Castor fiber* (melanistic) in the tract has been recorded. The Desenka distributary is also home to the common beaver. *Castor fiber* is the species with high indicatory significance in Kyiv Dnipro floodplane (PARNIKOZA and ZAGORODNIUK 2021).

Current state and recommendations for Horbachykha tract protection

Today, a difficult situation has developed in the Horbachykha tract. At present, most of the area of the tract has been allocated for residential buildings, which cannot be allowed. Only the coastal strip remained free from the construction's plans. Considering this it is necessary to implement the protection of the tract in several stages. At the first stage, it is necessary to declare the coastal strip of the tract, which has not yet been distributed for construction, a landscape reserve of local importance. In the future, through court, it is necessary to return the lands of the Horbachykha tract distributed for residential construction to Kyiv city community. After that, the entire area of the tract of about 88 ha must be included in the landscape reserve of local significance. At the final stage, the Horbachykha, as a unique left-bank tract, should become part of the strictly protected zone and regulated recreation zone of the planned National Park “Dnipro Islands” (PARNIKOZA et al. 2020). This object with Horbachykha tract as component needs to be included in Emerald (Natura 2000) network.

Conclusions

The history of the formation of the Horbachykha, demonstrate that this tract initially was a natural island, and in result of Dnipro regulation in beginning of 20th century finally was formed as left bank floodplain tract, that in 1960–1970s lost the original flood regime. Flora of Horbachykha tract consist of 161 species of vascular plants (22% of whole Dnipro floodplane Kyiv flora); 7 rare species of plants and 8 rare vegetation communities were registered. So historical and botanical data confirms the fact that the tract had rests of aboriginal ecosystems and it`s very high value. Main part of ecosystems of this type were completely destroyed by the development of the left-bank part of the city. Horbachykha is the largest fragment of alluvial forests on the left bank of Kyiv. The existing biotopes of this tract form one of the key elements of the ecological corridor along the Dnipro floodplain.

Horbachykha tract have native and typical fauna of Dnipro floodplane. 14 species that have the status of protection of were found in watercourses and reservoirs; *Rhodeus amarus* occupies the largest percentage (83.2%) among rare fish species. The presence of 7 representatives of the rheophilic group indicates very important specific – conservation of hydrological regime. Among amphibians and reptiles, four species with a protected status were found. The avifauna is represented by 34 species of birds (12 are listed in the Red Book of Ukraine), 35.4% and 29.4% of which are adapted to channel areas of river and forest biotopes (alluvial forests) correspondingly. According to the status of stay, 9 species are breeding, 10 are flying, and the rest are migratory. The registration of nesting *Otus scops* is only one current and very important registration for whole Kyiv area. The presence of 54 species protected by the Bonn Convention, which protects migratory species – is the strong reason to protect this tract as the part of whole migratory corridor. Several mammal species have been recorded within the research including *Castor fiber* – species with high indicatory significance.

A significant number of animals protected by Resolution 6 of the Bern Convention provide argument for including Horbachykha tract as part of the object Dnipro floodplain corridor, proposed as part of the Emerald (Natura 2000) Network.

Our research shows that the Horbachykha tract semi-natural area with documented natural origin is extremely valuable, in particular with regard to its biotope characteristics, vegetation and fauna. Initially this tract needs to be protected by creating a landscape reserve of local significance, and then by including it in the "Dnipro Islands" National Park.

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ASSESSING BACTERIAL DIVERSITY IN TROPICAL BOVINE COW DUNG THROUGH ILLUMINA SEQUENCING

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Abstract

Cow dung is the undigested remnant of plant matter of *Bos indicus* (cow), consisting of cellulose and lignin, hemicellulose, crude protein, and minerals. Despite its numerous benefits and due to the use of cultural base techniques, little is known about cow dung microbiota because of the shortcomings associated with the use of conventional culture methods. This has necessitated the use of a robust high-throughput technique to determine the bacterial community of cow dung. Total DNA was extracted from a fresh cow dung sample, and the bacterial 16S rRNA community was sequenced via the Illumina platform. The bacterial phyla identified included *Firmicutes* (51.12%), *Proteobacteria* (36.53%), *Actinobacteria* (11.44%) and another unclassified group (0.92%). The most predominant class was *Bacilli* (49.71%) followed by *Proteobacteria* (gamma-type 29.85%), *Actinobacteria* (11.44%) and the least abundance was recorded by *Proteobacteria* (alpha-type 6.47%). The common genera in this group included *Staphylococcus* (46.31%), *Legionella* (13.48%), *Micrococcus* (9.42%), *Acinetobacter* (5.53%), *Alishewanella* (5.00%), *Pseudomonas* (5.22%), *Paracoccus* (4.21%) with 10.33% of the group yet to be classified. This study uncovers a high diverse bacteria community in the examined cow dung that could be harnessed for usage in different areas such as medicine, agriculture, and industry.

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Introduction

Cow dung is the undigested solid waste of *Bos indicus* (cow). It consists of cellulose, lignin, hemicellulose, crude protein, and minerals such as nitrogen, potassium, sulfur, cobalt, iron, magnesium, calcium, etc. It is a mixture that consists of feces and urine, usually in a ratio of 3:1 (RANDHAWA and KULLAR 2011). Cow dung as a community is rich in diverse types of microorganisms, such as bacteria, fungi, yeast, and protozoa. Some different genera of bacteria that have been reported in cow dung include *Klebsiella oxytoca, Klebsiella pneumoniae*, *Enterobacter aerogenes, Escherichia coli, Morgarella morganii, Pasteurella spp., Providencia alcaligenes,* and *Pseudomonas* spp. (SAWANT et al. 2007). Cow dung is more than just a waste because of its diverse applications including medicine, environmental management, energy sources, and agriculture. Cow dung possesses antiseptic and prophylactic or disease preventive properties (THENMOZHI et al. 2018). It destroys the microorganism that causes disease and putrefaction. Medicinal properties of five products collectively known as panchgavya obtained from cow namely milk, ghee, curd, dung, and urine are supported by their use in the preparation of various herbal medicines (PATHAK and KUMAR 2003, JARALD et al. 2008). Possible applications of cow dung microorganisms in pharmaceutical industry have been indicated by TEO and TEOH (2011) and it was shown that isolate K4 possessed antibacterial activity against *E. coli.* Research has also been conducted on water, ethanol, and n-Hexane extract of whole cow dung against *Candida*, *E. coli*, *Pseudomonas* and *Staphylococcus aureus* by SHRIVASTAVA et al. (2014) revealing their antimicrobial properties. Cow dung is also used as a co-product in agriculture, such as manure, biofertiliser, biopesticides, pestrepellent and as a source of energy (DHAMA et al. 2005). LI et al. (2009) reported 67 ml/g methane yield from anaerobic digestion of cow manure, whose total and volatile solids were 23.4 and 13.8 g/l, respectively. Thus, cow dung may not only act as a substitute for chemical fertilisers because it supplements organic matter, but also as a conditioner for soil (GARG and KAUSHIK 2005, YADAV et al. 2013, BÉLANGER et al. 2014). As reported by VAKILI et al. (2015), adding cow dung to palm oil biomass improves the compost's physical and chemical properties, as well as its nutritional composition. ARSLAN et al. (2008) and VAKILI et al. (2015) recognize that compost improves soil nutrients and water retention. Among the microorganisms present in cow dung are *Acinetobacter*, *Bacillus*, *Pseudomonas*, *Serratia*, and *Alcaligenes* spp., making them suitable for biodegradation of pollutants (ADEBUSOYE et al. 2007, UMANU et al. 2013). Thus, cow dung may not only act as a substitute for chemical fertilisers because it supplements organic matter, but also as a conditioner for soil (GARG and KAUSHIK 2005, YADAV et al. 2013). Due to its richness in microbial diversity, cow dung had been employed in removing toxic pollutants from the environment (UMANU et al. 2013). Cow dung slurry maintained in the ratio of 1:10 or 1:25 is able to degrade the rural, urban and hospital wastes, including oil spillage to five basic elements (RANDHAWA and KULLAR 2011). A study by ORJI et al. (2012) highlights the importance of cow dung isolates, both bacterial and fungal, for reducing total petroleum hydrocarbons to 0 % in polluted mangrove soil. UMANU et al. (2013) suggested that the application of cow dung in an appropriate concentration may prove very efficient in biodegradation of water contaminated with motor oil. WYSOCKA-CZUBASZEK (2019) investigated by comparing the influence of digestate addition on soil chemical properties with traditional organic fertilizers such as liquid and solid cattle manure and with mineral fertilizer. Finding by the same author was that the digestate supplied soil with a significant amount of NH_4-N, whose nitrification was slower comparing to soils treated with mineral fertilizer and liquid cattle manure.

Because microorganisms can be easily cultivated, microbial enzyme application in industry is on the rise. The microbial diversity of cow dung makes it a suitable source of important industrial enzymes. One member of the xylanolytic bacteria *Paenibacillus favisporus* from cow dung has been reported to produce various types of hydrolytic enzymes such as xylanases, cellulases, amylases, gelatinase, urease, and β-galactosidase (ENCARNA et al. 2004). In addition, cow dung can also serve as a suitable substrate to produce enzymes (VIJAYARAGHAVAN et al. 2012). It is also used in the production of biogas as an alternative source of renewable energy. Biogas, a mixture of different gases produced by anaerobic fermentation of organic matter from methanogenic bacteria, mainly constitutes methane (50–65%) and CO_2 (25–45%) (SHARMA 2011).

The mycelial growth of *Sclerotinia sclerotiorum* has been reported by BASAK et al. (2002) to be suppressed by cow urine and cow dung. The fungus is one of the most common pathogens that cause sclerotina rot in cucumber and other vegetables. Similarly, BASAK and LEE (2001) also reported that fresh cow urine and cow dung have inhibitory action on mycelial growth of *Fusarium solani*, f. sp. *cucurbitae* and *F. oxysporum* f. sp. *cucumerinum*, which are responsible for *Fusarium* root rot and wilt of cucumber. *Bacillus subtilis* isolated from cow dung has been reported to have antagonistic activity against plant diseases (GUPTA et al. 2016). The bacterium can be employed as a biocontrol agent and due to the high heat tolerance of *Bacillus* sp., it can be employed industrially to produce amylase (RAMACHANDRAN et al. 2016). *Mycobacterium vaccae*, a nonpathogenic bacterium first isolated from cow dung, possesses antidepressant properties. When inhaled, it enhances the growth of neurons, which stimulates the production of serotonin and norepinephrine in the brain (LOWRY et al. 2007). Smoke generated from burnt cow dung is also reported to be effective as a mosquito repellant (GUPTA et al. 2016).

Cow dung has also been employed over the years as organic manure in agriculture which serves as an alternative to fertilizer. According to the US Department of Agriculture, in California alone, up to 60 million tons (at 30 kg/head) of animal waste are produced per year by 5.2 million cattle and calves, and a large portion of this is waste used as manure in cropland (USDA 2016). This has reduced the use of chemical fertilizers that are not eco-friendly. Some of the microbiomes found in dung can promote plant growth. Zinc, a micronutrient required for plant growth and productivity has been reported to be solubilized by *Bacillus* sp. isolated from cow dung. This implies that cow dung is rich in microorganisms that can be used as a bioinoculant. Some of these cow dung bacteria have also been implicated in phosphorus solubilization, and siderophore, HCN and indole acetic acid (plant hormone) production (KALPANA and DINESH 2019).

The utilization of cow dung as a fertilizer is associated with negative consequences. This is mostly due to the prevailing practice of disposing of cow dung in piles, slurries, or lagoons, which leads to significant greenhouse gas emissions of methane, environmental degradation, negative health impacts, and loss of valuable nutrients that could otherwise be utilized to enhance soil fertility. It is essential to consider alternative methods of disposal and explore environmental friendly options for the utilization of cow dung as a fertilizer. This will not only mitigate the negative impacts but also provide a valuable source of nutrients to improve soil health and fertility. The high level of pathogens in surface water has been attributed to run-off from farmland into surface water (PANDEY et al. 2014). In addition, harmful pathogens in untreated manure can contaminate crops and vegetables on farmland (ERICKSON et al. 2014, RAYMOND et al. 2021).

Despite this wide application of cow dung, little is known about the cow dung microbiota. This lack of knowledge may be due to the method used to analyze the cow dung community. Cultural-dependent methods have been used to study cattle intestinal microflora. In addition, this method is time consuming, and only approximately 1% of bacteria have been successfully cultured, necessitating metagenomic analytical techniques. The remaining 99% is yet to be cultured; hence the need for metagenomics approaches (RADA et al. 2006). This study aimed to analyze the bacterial diversity of cow dung from a tropical *Bos indicus* using Illumina sequencing technology. This study delves into the depths of bacterial diversity found within tropical *Bos indicus* cow dung. The results promise to offer an enlightening glimpse into the microbial world thriving within this unique ecosystem.

Materials and Methods

Sample collection and DNA extraction

Fresh cow dung was collected from a cattle farm in Gbagada, Lagos Nigeria and transported immediately in an ice pack (4°C) to Africa Bioscience Laboratory, Ibadan, Oyo State, Nigeria for community DNA extraction. The cow dung properties had been previously determined by ADEGUNLOYE and ABE (2020). DNA extraction from the cow dung sample was carried out using a Presto Soil DNA Extraction kit (Geneaid Biotechnology Limited, Taiwan) according to the manufacturer's instructions and sent to Xcelris Genomics Laboratory Gujarat, India for Illumina sequence analysis. The quality of gDNA was checked on a 0.8% agarose gel (loading 5 µl of the sample) for the presence of intact bands at 110 V for 30 mins. The sample (1 µl) was loaded in a Thermo NanoDrop ND-1000 UV/VIS Spectrophotometer (Thermo Fisher Scientific, UK) to determine the A260/280 ratio. The DNA was also quantified using a Qubit dsDNA HS Assay kit (Life Technologies, Madison, USA). One microliter of each sample was used for determining concentration using Qubit® 2.0 Fluorometer.

Library preparation

The amplicon library was prepared using the Nextera XT Index Kit (Illumina Inc., San Diego, CA, USA) according to the 16S metagenomic sequencing library preparation protocol (Part #15044223 Rev. B). Primers for the amplification of the V3-V4 hypervariable region (V3-R: CCTACGGGNBGCASCAG; V4-R: GACTACNVGGGTATCTAATCC) of the 16S rDNA gene of bacteria and archaea were designed by Xcelris Labs Limited, Gujarat, India and synthesized in Xcelris PrimeX facility. The amplicons, together with the Illumina adaptors, were amplified by using i5 and i7 primers that add multiplexing index sequences, as well as common adapters required for cluster generation (P5 and P7) according to the standard Illumina protocol. The amplicon libraries were purified by 1X AMpureXP beads, checked on an Agilent DNA1000 chip on a Bioanalyzer 2100 and quantified by a Qubit Fluorometer 2.0 using Qubit dsDNA HS Assay kit (Life Technologies, Madison, USA).

Cluster Generation and MiSeq Illumina Sequencing

After obtaining the Qubit concentration for the library and the mean peak size from the Bioanalyzer profile, the library was loaded onto the Illumina MiSeq platform at an appropriate concentration (10–20 pM) for cluster generation and sequencing. Paired-end sequencing allows the template fragments to be sequenced in both the forward and reverse directions on the Illumina platform. The kit reagents were used to bind the samples to complementary adapter oligos on a paired-end flow cell. The adapters were designed to allow selective cleavage of the forward strands after resynthesis of the reverse strand during sequencing. The copied reverse strand was then used to sequence from the opposite end of the fragment.

Sequence data analysis

The generated sequence data were analyzed by QIIME (Quantitative Insight into Microbial Ecology) pipeline with the following workflow: filtering chimeras → OTU (Operational Taxonomic Unit) picking → Taxonomic assignment → Diversity calculation, using the USEARCH61. The forward and reverse sequences were stitched to form longer sequences using PANDAseq (MASELLA et al. 2012), followed by data cleaning by removal of chimeras using USEARCH61 (*de novo* and abundance-based options). The cleaned data were further subjected to OTU picking, taxonomic assignment and diversity calculation utilizing the UCLUST algorithm within the QIIME pipeline. OTU picking involves the clustering of highly similar sequences together and then the generation of a consensus sequence to represent the cluster. OTUs were picked from the cleaned reads with a benchmark of 97% sequence similarity. Singletons, that is, clusters containing single sequences, were removed from the list of OTUs before taxonomic assignment. Taxonomy assignment was carried out by mapping the OTUs to the Greengenes database at a 90% similarity level.

Results

Alpha diversity

Alpha diversity or within-sample diversity is calculated using an OTU table that gives ideas about species richness. Table 2 summarizes the $\boldsymbol{\alpha}$-diversity, where the columns correspond to alpha diversity metrics and the rows correspond to samples and their calculated diversity measurements. After sequencing, the number of flash reads was 523 117, out of which 400 590 were non-chimeric sequences, while the number of OTUs was 26 527 (Table 1). The number of OTUs with zero singletons was 3,189. Shannon and Chao1 are the diversity indices used in this study to show alpha diversity. Chao1 focuses on richness, while Shannon shows the number of species and the effect of evenness. The calculated alpha diversity was Shannon (4.70), and Chao1 (3 214.01), and the observed species was 3 189.00 (Table 2).

Table 1

Summary of the OTUs obtained from cow dung

Flash/stitch reads	Non-chimeric sequences	Number of OTUs	Number of OTUs with zero singletons
523 117	400 590	26 527	3 189

Table 2

Alpha-diversity metrics of the bacteria community within a tropical cow dung

Shannon	Observed species	chao1
4.70	3 189.00	3 214.01

Cow dung microbial diversity

The bacteria order *Bacillales* was the most predominant, followed by *Legionellales*, *Actinomycetales*, *Pseudomonadales*, *Alteromonadales*, *Rhodobacterales*, *Rhizobiales*, *Lactobacillales*, *Clostridiales* and an unidentified group (Figure 1). Within the family, the most abundant were *Staphylococcaceae* (46.31%), *Legionellaceae* (13.48%), *Micrococcaceae* (9.42%), *Moraxellaceae* (5.55%), *Chromatiaceae* (5.50%), *Pseudomonadaceae* (5.22%), *Rhodobacteraceae* (4.21%) and other belonging to unclassified group (15.81%) – Figure 1. The phyla *Firmicutes*, *Proteobacteria* and *Actinobacteria* were fully represented in the cow dung community (Figure 2). Predominantly, *Firmicutes* constituted 51.12% followed by *Actinobacteria* 11.44%, *Proteobacteria* 36.53% and other unclassified group (0.92%) of the entire population (Figure 2). The most predominant class was *Bacilli* (49.71%) followed by *Proteobacteria* (Gamma – 29.85%), *Actinobacteria* (11.44%) and *Proteobacteria* (Alpha-6.47%) had the least abundance (Figure 2).

In this study, the common genera included *Staphylococcus* (46.31%), *Legionella* (13.48%), *Micrococcus* (9.42%), *Acinetobacter* (5.53%), *Alihewanella* (5.00%), *Pseudomonas* (5.22%), *Poracoccus* (4.21%) (Figure 3). *Staphylococcus* (46.31%) was the most predominant followed by *Legionella* (13.48%), *Micrococcus* (9.42%), *Acinetobacter* (5.53%, *Alihewanella* (5.00%), *Pseudomonas* (5.22%) and *Poracoccus* (4.21%) had the least abundance. However, there was 10.33% abundance by the group yet to be classified (Figure 3).

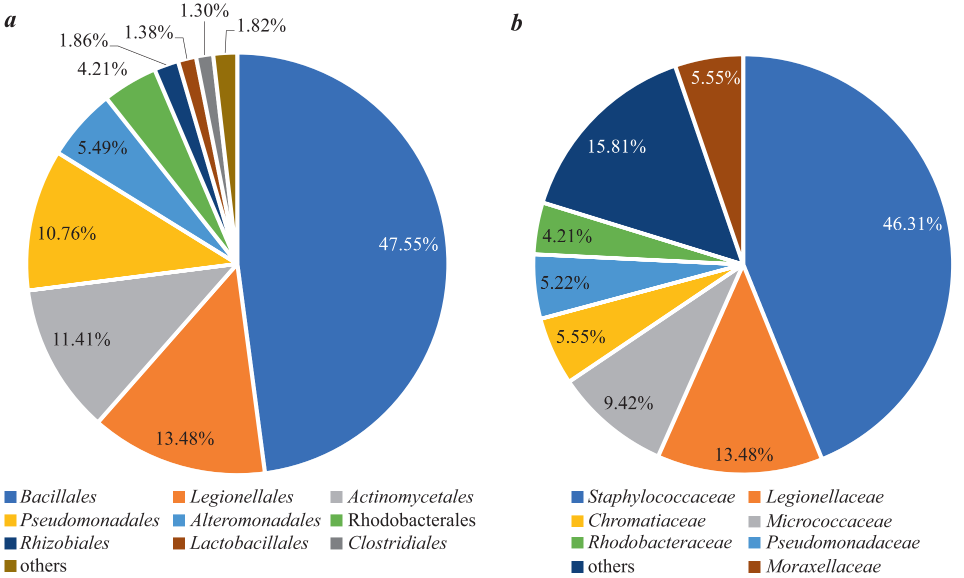

Fig. 1. Taxonomic distribution of bacteria from a tropical cow dung at the order (*a*) and family (*b*) levels

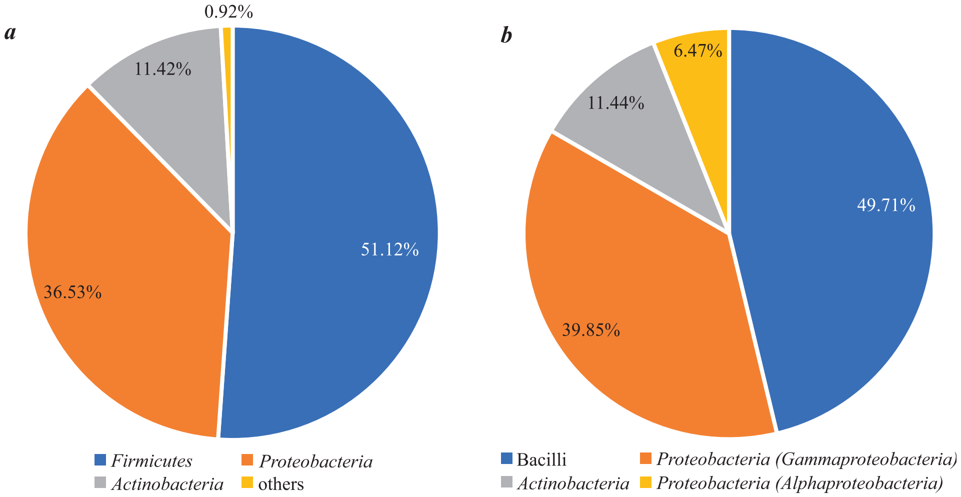

Fig. 2. Taxonomic distribution of bacteria from a tropical cow dung at the phylum (*a*) and class (*b*) levels

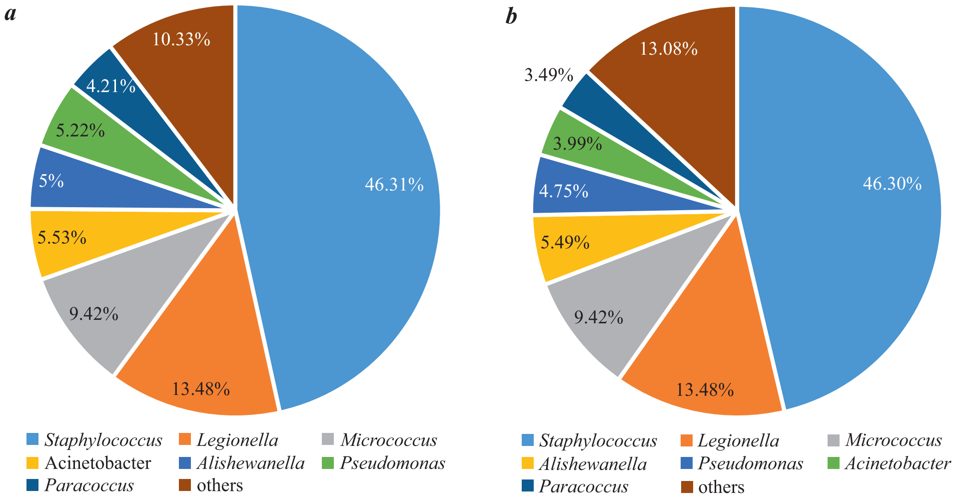

Fig. 3. Taxonomic distribution of bacteria from a tropical cow dung at the genus (*a*) and species (*b*) levels

Discussion

Knowledge of the composition, diversity and structure of the microbial community was limited until the emergence of fingerprinting techniques and subsequent molecular approaches. These new techniques broaden scientists' understanding of the relationship between microbes and their environment (Green et al. 2008). The bacterial diversity of cow dung had in the past been assessed by a culture-dependent method. However, according to Girija et al. (2013), culture-based methods show bias to facultative anaerobes because they can be easily cultured under laboratory conditions, while strict anaerobes are underestimated because they fail to grow under normal growth conditions. Previous studies by the same authors reports the bacterial diversity and phylogenetic relationship of indigenous bacteria of cow dung by 16S rRNA gene libraries (Girija et al. 2013). Mtshali et al. (2022) studied the bacterial communities present in bovine faeces, milk, and blood. Alpha diversity was calculated using the Chao1 index, which measures richness, and the Simpson's and Shannon indexes, which combine richness and evenness. (Gotelli and Colwell, 2001, Hoque et al. 2020). Alpha diversity values were significantly higher in feces than in milk or blood. This present study obtained a Shannon of 4.70, which was lower than the 6.7251 recorded by Mtshali et al. (2022) for bovine faeces, while this study obtained a Chao1 of 3214.01, which was higher than 1710.5 recorded by Mtshali et al. (2022).

Bacteria belonging to the phyla *Bacteriodetes* (38.3%), *Firmicutes* (29.8%), *Proteobacteria* (21.3%), and *Verrucomicrobia* (2%) were identified (GIRIJA et al 2013). In this study we explored the microbial structure and composition of cow dung (bovine faeces) through sequencing of the V3-V4 hypervariable region of the 16S rRNA gene, employing the Illumina Miseq platform. This is an ideal platform for small-scale research due to its cost effectiveness, short turnaround time and comparatively high sequencing depth (GUPTA and VERMA 2019). This study examined the number of reads by only cow dung (bovine faeces) and had a high number of reads. Similarly report by MTSHALI et al (2022) accessed the number of reads returned by sample type and showed that they were disproportionate with the highest number recorded among faeces, followed by milk and blood. The high microbial biomass recorded for faecal samples was anticipated due to the difference in the type of samples being analyzed, for instance, blood samples generally contain low microbial biomass while faecal samples contain high microbial biomass (EISENHOFER et al. 2019).

The most prevalent bacterial groups detected in cow dung samples in this study included members of *Firmicutes*, *Proteobacteria*, *Actinobacteria* and unclassified group. MTSHALI et al (2022) found the most prevalent bacterial groups in the faeces and milk included members of the *Firmicutes* and *Bacteroidota* phyla; while bacterial sequences from blood were predominantly members of *Proteobacteria*, a similar observation to findings of YOUNG et al. 2015. It has been proven that the gastrointestinal tract (GIT) of calves is seeded before birth with a diverse array of microbiota, changing drastically post-partum and successively predominated by *Firmicutes*, *Bacteroidota*, *Proteobacteria* and *Actinobacteriota* in decreasing order of abundance post-weaning (O'HARA et al. 2020, CENDRON et al. 2020, KOESTER et al. 2020, YOUNG et al. 2015, MALMUTHUGE et al. 2015, MAO et al. 2013, OIKONOMOU et al. 2013). In contrast to popular reports however, the *Firmicutes*, *Proteobacteria* and *Actinobacteria* were succeeded by *Verrucomicrobiota* in this study, following a similar microbial distribution pattern to donkey gut microbiota reported by LIU et al. (2014).

The observed faecal microbiota represented a mixture of taxa containing known anaerobic gut microbes (*e.g.*, *Clostridium sensu stricto_1*, *Romboutsia* and *Bacteroides*) (CENDRON et al. 2020, DOWD et al. 2008). Initial gut colonizers or bacteria found in the intestine but typically present on other mucosae (*e.g.* *Streptococcus* and *Staphylococcus*) (ALIPOUR et al. 2008); and bacterial genera with potential health effects on cattle and human hosts (*e.g.* *Bacillus* and *Clostridium_sensu_stricto_1*) (DOWD et al. 2008).

It has been reported that the suppression and/or over colonization of certain microbes in a particular niche result in disease pathogenicity, thus emphasizing the need to understand the interaction between the host environment and its inhabiting microbes (DENG et al. 2019). Furthermore, since microbes with zoonotic potential were detected, precaution should be taken to prevent human infection in the sampled community. The routes of infection can be through consumption of contaminated meat and milk; via aerosol due to the proximity of the animal enclosures to their homes; occupational exposure through handling of infected animals as well as aborted foetal material (MAITY and AMBATIPUDI 2021); and most importantly through the unsanitary practices associated with the use of cattle products and by-products by this community (DARIA and ISLAM 2021).

The *Bacillales* order includes several families, such as the *Listeriaceae*, *Planococcaceae*, *Staphylococcaceae*, and *Bacillaceae* (BECKER et al. 2021). Within the family Micrococcaceae, the genus *Staphylococcus* comprises Gram-positive, non-spore-forming cocci that frequently colonize the skin and nasal cavities as common human microorganisms. Five possible human pathogens are found in this genus: *S. aureus*, *S. epidermidis*, *S. saprophiticus*, *S. haemolyticus*, and *S. hominis*; nevertheless, the first three isolates are the most frequently occurring. The capacity to coagulate sets *S. aureus* apart from the other two infections, which are thought to be the most dangerous. In addition to dangerous systemic infections, *S. aureus* can cause several superficial pyogenic (pus-forming) infections of the dermis and underlying tissues. It can produce a variety of toxins, such as poisonous substances, cytotoxins (widely distributed toxins), and enterotoxins (food poisoning). Although they are far less common as pathogens, the other coagulase-negative staphylococci, *S. epidermidis* and *S. saprophiticus*, are occasionally linked to wound infections, endocarditis, and infections in prosthetic joints, to mention a few (BECKER et al. 2021).

Gram-negative bacilli are species of *Legionella*. In the family *Legionellaceae* and the genus *Legionella*, there are currently 42 species of legionellae that have been identified, representing 64 serogroups (BENSON and FIELD 1998). *Legionellae* are Gram-negative bacilli that are thin and somewhat pleomorphic, with a diameter ranging from 2 to 20 µm. It is possible for long, filamentous forms to emerge, especially following growing on agar. *Legionella* is characterized ultrastructurally by having the exterior and inner membranes of Gram-negative bacteria. The majority of its species are motile using a single polar flagellum, and it has pili (fimbriae) (BENSON and FIELD 1998, FANG et al. 1989, WINN 1988, WINN and MYEROWITZ 1981).

The present study identified four genera including *Staphylococcus*, *Legionella*, *Alishewanella* and *Paracoccus*. *Legionella* is the only genus in the family *Legionellaceae*. Fifty species of *Legionella* and more than 70 different serogroups now are recognized (MORONTA 2022). *Legionella* is a genus in the phylum, the majority of which have been isolated only from environmental, rather than from clinical sources. In the environment, these organisms may inhabit complex communities composed of multiple bacterial species that grow within biofilms (MORONTA 2022). They have been isolated from waters with temperatures ranging from 5 to 50°C; however, they can grow to abundance at the warmer end of this spectrum, particularly in water distribution systems with water heaters (MORONTA 2022). According to BENSON and FIELD (1998), the intricacy of environmental interactions is comparable to that of viral and parasite illnesses. Water is the only known source of *Legionella* species, especially surface waters from lakes, rivers, and drinking water. *Legionella* does not grow in sterile tap water, but it does grow in vitro when free-living amoebae are added (BENSON and FIELD 1998).

Alishewanella is a genus in the phylum *Pseudomonadota* (bacteria). *Gammaproteobacteria* is a class of bacteria in the phylum *Pseudomonadota*. It contains about 250 genera, which makes it the most genus-rich taxon of the prokaryotes (KIM et al. 2009). Several medically, ecologically, and scientifically important groups of bacteria belong to this class *Alishewanella*. There has been paucity of information to the diversity of *Alishewanella* specie. It just recently studies have been explored on this genus (VOGEL et al. 2000). According to NCBI taxonomy, there are 36 isolates from different environments, 27 uncultured *Alishewanella* strains with 16S rRNA gene sequences, and only 5 species of *Alishewanella* with officially published names (VOGEL et al. 2000, KIM et al. 2009, ROH et al. 2009, JUNG et al. 2013). Fermented foods, tidal flat sediments, plant leaf and root surfaces, soils, cold temperature deserts, sludge, permafrost soils, freshwater biofilms, metal tailings, beetle larvae guts, lakes, wastewater, and heavy metal-resistant communities are some isolation sources of the group. These many isolation sources suggest that the *Alishewanella* species are highly adaptable and occupy a wide variety of habitats. Furthermore, a culture-dependent analysis of a lake's bacterial population revealed a prevalence of *Alishewanella* species (POLZ et al. 2013).

The *Paracoccus* genus classification, belonging to the alpha subgroup of *Proteobacteria*, has undergone significant and extensive changes. Numerous new species have been discovered, and the status of existing species has been reevaluated. Currently, the genus comprises 17 species found in diverse environments. Some of these species, including *Paracoc-*

cus alcaliphilus (URAKAMI et al. 1989), *P. carotinifaciens* (TSUBOKURA et al. 1999), *P. aminophilus*, *P. aminovorans* (URAKAMI et al. 1990), and *P. kondratievae* (DORONINA et al. 2002), were isolated from soil. Other species were found in environments containing toxic components, such as *P. alkenifer*, which was isolated from biofilters used in treating waste gases from an animal rendering plant (LIPSKI et al. 1998), *P. methylutens*, which was discovered in groundwater contaminated with dichloromethane (DORONINA et al. 1998), *P. pantotrophus*, which was isolated from sulfide-oxidizing, denitrifying fluidized-bed reactors in plants (ROBERSTON and KUENEN 1983), and *P. kocurii*, which was found in wastewater from semiconductor manufacturing processes (OHARA et al. 1990). Some strains of *P. denitrificans*, the first *Paracoccus* species isolated (BEIJERINCK and MINKMAN 1910), were also found in several different habitats, including sewage, sludge, horse manure, cow dung (LIPSKI et al. 1998), and soil. Bacteria belonging to the *Paracoccus* genus are likely to be essential components of many wastewater treatment system communities (NEEF et al. 1996). Recently, the number of known habitats for these bacteria has expanded, with two new species discovered from the marine environment; *P. seriniphilus* was isolated from the marine bryozoan *Bugula plumosa* (PUKALL et al. 2003, KOESTER et al. 2020), and *P. zeaxanthinifaciens* was isolated from seaweed from the coast of the African Red Sea (ÅRHEM 1989). Moreover, the first *Paracoccus* species associated with human infection (*P. yeei*) was isolated from the dialysate of a patient with peritonitis (TSCHOPP et al. 2013). These findings suggest that these bacteria are more widespread than previously thought.

Conclusion

The characterization of cow faecal microbiota can offer valuable insights into the microbial structure and composition of cow dung samples, particularly in the Nigerian context. By utilizing high throughput sequencing of the V3-V4 hypervariable region of the 16S rRNA gene, the microbiota of faeces from cows was analyzed. The results of the study reveal a novel understanding of the microbial diversity of cow dung samples and can potentially contribute to knowledge acquisition concerning the hypothesized pathway in ruminants. The concurrent detection of microbes in the cow dung samples can offer further insights into the intricate relationships among microbiota, and thus, facilitate a more comprehensive understanding of the microbial ecology of the cow faecal microbiota.

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