UNIWERSYTET TECHNOLOGICZNO-PRZYRODNICZY
IM. JANA I JĘDRZEJA ŚNIADECKICH
W BYDGOSZCZY

WYDZIAŁ HODOWLI
I BIOLOGII ZWIERZĄT

ZESZYTY NAUKOWE NR 255

ZOOTECHNIKA
38

BYDGOSZCZ – 2010

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ISSN 1899-0096

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Wyd. I. Nakład 80 egz. Ark. aut. 2,5. Ark. druk. 2,75.
Uczelniany Zakład Małej Poligrafii UTP Bydgoszcz, ul. Ks. A. Kordeckiego 20

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POLYMORPHISM OF CHROMOSOME SIZE IN THE SOWS OF POLISH LANDRACE BREED (PBZ)

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Assessment was made of sex chromosomes and autosomes based on measuring their areas in the Polish landrace, and of the connection of the observed polymorphism with reproductive traits. The average area of sex chromosomes in examined sows was 7.4779 μm^2, with the values ranging from 6.9739 μm^2 to 8.1331 μm^2. And the average autosomes area was 143.7742 μm^2. Considerably greater variability was found within the sex chromosomes area than the autosomes area. The variability index of the chromatids area of sex chromosomes was between 0.3182% and 7.9053%. The variability of autosomal chromosomes area, however, was between 1.0491% and 1.3069%. The average areas of sex chromosomes and autosomes as well as the average total areas of chromosomes proved relatively highly and positively correlated with the number of piglets born in the fourth litter, and the values of correlation indexes were respectively $r = 0.4044$, $r = 0.3257$ and $r = 0.3488$.

Keywords: polymorphism, chromosomes, reproductive traits, sows, Polish landrace breed

1. INTRODUCTION

Each animal breed is characterized by a specific complement of chromosomes, both in terms of their number and morphology. Assessing whether the chromosome complement is normal requires taking into consideration the fact of occurrence of chromosome polymorphism. In respect of chromosomes, the following forms of polymorphism can be distinguished:

- chromosome length polymorphism (the relative length of sex chromosomes was assessed, particularly the Y-chromosome in various animal breeds – sheep, cattle, horses, and pigs) [3, 5, 9],
- polymorphism of the number and size of specific chromosome sections in terms of structure and function (the size of centromeric heterochromatin blocks and the nucleolus organizer areas) [9, 10],
- polymorphism of the number of chromosomes (may arise from centric fusions or occurrence of a varied number of chromosomes) [2, 5].

The objective of the study is to analyze the polymorphism of chromosomes based on measurement of the sex chromosome area and the autosomal chromosome area in sows of the Polish landrace breed, as well as the connection between the observed polymorphism and reproductive traits.

2. MATERIAL AND METHODS

The research material was constituted by blood coming from 20 sows of the Polish landrace breed. Animals came from two brood herds from the land of the Kujawsko-Pomorskie province. Whole blood lymphocytes were maintained on RPMI1640 medium with an addition of calf serum LF-7, and antibiotic. The metaphase spread preparations were made in accordance with generally accepted methods [7]. The metaphase spreads were stained using the GTG method and the Giemsa stain [7]. The preparations were analyzed in a light microscope with the magnification of 1250X, and using the Multi-Scan Karyotype computer software v. 8.01 [4].

Size of the chromosomes was measured in minimum three metaphase platelets with the use of the 'surface' function and recorded in the Microsoft Excel program. Average values of sex chromosomes and autosomes were calculated (μm^2).

The relative size of the sex chromosome area (%) and participation of heterosomes were calculated according to the following formulas:

Relative size of sex chromosomes = [total of heterochromosome area (μm^2) / total of autosome area (μm^2)] x 100%.

Sex chromosomes participation = [total of heterochromosome area (μm^2) / total of autosomes and heterochromosomes (μm^2)] x 100%.

Variability of the examined chromosome traits was estimated by calculating the standard deviation (S_x) and the variability index (V_x) [8]. Simple correlations between the analysed chromosome traits and the first littering as well as the number of piglets born alive were estimated in the first, second, and third litter [8].

3. RESULTS

Table 1 presents average values of sex chromosome and autosome area, as well as the average relative area and chromosomes participation in all metaphase chromosomes.

Average sex chromosome area in sows of the Polish landrace breed was 7.4779 μm^2. The smallest average sex chromosome area was observed in sow no. 33 – 6.9739 μm^2, and the largest of 8.1331 μm^2 in sow no. 45 (Table 1).

In terms of average values of the areas of autosomal chromosome chromatids areas, values observed in sows number 35 and 50 are worth noting (Table 1). Sow no. 50 was characterized by the largest autosome area of 158.9862 μm^2, and sow number 35 the smallest of 126.3322 μm^2. The average chromosome area in the examined group of sows was 143.7742 μm^2 (Table 1).

Table 1. Average areas of sex chromosomes and autosomes, and the relative value and percentage of heterochromosomes of Polish landrace sows

Tabela 1. Średnie wielkości powierzchni chromosomów płci i autosomów oraz względna wartość i udział heterochromosomów loch rasy pbz

Sow no. Nr lochy	Average area of sex chromosomes [μm^2] Średnia powierzchnia chromosomów płci	Average area of chromatids of autosomal chromosomes [μm^2] Średnia powierzchnia chromatyd chromosomów autosomalnych	Average area of sex chromosomes and autosomal chromosomes [μm^2] Średnia powierzchnia chromosomów płci i chromosomów autosomalnych	Average relative area of sex chromosomes [%] Średnia powierzchnia względna chromosomów płci	Percentage of chromatids of sex chromosomes [%] Udział chromatyd chromosomów płci
13	7.0674	156.6813	163.7487	4.5107	4.3160
14	7.3393	141.5705	148.9099	5.1842	4.9287
15	7.4612	140.7087	148.1699	5.3026	5.0356
16	7.2644	142.0309	149.2952	5.1146	4.8658
24	7.6749	140.5813	148.2562	5.4594	5.1768
27	7.1342	141.7830	148.9172	5.0318	4.7907
28	7.3540	142.1166	149.4707	5.1746	4.9201
33	6.9739	142.0519	149.0257	4.9094	4.6797
35	7.2841	126.3322	133.6163	5.7658	5.4515
36	7.4285	136.2987	143.7272	5.4501	5.1685
38	7.9078	136.0207	143.9285	5.8137	5.4942
39	7.3417	142.4695	149.8112	5.1531	4.9006
40	7.8043	144.1579	151.9622	5.4137	5.1357
41	8.1020	146.5895	154.6915	5.5270	5.2375
42	7.7914	150.5954	158.3868	5.1738	4.9192
44	8.1250	147.4180	155.5430	5.5116	5.2237
45	8.1331	146.1240	154.2571	5.5659	5.2725
49	7.2623	142.4365	149.6988	5.0987	4.8513
50	7.0492	158.9862	166.0354	4.4338	4.2456
51	7.0591	150.5310	157.5901	4.6895	4.4794
Average Średnia	7.4779	143.7742	151.2521	5.2142	4.9440

The average chromosome area (the total of autosomes and sex chromosomes) in the metaphase platelets in examined sows was 151.2521 μm^2, assuming values from 133.6163 μm^2 (sow no. 35) to 166.0354 μm^2 (sow no. 50) (Table 1).

In the examined group of sows, the average relative area of sex chromosomes was 5.2142%, and participation of sex chromosomes was 4.9440% (Table 1). The sow numbered 50 was characterized by the smallest values of the average relative area, equalling to 4.4338% and participation of sex chromosomes in all metaphase chromosomes (4.2456%). On the other hand, the highest values of the average relative area of sex chromosomes and the participation of sex chromosomes was observed in sow no. 38 (Table 1).

Analyzing the variability of the metaphase chromosomes area in the examined group of Polish landrace sows, significantly higher variability was found within the sex chromosomes than autosomes. The variability index of the sex chromosome chromatids

was between 0.3182% (sow no. 27) and 7.9053% (sow no. 42), whereas the variability of autosomal chromosome area was between 1.0491% (sow no. 13) and 1.3069% (sow no. 42) (Table 2). Taking into consideration the total area of sex chromosomes and autosomes, the lowest variability was observed in sow no. 1 (Vx = 0.9833%), and the highest in sow no. 42 (Vx = 1.2127%) (Table 2). Among the 20 sows, the highest variability, in terms of chromosome area in respect of both sex chromosomes and autosomes, was found in sow no. 42 (Table 2).

Tabele 2. Variability of the area of sex chromosomes and autosomes in sows of the Polish landrace breed

Tabela 2. Zmienność wielkości powierzchni chromosomów płci i autosomów loch rasy pbz

Individual Osobnik	Trait – Cecha					
	Area of chromatids of sex chromosomes Powierzchnia chromatyd chromosomów płci		Area of chromatids of autosomal chromosomes Powierzchnia chromatyd chromosomów autosomalnych		Area of sex chromosomes and autosomal chromosomes Powierzchnia chromosomów płci i chromosomów autosomalnych	
	Statistical measures – Miary statystyczne					
	Sx [µm^2]	Vx [%]	Sx [µm^2]	Vx [%]	Sx [µm^2]	Vx [%]
13	0.1014	1.4341	1.6438	1.0491	1.6102	0.9833
14	0.0529	0.7202	1.6997	1.2006	1.6551	1.1115
15	0.0465	0.6227	1.6102	1.1444	1.5674	1.0579
16	0.3261	4.4887	1.7679	1.2447	1.7239	1.1547
24	0.2799	3.6472	1.7572	1.2500	1.7110	1.1541
27	0.0227	0.3182	1.6345	1.1528	1.5927	1.0695
28	0.2231	3.0344	1.7383	1.2232	1.6933	1.1329
33	0.1211	1.7368	1.8237	1.2838	1.7778	1.1929
35	0.3018	4.1432	1.4139	1.1192	1.3776	1.0310
36	0.1298	1.7476	1.5610	1.1453	1.5193	1.0571
38	0.3155	3.9902	1.6133	1.1861	1.5718	1.0921
39	0.1882	2.5639	1.7585	1.2343	1.7128	1.1433
40	0.0764	0.9786	1.8493	1.2828	1.7998	1.1843
41	0.3104	3.8313	1.8589	1.2681	1.8102	1.1702
42	0.6159	7.9053	1.9682	1.3069	1.8102	1.2127
44	0.5046	6.2098	1.7149	1.1633	1.6721	1.0750
45	0.6079	7.4747	1.8303	1.2525	1.7852	1.1573
49	0.4169	5.7404	1.7698	1.2425	1.7260	1.1530
50	0.1151	1.6326	1.8181	1.1436	1.7806	1.0724
51	0.1393	1.9734	1.6698	1.1093	1.6317	1.0354
Average Średnia	0.3948	5.2793	7.0836	4.9269	7.1551	4.7306

The Polish landrace breed is counted as a maternal breed, therefore some of the most important production traits are the traits characterizing reproduction. The examined group of sows littered for the first time at the age of 353 days on average. Attention should be drawn to considerable diversity of sows as regards the age of first littering, ranging from 303 days (sow no. 33) up to 397 days (sow no. 49) (Table 3). The average number of piglets born alive in subsequent four litters in the examined group was relatively high and equalled 13 (first litter) up to 15 (third litter) piglets (Table 3).

Tabele 3. Values of selected reproduction traits of Polish landrace sows

Tabela 3. Wartości wybranych cech rozrodczych loch rasy pbz

Sow no. Nr lochy	Age of first littering Wiek pierwszego oproszenia	Number of piglets born alive in the first litter Liczba prosiąt żywo urodzonych w 1. miocie	Number of piglets born alive in the second litter Liczba prosiąt żywo urodzonych w 2. miocie	Number of piglets born alive in the third litter Liczba prosiąt żywo urodzonych w 3. miocie	Number of piglets born alive in the fourth litter Liczba prosiąt żywo urodzonych w 4. miocie
13	369	13	14	–	–
14	369	15	12	14	–
15	316	14	13	–	–
16	354	13	12	–	–
24	372	12	14	17	16
27	353	9	10	13	14
28	324	15	14	20	14
33	303	14	17	14	14
35	346	11	12	13	14
36	323	15	13	15	–
38	328	14	13	14	13
39	358	14	14	14	13
40	375	12	13	–	–
41	397	11	–	–	–
42	337	12	12	–	–
44	396	14	13	15	15
45	352	13	13	14	16
49	397	13	14	15	13
50	345	13	15	16	15
51	344	12	12	16	14
Average Średnia	353	13	13	15	14

The observed polymorphism of the size of sex chromosomes and autosomes in the examined sows may be connected with production traits. Relations between the size of the chromosome area and the selected reproduction traits of the group of examined sows are shown in Table 4. In the examined group of sows, the values of correlation indexes were between [–0.2733] (the number of piglets born alive in the second litter – percentage of sex chromosomes) and 0.4044 (the number of piglets born alive in the fourth litter – average sex chromosome area) (Table 4).

The age of the first litter turned out to be positively correlated with all examined chromosome parameters. However, the highest correlation value was found in the case of the average sex chromosome area – r = 0.3598 (Table 4). Correlations between the examined average chromosome areas (sex, autosomes, and total) and the number of piglets born alive in the first litter turned out to be negative with the value near to zero (Table 4).

However, the relative sex chromosomes size, their percentage and average area turned out to be negatively correlated with the number of piglets born alive in the second and third litters. The average autosome area and the average chromosome area turned out to be positively correlated with the number of piglets born alive in the second, third, and fourth litter (Table 4).

Table 4. Simple correlation indexes between the examined traits
Tabela 4. Współczynniki korelacji prostych pomiędzy badanymi cechami

Correlated traits Cechy korelowane	Age of first littering Wiek pierwszego oproszenia	Number of piglets born alive in the first litter Liczba żywo urodzonych prosiąt w 1. miocie	Number of piglets born alive in the second litter Liczba żywo urodzonych prosiąt w 2. miocie	Number of piglets born alive in the third litter Liczba żywo urodzonych prosiąt w 3. miocie	Number of piglets born alive in the fourth litter Liczba żywo urodzonych prosiąt w 4. miocie
Age of first littering Wiek pierwszego oproszenia	–	–0.3050	–	–	–
Relative size of sex chromosomes Względna wielkość chromosomów płci	0.0876	0.0067	–0.2728	–0.2448	–0.0568
Percentage of sex chromosomes % udział chromosomów płci	0.0878	0.0071	–0.2733	–0.2443	–0.0564
Average area of sex chromosomes Średnia powierzchnia chromosomów płci	0.3598	–0.0097	–0.1876	–0.0331	–0.4044
Average area of autosomal chromosomes Średnia powierzchnia chromosomów autosomalnych	0.2250	–0.0306	0.2234	0.3189	0.3257
Average area of chromosomes (autosomes, heterochromosomes) Średnia powierzchnia chromosomów (autosomy, heterochromosomy)	0.2448	–0.0312	0.2153	0.3185	0.3488

Interesting relations were observed between the examined chromosome traits and the number of piglets born alive in the fourth litter. The average areas of sex chromosomes and autosomes proved to have a relatively high positive correlation with the number of piglets born alive in the fourth litter, the values being respectively $r = 0.4044$, $r = 0.3257$ and $r = 0.3488$ (Table 4). Obtained values of correlation indexes might come in useful as indexes concerning prediction of the number of piglets to be born alive in the fourth litter.

4. DISCUSSION

Polymorphism of the relative length of sex chromosomes was assessed in several breeds of farm animals, including pigs. Polymorphism of the chromosome length was examined in sex chromosomes based on their relative length expressed by the centromeric index, that is the ratio of the long arms to the short arms (q:p), or the percentage of length of the haploidal autosomes complement and the sex X-chromosome [4]. In several breeds and synthetic lines of breeding pigs in Poland, a polymorphism was observed of the relative length of the sex Y-chromosome, the smallest and relatively easy to identify in the animals' karyotype. It was found that polymorphic variants of the relative length of the Y-chromosome may be considered as characteristic traits of particular pig breeds. It seems that the observed differences in the relative length of the Y-chromosome stem from the varied size of the large heterochromatin block, which includes the q arm of this chromosome. Measuring the length of chromosomes, chiefly sex chromosomes, correlation was sought between polymorphic variants and determined fertility indexes [4, 5].

It was not concluded explicitly what the influence of the chromosome size polymorphism was on the animals' production traits. However, the research has proved the thesis that chromosome polymorphism can be applied in seeking chromosome markers and gene mapping [1, 2, 3].

Chromosome polymorphism observations conducted in population covering one breed allow one to reveal inter-individual differences, as well as to determine the breed trend [5, 6].

5. CONCLUSION

1. The examined sows, belonging to the Polish landrace breed, had the number of chromosomes normal for this breed and sex, namely 2n = 38 XX.
2. Significant differences were found in terms of the area of autosomal chromosomes and the total area of sex chromosomes and autosomes in diploidal cells of the examined sows. From among the calculated correlation indexes, the phenotypic correlation index between the average sex chromosome area and the number of piglets born alive in the fourth litter (r = 0.4044) is worth noting.
3. The observed relations between traits determining the size of chromosomes (autosomes and sex chromosomes) and the traits regarding the sows reproduction indicate the possibility of using the chromosome polymorphism as a marker of reproductive traits.
4. The results, which are to be considered preliminary, provide the basis for further research with the objective of seeking production (reproduction) traits markers in sows.

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POLIMORFIZM WIELKOŚCI CHROMOSOMÓW U LOCH RASY POLSKA BIAŁA ZWISŁOUCHA (PBZ)

Streszczenie

Oceniono polimorfizm chromosomów płci i autosomów na podstawie pomiaru ich powierzchni u loch rasy polska biała zwisłoucha oraz związek zaobserwowanego polimorfizmu z cechami rozrodczymi. Średnia powierzchnia chromosomów płci u badanych loch wynosiła 7,4779 μm^2, przy zakresie wartości od 6,9739 μm^2 do 8,1331 μm^2. Średnia powierzchnia autosomów wynosiła natomiast 143,7742 μm^2. Stwierdzono znacznie większą zmienność w obrębie chromosomów płci niż autosomów. Współczynnik zmienności powierzchni chromatyd chromosomów płci wahał się w granicach od 0,3182% do 7,9053%. Zmienność powierzchni chromosomów autosomalnych zawierała się w granicach od 1,0491% do 1,3069%. Średnie powierzchnie chromosomów płci i autosomów oraz średnie powierzchnie całkowite chromosomów okazały się stosunkowo wysoko dodatnio skorelowane z liczbą prosiąt żywo urodzonych w czwartym miocie, a wartości współczynników korelacji wynosiły odpowiednio: r = 0,4044; r = 0,3257 i r = 0,3488.

Słowa kluczowe: polimorfizm, chromosomy, cechy rozrodcze, lochy, rasa pbz

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EFFECT OF CATTLE LIQUID MANURE FERTILIZATION ON SOIL MITES (ACARI) OF LOWLAND MEADOW

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The effects of cattle liquid manure, treated with Effective Microorganisms (EM) or bactericidal agent, on soil mites of lowland meadow was investigated, with species analysis of Oribatida. Doses of cattle liquid manure 30 $m^3 \cdot ha^{-1}$ and 60 $m^3 \cdot ha^{-1}$ increased the crop of green forage, more with EM than with bactericidal agent, while a dose 90 $m^3 \cdot ha^{-1}$ had no effect. A cattle liquid manure reduced the density of mites, including the Oribatida and comparing to the control plot, but with bactericidal agent reduced the density more than with EM. Among Oribatida *Liebstadia similis*, *Scheloribates laevigatus*, *Eupelops occultus*, *Achipteria coleoptrata* and *Tectocepheus velatus* were relatively abundant, while the other species occurred in low densities. The mites lived mostly on the lower parts of plants, and the density decreased with the soil depth.

Keywords: cattle liquid manure, grassland, Acari, Oribatida, Effective Microorganisms

1. INTRODUCTION

Mites are one of the largest group of soil mesofauna, which inhabit mainly the upper soil layer [13]. They participate in transformation of soil organic matter and mix it with the mineral soil [3, 4, 13]. Therefore, a high activity of mites results in faster circulation of elements, which are necessary for plant growth and are important for production of ecosystem.

Generation of huge amounts of liquid manure at industrial farms creates environmental problems. If liquid manure is improperly stored, it drains in the soil and ground water, and pollutes it. Liquid manure can be also used as a fertilizer on grasslands, but it contains pathogenic microorganisms, and should be disinfected before using. Usually, chemicals are used, which also effect the soil, but Effective Microorganisms (EM) are without chemicals, and also limit the development of pathogenic microorganisms. Properly used liquid manure is an important source of macro- and microelements for plants, and also enriches the soil in organic matter, improving its fertility. This paper aims to know the effects of cattle liquid manure with EM or bactericidal agent on soil mites (Acari), with species analysis of Oribatida.

2. MATERIAL AND METHODS

This experiment was performed on permanent lowland meadow, which belongs to the Agricultural Experimental Station in Minikowo (University of Technology and Life Sciences in Bydgoszcz), situated in the Valley of Bydgoszcz Canal. Seven plots (4 x 5 m each) were chosen, with 5 m buffer zones between them, from which one was a control (0), and the other were fertilized with cattle liquid manure in doses 30 $m^3 \cdot ha^{-1}$, 60 $m^3 \cdot ha^{-1}$ and 90 $m^3 \cdot ha^{-1}$, either with EM (plots 1–3, respectively) or bactericidal agent (plots 4–6, respectively).

Soil samples of 17 cm^2 and 9 cm deep were taken from each plot in spring of 2008 in 10 replications. The samples were next divided into lower part of plants (3–0 cm) and two soil layer (0–3 and 4–6 cm). Oribatid mites were extracted in high gradient Tullgren funnels, conserved and determined to species, including the juvenile stages. Totally 5333 mites, including 1628 oribatid mites were investigated. We compared the species with the abundance (*A*) and dominance (*D*) indices, and mite communities with abundance, number species of Oribatida, and the Shannon *H* index [8]. The results were verified using U Manna-Whitney test at $P \leq 0.05$ (Statistica 6.0), with earlier logarithmic transformation of data [1, 12]. Names of oribatid species follow Weigmann [15].

3. RESULTS AND DISCUSSION

A low and medium doses of cattle liquid manure slightly increased the crop of green forage, compared to the control plot, more with EM than with bactericidal agent, while the highest dose has no effect on this crop (Table 1).

Table 1. Green forage and abundance of mites (*A* in thousand individuals · m^{-2}), number of species (*S*) and Shannon *H* index of Oribatida in the investigated plots

Tabela 1. Plon zielonki a abundancja roztoczy (*A* w tysiącach sztuk · m^{-2}), liczba gatunków (*S*) i indeks *H* Shannona Oribatida na badanych poletkach

	Plots – Poletka						
Group – Grupa	0	1	2	3	4	5	6
Green forage Plon zielonki	11.6	13.1	13.5	11.3	12.9	13.2	10.9
Acari – Roztocze	61.0	51.5	44.8	38.6*	46.8	44.4	37.3*
Gamasida	0.3	2.7*	0.3[a]	0.1[a]	1.3*[bc]	1.8*[bc]	1.2*[bc]
Actinedida	40.2	34.3	31.3	26.1	31.2	29.7	23.5*
Other – Inne	0.5	0.3	0.4	0.0	0.5	0.3	0.4
Oribatida	20.0	14.2	12.8	12.4*	13.8	12.6*	12.2*
S	9	7	7	7	7	5	6
H	1.47	1.46	1.49	1.44	1.46	1.61	1.72

Significant differences at $P \leq 0.05$ between – Istotne różnice przy $P \leq 0.05$ pomiędzy: *control plot and plots 1–6 – poletkiem kontrolnym a poletkami 1–6: [a] plot 1 and plots 2–6 – poletkiem 1 a poletkami 2–6: [b] plot 2 and plots 3–6 – poletkiem 2 a poletkami 3–6: [c] plot 3 and plots 4–6 – poletkiem 3 a poletkami 4–6: [d] plot 4 and plots 5–6 – poletkiem 4 a poletkami 5–6; [e] plot 5 and plot 6 – poletkiem 5 a poletkiem 6

A cattle liquid manure fertilization reduced the density of mites, comparing to the control plot, along with increasing doses of fertilizer, but bactericidal agent reduced the density more than EM, and the results were significantly lower only in plots with the highest doses of liquid manure. Among the mites the most abundant was Actinedida, and the second most abundant was Oribatida, while the other groups occurred in low densities. The oribatid mites were sensitive to cattle liquid manure, which is partly consistent with literature [2, 7, 14]. The influence of cattle liquid manure on oribatid mites in the nearby meadows was negative at doses of 40 $m^3 \cdot ha^{-1}$ and 80 $m^3 \cdot ha^{-1}$ [7], while the influence of pig liquid manure was negative at doses 20 $m^3 \cdot ha^{-1}$ and 40 $m^3 \cdot ha^{-1}$, and positive at dose 60 $m^3 \cdot ha^{-1}$ of this fertilizer [14]. Bielska [2] also observed negative influence of liquid manure on the density, species number and age structure of oribatid mites of grassland.

Among Oribatida *Liebstadia similis*, *Scheloribates laevigatus*, *Eupelops occultus*, *Achipteria coleoptrata* and *Tectocepheus velatus* were relatively abundant, while the other species occurred in low densities (Table 2).

Table 2. Abundance (*A* in thousand individuals · m^{-2}) and dominance (*D*) indices of some oribatid species in the investigated plots: tot – total, juv – *juveniles*

Tabela 2. Abundancja (*A* w tysiącach sztuk · m^{-2}) i dominacja (*D*) niektórych gatunków Oribatida na badanych poletkach: tot – ogółem, juv – formy młodociane

Species Gatunki		Plots – Poletka						
		0	1	2	3	4	5	6
Oribatida	*A* tot	20.0	14.2	12.8	12.4*	13.8	12.6*	12.2*
	A juv	4.1	3.5	2.2	2.5	2.6	2.2*	2.1*
	D	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Liebstadia similis	*A* tot	9.0	6.9	5.2	5.7	4.9	4.5*	4.3*
	A juv	2.1	1.8	1.0	1.4	1.0*	0.9*	0.8*
	D	44.7	48.9	40.4	45.6	45.4	35.9	35.2
Scheloribates laevigatus	*A* tot	3.9	2.5	3.1	2.6	3.8	3.0	2.7
	A juv	0.8	0.4	0.5	0.4	0.8	0.7	0.7
	D	19.5	17.9	24.4	20.9	27.5	23.9	21.3
Eupelops occultus	*A* tot	3.5	2.5	2.2	2.6	3.3	2.7	2.6
	A juv	1.0	0.8	0.4*	0.7	0.6	0.5	0.5
	D	17.7	17.4	17.4	20.9	24.0	21.5	21.3
Achipteria coleoptrata	*A* tot	2.0	1.3	1.4	0.6*	0.9	0.8	0.7*
	A juv	0.2	0.4	0.2	0.0[a]	0.1	0.1	0.1
	D	9.9	8.9	10.8	4.9	6.5	6.7	5.5
Tectocepheus velatus	*A* tot	1.0	0.4[b]	0.5	0.4*	0.7	0.5	0.7
	A juv	0.0	0.0	0.0	0.0	0.0	0.0	0.1
	D	4.8	3.0	4.2	3.4	4.8	4.3	5.9

Significant differences at $P \leq 0.05$ between – Istotne różnice przy $P \leq 0.05$ pomiędzy: *control plot and plots 1–6 – poletkiem kontrolnym a poletkami 1–6: [a] plot 1 and plots 2–6 – poletkiem 1 a poletkami 2–6: [b] plot 2 and plots 3–6 – poletkiem 2 a poletkami 3–6; [c] plot 3 and plots 4–6 – poletkiem 3 a poletkami 4–6: [d] plot 4 and plots 5–6 – poletkiem 4 a poletkami 5–6: [e] plot 5 and plot 6 – poletkiem 5 a poletkiem 6

Four former species represent typical meadow species, and often dominate in permanent meadows [7, 14], while the latter species is more abundant in forests [9]. *Tectocepheus velatus* dominated in oribatid mite communities in alternating meadow, and tolerated both cattle and pig liquid manure [6, 11], but in permanent lowland meadows it was not abundant [7, 14]. A cattle liquid manure slightly limited the participation of juveniles in oribatid mite communities, but the results were significantly lower only in plots with medium and higher doses of liquid manure with bactericidal agent.

The mites occupied mainly lower parts of plants, and their density decreased with the soil depth. The influence of cattle liquid manure on vertical distribution of oribatid mites was indistinct, and oribatid mites occupied mainly lower part of plants. The densities of these mites on plants in plots 0, 1, 2, 3, 4, 5 and 6 were 31.1, 22.2, 19.8, 20.3, 20.8, 18.6 and 17.7 individuals · 50 cm^{-3}, respectively, while in upper soil horizon were 2.3, 1.3, 1.5, 0.4, 2.2, 2.3 and 2.5 respectively, which was consistent with Graczyk et al. [7] and Wasińska-Graczyk et al. [14]. Presence of abundant typical meadow species like *Achipteria coleoptrata*, *Scheloribates laevigatus* on lower parts of grasses can create economic problems. These mites are intermediate hosts of tapeworms [5, 9], which parasite on some domestic animals.

4. CONCLUSIONS

1. A low and medium doses of cattle liquid manure slightly increased the crop of green forage, compared to the control plot, more with EM than with bactericidal agent, while the highest dose has no effect on this crop.
2. A cattle liquid manure reduced the density of mites, including the Oribatida and comparing to the control plot, but bactericidal agent reduced the density more than EM.
3. Among Oribatida *Liebstadia similis*, *Scheloribates laevigatus*, *Eupelops occultus*, *Achipteria coleoptrata* and *Tectocepheus velatus* were relatively abundant, while the other species occurred in low densities.
4. The mites lived mostly on the lower parts of plants, and the density decreased with the soil depth.

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WPŁYW NAWOŻENIA GNOJOWICĄ BYDLĘCĄ NA ROZTOCZE GLEBOWE (ACARI) ŁĄKI NIZINNEJ

Streszczenie

Wpływ gnojowicy bydlęcej z dodatkiem Efektywnych Mikroorganizmów (EM) lub czynnika bakteriobójczego na roztocze glebowe łąki nizinnej badano za pomocą analizy gatunkowej Oribatida. Gnojowica bydlęca w dawkach 30 $m^3 \cdot ha^{-1}$ i 60 $m^3 \cdot ha^{-1}$ stosowana z dodatkiem EM powodowała wyższy wzrost plonu zielonki niż z dodatkiem czynnika bakteriobójczego, natomiast dawka 90 $m^3 \cdot ha^{-1}$ nie wywarła żadnego wpływu. Gnojowica bydlęca zmniejszała zagęszczenie roztoczy, łącznie z Oribatida, w porównaniu z poletkiem kontrolnym, przy czym redukowała je w większym stopniu z dodatkiem czynnika bakteriobójczego niż EM. Wśród Oribatida stosunkowo licznie występowały *Liebstadia similis*, *Scheloribates laevigatus*, *Eupelops occultus*, *Achipteria coleoptrata* i *Tectocepheus velatus*, podczas gdy pozostałe gatunki występowały w niskim zagęszczeniu. Roztocze żyły przeważnie na niższych częściach roślin, a ich zagęszczenie zmniejszało się wraz z głębokością gleby.

Słowa kluczowe: gnojowica bydlęca, użytki zielone, Acari, Oribatida, Efektywne Mikroorganizmy

UNIWERSYTET TECHNOLOGICZNO-PRZYRODNICZY
IM. JANA I JĘDRZEJA ŚNIADECKICH
W BYDGOSZCZY
ZESZYTY NAUKOWE NR 255 – ZOOTECHNIKA 38 (2010) 19-26

ANALYSIS OF CAG/AAG POLYMORPHISM INCIDENCE AT CODON 171 OF THE OVINE PRION PROTEIN GENE

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The ovine *PRNP* gene is responsible for the production of cell prion protein and its polymorphism significantly affects the sheep susceptibility/resistance to scrapie. The aim of the study presented herein was to detect variation (CAG/AAG) occurring at codon 171 of the ovine prion protein gene. The test covered 241 animals from the following sheep breeds: Polish Merino, Blackheaded Mutton Sheep, Polish Mountain Sheep, Ile de France, Berrichon du Cher and Suffolk. The test itself was conducted with the application of the PCR-RFLP method and with the use of the *Mbo*I enzyme. A lysine coding triplet was found in the 171 position in case of the Blackheaded Mutton Sheep group. The XXK allele occurred in a heterozygous combination with a frequency of 0.69%, constituting 1.33% of genotypes of the analysed Blackheaded Mutton Sheep group and 0.4% of genotypes of the whole population subject to study.

Keywords: scrapie, *PRNP*, polymorphism, lysine, sheep

1. INTRODUCTION

Scrapie is a degenerative disease that affects the nervous system of sheep and goats. Scrapie was first described in 1723 in Scotland. Both scrapie and other diseases from the brain amyloidoses group has up until today remained incurable. The *PRNP* gene is responsible for coding the prion protein which in case of sheep is located within the long arm of chromosome 13, in the 13q17-q18 position [14]. Sheep have revealed polymorphisms at the following codons of the prion protein gene: 83, 85, 101, 112, 127, 136, 137, 138, 141, 142, 143, 146, 151, 154, 167, 168, 171, 172, 175, 176, 180, 189, 195, 196, 231, 237, 241 [1, 4, 7, 8, 9, 10, 13, 17, 18]. Polymorphism of the prion protein gene leads to synthesis of prion proteins of various amino acid sequences, which constitutes the cause of diversified resistance to infections and disease development. The polymorphisms occurring particularly at three codons: 136 (GCC/GTC), 154 (CGG/CAT) and 171 (CGG/CAG, CAG/CAT) have a considerable influence on the degree of sheep resistance/susceptibility to scrapie [9]. Due to this variability, five main haplotypes (hereinafter referred to as alleles) may be distinguished: $A_{136}R_{154}R_{171}$, $A_{136}R_{154}Q_{171}$,

$A_{136}H_{154}Q_{171}$, $A_{136}R_{154}H_{171}$, $V_{136}R_{154}Q_{171}$. The ARR allele determines the highest degree of sheep resistance to this disease, followed by the AHQ, ARH, ARQ alleles, with the VRQ allele determining the highest susceptibility to scrapie. The aforesaid alleles combine to form 15 genotypes which were divided into five classes of sheep resistance to scrapie, from G1 to G5 [6].

In order to detect prion protein genotypes, molecular biology methods are used, such as, e.g.: the PCR-RFLP method [10], sequencing [12], SSCP, DGGE [17]. Selection of the applicable method depends on the number of tested animals and the costs of analysis. PCR-RFLP constitutes the most frequently used method for polymorphism detection at the three most important codons: 136, 154 and 171. Another CAG/AAG single nucleotide polymorphisms (SNP) responsible for coding the lysine amino acid was discovered in the 171 triplet as a result of a study on the ovine *PRNP* gene variability [7, 10, 11]. The most frequently used enzymes enabling the CGG/CAG, CAG/CAT (R/H/Q) polymorphism detection at codon 171 are the *Bsp*HI and *Bsp*DI enzymes recognizing the CGG and CAG and CAT sequence [16]. Unfortunately, these enzymes prevent detection of the CAG/AAG polymorphism responsible for coding lysine in this position. In case of utilization of the PCR-RFLP reaction in genotyping the prion protein gene at three codons: 136, 154, 171, it is necessary to trigger an additional reaction in order to detect the AAG sequence in the 171 triplet.

Tests carried out in order to detect the CAG/AAG polymorphism were performed in several countries: Mongolia [10], Greece [5], the United States of America [11] and Italy [3]. Unfortunately, there is currently no information available on the Polish population of sheep, even though the occurrence of such single nucleotide polymorphisms (SNP) may alter the result of genotyping carried out with the use of PCR-RFLP method. It was for this reason that the purpose of the study involved detection of the CAG/AAG polymorphism in the 171 triplet, responsible for coding lysine in this position in the case of the following group of sheep: Polish Merino, Blackheaded Mutton Sheep, Ile de France, Polish Mountain Sheep, Suffolk and Berrichon du Cher, that can be found in the territory of Poland.

2. MATERIAL AND METHODS

The study covered a population of 241 sheep. The following sheep breeds were subject to testing: Polish Merino (8 males and 27 females), Blackheaded Mutton Sheep (15 males and 60 females), Polish Mountain Sheep (13 females), Ile de France (5 males and 66 females), Berrichon du Cher (5 males and 25 females) and Suffolk (3 males and 14 females). Peripheral blood of sheep collected from the jugular vein into test tubes containing K_2EDTA anticoagulant served as the biomaterial. High quality genome DNA was isolated with the use of MasterPure™ DNA Purification Kit for Blood (Epicentre Technologies). In order to detect polymorphism at the 171 codon (CAG/AAG) the PCR-RFLP technique was utilized with the use of the *Mbo*I enzyme, as per the Lühken et al. [15] methodology, with certain own modifications. The polymerase chain reactions (PCR) were performed in a volume of 25 µl. The reaction mixture contained: 1.5U Dream Taq (Fermentas) polymerase, 200 µM of each dNTP, 2.0 mM $MgCl_2$ and 10 pmol of each of the following primers: Forward 5`AACCAACATGAAGCATGTGGC3`, Reverse 5`AAGCAAGAAATGAGACACCACC3` and 100ng DNA. The thermal reaction profile consisted of: preliminary denaturation at 94°C for 90 seconds, followed by 40 cycles

covering: 94°C for 15 seconds, 60°C for 20 seconds, 72°C for 45 seconds and final synthesis at 72°C for 5 minutes. The amplified fragment had a length of 545 base pairs. In order to detect the CAG/AAG polymorphism at codon 171 of the ovine *PRNP* gene responsible for coding lysine in this position, the amplicon was subject to enzymatic hydrolysis with 3U of the *Mbo*I (Fermentas) restriction enzyme at a temperature of 37°C, for 4 hours. Enzymatic digestion products were separated in 2.5% agarose gel with 0.5 μg/μl ethidium bromide in a 1 x concentrated TBE buffer (10xTBE: 0.89M Tris, 0.89M boric acid, 0.02M EDTA, pH 8.0) at 120 V for 60 min. In case of occurrence of the AAG sequence at codon 171 the *Mbo*I restriction enzyme hydrolysed the amplicon to a 379 bp long fragment proving the incidence of lysine and to two fragments with a length of 182 bp and 197 bp, proving the incidence of another allele. Subsequently, the XXK allele occurrence frequencies were calculated for the whole group of animals covered by the study as well as for each individual sheep breed.

3. RESULTS

As a result of the performed (CAG/AAG) SNP detection in triplet 171 of the ovine *PRNP* gene it has been revealed that the XXK allele occurred in one Blackheaded Mutton Sheep female. No incidence of a lysine coding sequence at codon 171 has been identified in the case of the following sheep breeds: Polish Merino, Polish Mountain Sheep, Suffolk, Ile de France, Berrichon du Cher. The XXK allele was found in one specimen, which constituted 0.2% of alleles of the whole analysed sheep population and 0.66% of the Blackface sheep group. The genotype containing lysine occurred in a heterozygous XXK/XXX combination. Proportion of the genotype containing this allele totalled 0.4% of all genotypes within the analysed sheep population and 1.33% of the Blackheaded Mutton Sheep group. Frequency of the allele responsible for coding lysine in triplet 171 is exceptionally low within the sheep population covered by the study. Owing to its low frequency of occurrence this allele has not been categorized into any of the classes of sheep resistance to scrapie.

Figure 1 presents electrophoretic distribution of the products of *Mbo*I restriction enzyme amplicon hydrolysis reaction: M – DNA fragment length marker pUC19 (Fermentas); 1-9 – specimens without a restriction site for the *Mbo*I enzyme at codon 171, DNA fragments with the following lengths were obtained: 197 bp and 182 bp; 10 – specimen possessing a restriction site for the *Mbo*I enzyme at codon 171, DNA fragments with the following lengths were obtained: 379 bp, 197 bp and 182 bp (Fig. 1.)

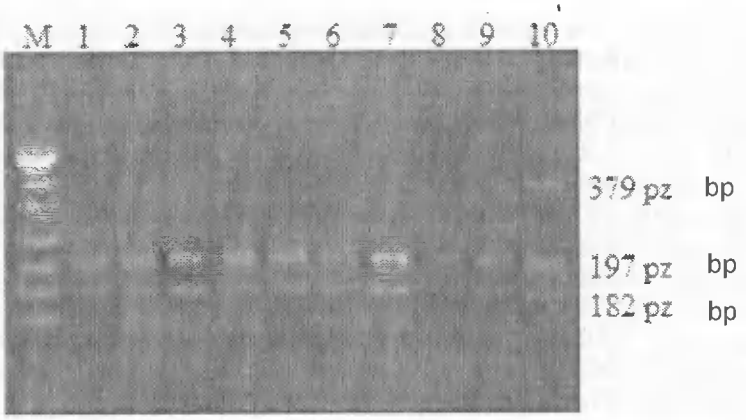

Fig. 1. Electrophoretic distribution of the products of *Mbo*I restriction enzyme amplicon hydrolysis reaction: M – DNA fragment length marker pUC19 (Fermentas): 1-9 – specimens without a restriction site for the *Mbo*I enzyme at codon 171. DNA fragments with the following lengths were obtained: 197 bp and 182 bp; 10 – specimen possessing a restriction site for the *Mbo*I enzyme at codon 171. DNA fragments with the following lengths were obtained: 379 bp. 197 bp and 182 bp

Rys. 1. Rozdział elektroforetyczny produktów rekcji hydrolizy amplikonów enzymem restrykcyjnym *Mbo*I: M – marker długości fragmentów DNA pUC19 (Ferments): 1-9 – osobniki nieposiadające miejsca restrykcyjnego dla enzymu *Mbo*I w kodonie 171, otrzymano fragmenty DNA o długości: 197 pz i 182 pz; 10 – osobnik posiadający miejsce restrykcyjne dla enzymu *Mbo*I w kodonie 171, otrzymano fragmenty DNA o długości: 379 pz, 197 pz i 182 pz

4. DISCUSSION

The genetic tests revealed a very low frequency of CAG/AAG polymorphism incidence at codon 171 of the ovine prion protein gene within the sheep population covered by the studies. Furthermore, only the XXK allele occurrence in a heterozygous combination has been confirmed. Studies carried out by researchers all around the world confirm occurrence on the ARK allele only in heterozygous combination [2, 3, 5, 10, 11]. This allele has been identified in a population of the following sheep breeds: Khalkh, Yeroo and Orkhon [10], Biellmont [2], Chios and Karagouniko [5] as well as in case of Dorper, Barbados Blackbelly, Barbados/St. Croix and Suffolk [11]. The highest frequency of the XXK allele has been noted in the case of the Biellese sheep breed in Italy [3] and amounted to 2.5%. This result was followed by dairy sheep from Greece [5] followed in turn by the Khalkh breed in Mongolia with 0.6% [10] and the Black-headed Mutton Sheep breed (own research) with 0.4%. The lowest frequency has been identified in Oklahoma, United States, at a level of 0.35% [11].

Studies carried out in Italy in 2004 covered 1207 sheep of the Biellmont breed from the Piedemount region [3]. The AAG sequence in triplet 171 was discovered in a group of 59 sheep, which amounted to 4.9% of all sheep subject to the study. The ARK allele occurred in a homozygous ARK/ARK combination in case of 2 specimens, totalling 0.2% of all genotypes. The percentage proportion of heterozygotes with the ARK allele was as follows: ARQ/ARK (n = 46) 3.8%, ARH/ARK as well as

AHQ/ARK in 4 specimens, which constituted 0.3%, VRQ/ARK in 2 specimens, totalling 0.2% and ARR/ARK in case of a single specimen, placed last in terms of percentage proportion in the frequency of genotypes within the analysed population [3].

In Greece the studies covered 216 sheep of the Chios and Karagouniko breed (Billinis, 2004). Polymorphism in triplet 171 responsible for coding lysine was discovered in case of 7 specimens in a heterozygous ARQ/ARK combination, which totalled 3.2% of the analysed population. No incidence of the ARK allele in a homozygous combination has been observed [5].

In Mongolia the studies covered 271 sheep of four breeds: Khalkh, Yeroo, Orkhon and Khangai, all inhabiting the central region of Mongolia. The ARK allele in a homozygous combination was discovered only in case of one specimen of the Khalkh breed, which amounted to a 0.6% frequency both for genotypes as well as alleles [10].

In Oklahoma, the XXK allele was discovered in case of 8 specimens of the following breeds: Dorper (n = 1), Barbados Blackbelly (n = 2), Barbados/St. Croix (n = 2) and Suffolk (n = 3) [11].

The discovery of another lysine coding mutation in triplet 171 of the *PRNP* gene initiated researches on the connection between the ARK allele and the sheep susceptibility to scrapie. The allele was found in Italy in a group of Biellmont breed specimens, both in homozygous as well as heterozygous combinations. It has been proved that the incidence of the ARK allele is related to low resistance to scrapie. It has further been discovered that the ARK allele occurred more frequently in a group of sick sheep. Due to an exceedingly low level of the ARK allele, genotypes in which it occurred have not been categorized into any of the scrapie resistance classes [2]. The same group of researchers conducted further studies in order to establish the susceptibility to scrapie revealed by sheep with a genotype containing at least one ARK allele. Due to low frequency of this allele and insufficient amount of analyses, ARK has not been categorized into any of the scrapie resistance classes [2].

Own researches as well as the studies carried out in Italy [3], Greece [5], Mongolia [10] and the United States of America [10] this polymorphism occurred with a very low frequency in case of the following sheep breed populations: Blackheaded Mutton Sheep, Biellmont, Khalkh, Yeroo, Orkhon, Dorper, Barbados Blackbelly, Barbados/St. Croix and Suffolk. The inconsiderable amount of specimens with CAG/AAG polymorphism in the lysine coding triplet 171 of the *PRNP* gene does not occur frequently enough for this allele to be categorized into any of the scrapie resistance classes. Owing to the identification of polymorphism in the lysine coding triplet 171, it is necessary to continue the studies leading to classification of the ARK allele to the relevant scrapie resistance class.

The frequency of this allele in the case of sheep populations covered by the studies is exceedingly low, that is why it has not been categorized into any of the scrapie resistance classes as per DEFRA, Great Britain.

5. CONCLUSIONS

The SNP in triplet 171 of the ovine *PRNP* gene triggering lysine coding is undetectable by means of standard DNA tests employing the PCR-RFLP method to detect the five alleles responsible for animal susceptibility to scrapie: ARR, ARQ, ARH,

AHQ, VRQ. Low frequency of occurrence of this allele within the group of six sheep breeds covered by the studies does not indicate the necessity to introduce tests enabling detection of the AAG sequence at codon 171. Standard laboratory procedures enabling detection of the five most common alleles of the prion protein seem adequate in case of the analysed breeds. It is however advisable to conduct similar studies covering other sheep breeds kept in the territory of Poland.

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BADANIE OBECNOŚCI POLIMORFIZMU CAG/AAG W KODONIE 171 GENU BIAŁKA PRIONOWEGO OWIEC

Streszczenie

Owczy gen *PRNP* odpowiedzialny jest za produkcję białka prionowego komórkowego prawidłowego, a jego polimorfizm ma znaczący wpływ na podatność/oporność owiec na trzęsawkę (scrapie). Celem badań była detekcja zmienności (CAG/AAG) występującej w kodonie 171 owczego genu białka prionowego. Przebadano 241 osobników ras: merynos polski, czarnogłówka, polska owca górska, ile de france, berrichon du cher oraz suffolk metodą PCR-RFLP przy użyciu enzymu *Mbo*I. W pozycji 171 wykryto triplet kodujący lizynę w grupie owiec rasy czarnogłówka. Allel XXK wystąpił w układzie heterozgotycznym z częstością 0,69%, co stanowiło 1,33% genotypów przebadanej populacji czarnogłówki oraz 0,4% genotypów całej populacji objętej badaniami.

Słowa kluczowe: trzęsawka (scrapie), *PRNP*, polimorfizm, lizyna, owce

The following study was partly financed through scholarship granted as part of the "2008/2009-ZPORR scholarships for doctoral students" project – action 2.6 of the Integrated Operational Program for Regional Development (ZPORR), project no. Z/2.04/II/2.6/20/09, with 75% financed from the funds of the European Social Fund and 25% from the Budget funds.

Artykuł został sfinansowany ze stypendium otrzymanego w ramach projektu „Stypendia dla doktorantów 2008/2009-ZPORR" – działania 2.6 ZPORR, nr projektu Z/2.04/II/2.6/20/09 finansowanego w 75% ze środków Europejskiego Funduszu Społecznego Unii Europejskiej oraz w 25% ze środków Budżetu Państwa.

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ACTIVITY OF SELECTED BLOOD SERUM ENZYMES IN GROWING BROILER CHICKENS

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The objective of this study was to determine the effect of age on the response of enzyme activities in blood serum of growing broiler chickens. The research was conducted on Ross 308 chickens. Blood serum samples were collected three times at 14, 21 and 42 days of age. Significant effects of age were found for both aspartate aminotransferase (AST) and lactate dehydrogenase (LDH).There were no statistically significant age- dependent differences among alanine aminotransferase (ALT) and creatine kinase (CK). The results proved the effects of biochemical metabolic processes, resulting from selection for intensive growth in meat type chickens.

Keywords: broiler chickens, age, serum enzymes

1. INTRODUCTION

Meat type chickens are characterized by a fast rate of growth and good use of feed. For the economic reasons, broilers should also seal high performance slaughtered carcass with low proportion of fat, high quality of meat and good health and resistance to diseases [4]. In farm conditions fast-growing broiler chickens have health problems, manifested by constitutional weakness [9]. Both in the state of health or disease, it is possible to define by a certain level of systemic enzymes in blood serum, dependent on some factors, such as: breed, age, sex, nutrition, physiological state and welfare of animals. Measuring the level of indicator enzymes in broiler chicken blood serum can also be very helpful in monitoring herd health and disease diagnostics. Observations of enzyme activity are not generally appropriate in terms of production because of the modest amount or lack of data on physiological standards of hematological factors dependent on named above genetic and environmental factors [7, 6].

The aim of this study was to estimate the level of some enzymes in the blood serum of broiler chickens.

2. MATERIAL AND METHODS

The present study was performed with 14, 21 and 42 day-old male commercial broilers Ross 308. Birds were kept in a traditional poultry-house with an automatically controlled system of maintaining constant environmental conditions (temperature, air renewal and humidity), consistent with the recommendations of the technology of rearing chickens Ross 308. In the growth and development period all chickens had unlimited access to water and they were also fed *ad libitum* with a standard feed mixture corn-wheat-soya broiler starter mash until 21 days, followed by a grower mash from 22 to 35 days and a finisher type mash from 36 to 42 day of bird's life.

In 14, 21, 42 days, ten chicks with a similar body weight were chosen to the hematological tests. The obtained blood serum activity of the following enzymes was determined by means of a photometer Epoll 20 and reagents of Alpha Diagnostic:

1) aspartate aminotransferase AST (EC 2.6.1.1) in IU/l
2) alanine aminotransferase ALT (EC 2.3.1.2) in IU/l
3) lactate dehydrogenase LDH (EC 1.1.1.27) in IU/l
4) creatine kinase CK (EC 2.7.3.2) in IU/l

All data in the study were analyzed statistically using the Statistica 8.0 (Statsoft, Inc. 2008). A significance level of 0.05 was used.

3. RESULTS AND DISCUSSION

The results of enzyme activity in broiler chickens blood serum measured in the study are presented in Table 1.

Table 1. Enzymatic activity in blood serum of growing broiler chickens
Tabela 1. Aktywność enzymów w surowicy krwi rosnących kurcząt brojlerów

Enzyme Enzym	Age (days) Wiek (dni)		
	14	21	42
AST, IU/l	228.6[1a] 20.1[2]	234.8[a] 45.1	280.3[b] 36.9
ALT, IU/l	8.1[a] 2.4	10.6[b] 2.3	6.6[a] 1.2
LDH, IU/l	3097[a] 478.5	2546.6[a,b] 415.9	3923[b] 972.2
CK, IU/l	5369.3 1494.9	5619.4 1080.5	6368.3 1617.6

[1] Mean value – Wartość średnia
[2] Standard deviation – Odchylenie standardowe
[a, b] Mean values in the same row not sharing a common superscript are significantly different ($P < 0.05$) – Wartości średnie w tym samym rzędzie oznaczone różnymi literami różnią się istotnie ($P < 0.05$)

The highest activity of aspartate aminotransferase 280.30 IU/l was observed in the oldest group of 42 day-old broiler chickens and it was significantly higher ($P < 0.05$) than in the younger broiler chickens. A significant effect of age in AST level was observed by Vyboh et al. 2006. In the studies conducted by other authors, a significant effect of age of chickens on the enzymatic activity of AST was not confirmed [1, 7]. The results of AST activity levels in chickens of different ages obtained in our study were similar to data presented by other authors [7, 2, 5]. Definitely lower activity of ALT than AST in bird's blood serum with no pathological changes in growing turkey's liver [8] excludes inflammation of the organs.

In 14 day-old birds, the activity level of alanine aminotransferase ALT was 8.10 IU/l. A significant increase in ($P < 0.05$) the enzyme activity to 10.60 IU/l was observed in 3 week-old chickens. At 6 weeks of age, the lowest level of ALT, 6.56 IU/l, was observed. It was similar to Krasnodębska-Depta's & Koncicki's studies (2000), moreover no significant effect of age on enzyme activity in growing broiler chickens was found. ALT levels observed in this study are lower than in earlier observations [10, 2].

The lowest 2545.63 IU/l lactate dehydrogenase LDH activity was found in 21 day-old broilers. A significant increase in enzyme activity was observed in the oldest group of birds (Table 1). The results obtained in this study for LDH level in chickens of different ages are higher than data presented by other authors [1, 3, 7, 5].

In these studies, the lowest activity of creatine kinase, CK 5369.33 IU/l, was found in blood of the youngest 14 day-old chickens. The increase in CK activity was observed in blood serum in older broilers at the age of 21 and 42 days. The highest, 6368.33 IU/l, CK activity was observed in blood serum of the oldest 6 week- old chickens. although there was no statistically significant age-dependent difference among the activity of this enzyme. The studies conducted by other authors reported a statistically significant effect of age on the activity of CK [7, 10], although in this study higher values of the enzyme activity were obtained [3, 7, 5]. It should be noted that the increase in the level of CK activity is characteristic of fast growing broiler chickens [3, 9].

4. CONCLUSIONS

1. Significant effects of age in this study were found for both aspartate aminotransferase (AST) and lactate dehydrogenase (LDH).
2. There were no statistically significant age-dependent differences among alanine aminotransferase (ALT) and creatine kinase (CK).

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AKTYWNOŚĆ WYBRANYCH ENZYMÓW W SUROWICY KRWI ROSNĄCYCH KURCZĄT BROJLERÓW

Streszczenie

Celem badań było określenie wpływu wieku na aktywność enzymów w surowicy krwi rosnących kurcząt brojlerów. Badanie przeprowadzono na kurczętach Ross 308. Pobrano próbki osocza krwi trzy razy: w 14., 21. i 42. dniu życia. Stwierdzono istotny wpływ wieku zarówno dla aminotransferazy asparaginianowej (AST), jak i dehydrogenzay mleczanowej (LDH). Nie odnotowano statystycznie istotnych różnic w zależności od wieku w przypadku aminotransferazy alaninowej (ALT) i kinazy kreatynowej (CK). Wyniki wykazały wpływ biochemicznych procesów metabolicznych, wynikających z selekcji, na intensywny wzrost kurcząt typu mięsnego.

Słowa kluczowe: kurczęta brojlery, wiek, enzymy surowicy

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W BYDGOSZCZY
ZESZYTY NAUKOWE NR 255 – ZOOTECHNIKA 38 (2010) 31-37

MILK PERFORMANCE AND BODY TYPE AND BUILD SCORING AS WELL AS BODY CONDITION SCORING OF FIRST-CALF COWS

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The research was carried out on the grounds of milk performance as well as the traits related to condition, type, and build of first-calf cows from the Kujawsko-Pomorskie province. The research covered the body condition scores of 333 cows as well as build and conformation scores of 645 animals. A group of 135 cows was distinguished from the analyzed cows which met the following criteria: first-calf cows, their first calving took place in 2007, all the animals in their first lactation were scored in the area of their type and build as well as the condition up to the hundredth day of lactation. The highest productivity of milk and its components was found in cows with the highest type and build scores. A negative relation between body condition scoring and first-calf cow milk performance results as well as cow type and build scoring was found. High and positive correlations between build general scoring and partial scoring pertaining to conformation were found.

Keywords: milk productivity, cow type and build scoring, cow body condition

1. INTRODUCTION

Conformation traits are not directly connected with cow milk productivity, however, their indirect influence has been found. Most of the available research results indicate that there is a positive relation between the elements of conformation and cow milk performance [1, 2, 5, 6, 7]. An animal of appropriate build of legs and rump is used longer in a herd. Appropriately built and capacious udder as well as its correct attachment means a possibility of producing more milk, easier machine milking as well as a smaller risk of injuries or dangerous udder diseases [11].

Consistent growth of milk productivity of cows sets higher requirements pertaining to maintenance, care, nutrition, and proper disease prevention they need. Examination of the body condition of cows carried out regularly is one of the superior methods enabling the monitoring of nutrition, reproduction, and state of health of the animals [1].

The purpose of this study was to present the results of utility of first-calf cows, originating from a leading farm of the Kujawsko-Pomorskie province, together with their type and build scoring as well as body condition scoring.

2. MATERIAL AND METHODS

The research covered the body condition scores of 333 cows as well as build and conformation scores of 645 animals. A group of 135 cows was distinguished from the analyzed cows which met the following criteria: first-calf cows, their first calving took place in 2007, all the animals in their first lactation were scored in the area of their type and build as well as the condition up to the hundredth day of lactation.

The following categories were considered in the evaluation of type and build of the cows: calibre and capacity, type and build, legs and hooves, udder as well as general evaluation. The following traits related to milking capacity of the first-calf cows were considered: productivity of milk, productivity and content of fat and protein in milk.

Conformation of the animals was evaluated in accordance with the Institute of Animal Production regulations (2004) in the period of 15 – 180 days after calving. Each category was scored between 50 and 100. The presented body condition assessment was carried out in the 5-point Wildman et al. scale [13]. The data came from milking cows used in the leading farm of the Kujawsko-Pomorskie province in identical environmental conditions. The cows were divided into categories with regard to type, build, and condition scores depending on the number of points they had scored. The first-calf cows of the first category of body condition scores (up to 3 points) were evaluated in view of their condition up to the hundredth day of lactation.

Numeric data came from the SYMLEK system and were prepared statistically by means of a variance analysis in the Statistica PL application [10]. A relation between evaluation categories pertaining to type, build, and body condition of cows and milk performance in the first lactation was studied. Significance of differences in the area of levels of the studied factors was described by means of Tukey's test [10]. Correlation coefficients between milk performance, type and build scoring and body condition of the cows were calculated.

3. RESULTS

While examining the relation between condition and build of the cows and productivity of the first lactation it was found that there is a significant connection between evaluation of calibre, udder as well as general evaluation and most of the researched traits of milk performance in the first lactation (Table 1). No statistically confirmed relation was found between the evaluation category referring to the condition of cows and the productivity of first-calf cows (Table 1).

While analyzing the results pertaining to milking capacity of the cows it was found that the first-calf cows belonging to the second category, the type and build of which were scored higher, produced more milk, fat, and protein in lactation (Table 2). The differences in compared groups often turned out to be statistically significant and highly

significant. The animals in the condition up to 3 points produced more milk and fat than the cows in better body condition. These differences were not confirmed as statistically significant (Table 2). More protein was found in milk of the cows in better body condition, the differences between the groups turned out to be statistically significant (Table 2).

Table 1. Value of F_{emp} and the level of the effect of the factors studied and dairy milk yield in first lactation

Tabela 1. Wartość F_{emp} oraz istotność zależności pomiędzy badanymi czynnikami a wydajnością mleka w pierwszej laktacji

Factor Czynnik	Trait – Cecha				
	Milk Mleko	Fat Tłuszcz		Protein Białko	
	[kg]	[kg]	[%]	[kg]	[%]
Condition Kondycja	3.03	2.38	0.56	4.59	0.31
Calibre Kaliber	15.10***	6.02**	5.70**	9.62**	7.40**
Type and conformation Typ i budowa	8.74***	2.70	4.23*	4.38*	7.80**
Legs and hooves Nogi i racice	4.76*	3.73	1.01	6.14*	0.01
Udder Wymię	12.00***	10.83***	1.98	10.34***	2.18
General score Ocena ogólna	24.73***	15.98***	5.80**	22.40***	2.92

*** – $P \leq 0.001$; ** – $P \leq 0.01$; * – $P \leq 0.05$

Table 2. Relationship between milk performance and overall conformation score

Tabela 2. Zależność pomiędzy użytkowością mleczną a oceną za pokrój

Evaluation of cows Ocena krów			Trait – Cecha				
			Milk Mleko	Fat Tłuszcz		Protein Białko	
Category (pts) – Kategoria (pkt)		n	[kg]	[kg]	[%]	[kg]	[%]
Condition	≤ 3	47	9859.10	377.23	3.86	314.98[a]	3.20
Kondycja	> 3.	88	9348.90	362.31	3.92	396.70[a]	3.18
Calibre	< 84	67	9002.60[A]	356.27[A]	4.00[A]	290.60[A]	3.23[A]
Kaliber	≥ 84.	68	10043.00[A]	378.57[A]	3.80[A]	315.35[A]	3.15[A]
Type and conformation	< 82	66	9112.9[A]	359.77	3.99[a]	294.36[a]	3.24[A]
Typ i budowa	≥ 82.	69	9922.2[A]	374.90	3.82[a]	311.39[a]	3.15[A]
Legs and hooves	< 80	51	9137.80[a]	356.14	3.96	290.22[a]	3.19
Nogi i racice	≥ 80.	84	9762.60[a]	374.40	3.87	310.87[a]	3.19
Udder	< 79	47	8885.40[A]	347.38	3.98[a]	285.55	3.22[A]
Wymię	≥ 79.	88	9869.00[A]	378.25	3.86[a]	312.42	3.17[A]
General score	< 80	44	8599.10[A]	342.27[A]	4.05[A]	277.05[A]	3.24
Ocena ogólna	≥ 80.	91	9975.00[A]	379.70[A]	3.84[A]	315.65[A]	3.17

[AA, aa] – values marked with the same capital are significantly different at $P \leq 0.01$ ($P \leq 0.05$)

[AA, aa] – wartości oznaczone tymi samymi literami różnią się od siebie istotnie przy $P \leq 0.01$ ($P \leq 0.05$)

A relation between body condition scoring and conformation scoring of the cows was tried to be analyzed and no statistical relation between body condition and build indices of the cows was found, the value was close to zero (Table 3). It is possible that the found relations resulted from various moments both evaluations had been made at. High and positive correlations between build general scoring and partial scoring pertaining to conformation were found. Also a very strong relation between type and build scoring and cow calibre scoring was found (Table 3).

A negative correlation between cow body condition scores and remaining researched traits of milk performance was found with the only exception of percentage of fat and protein in milk, the value close to zero (Table 3). All the type and build scoring was positively correlated with the productivity of milk, fat and protein in milk of first-calf cows. Negative relations between type and build scoring and fat and protein content in milk were found (Table 3).

Table 3. Correlation between condition and overall conformation score

Tabela 3. Korelacje pomiędzy kondycją a oceną za pokrój

Trait Cecha		$\overline{X}$	S_x	Condition Kondycja	Calibre Kaliber	Type and conformation Typ i budowa	Legs and hooves Nogi i racice	Udder Wymię	General score Ocena ogólna
				n					
				333	645	645	645	645	645
Condition Kondycja		3.42	0.15						
Calibre Kaliber		84.10	3.72	0.021					
Type and conformation Typ i budowa		81.02	2.76	0.039	0.748**				
Legs and hooves Nogi i racice		79.22	3.48	0.014	0.164**	0.318*			
Udder Wymię		79.88	2.87	0.014	0.357**	0.437**	0.196**		
General score Ocena ogólna		80.38	2.48	0.039	0.549**	0.663**	0.864**	0.531**	
Milk Mleko (kg)		9526.54	1634.51	–0.074	0.367**	0.301**	0.217**	0.255**	0.368**
Fat	kg	367.50	53.76	–0.005	0.247**	0.220**	0.149	0.162	0.241**
Tłuszcz	%	3.90	0.48	0.095	–0.236**	–0.169**	–0.144	–0.191**	–0.256**
Protein	kg	303.06	47.83	–0.074	0.301**	0.259**	0.217**	0.244**	0.338**
Białko	%	3.19	0.19	0.009	–0.259**	–0.183**	–0.041	–0.093	–0.165

** – $P \leq 0.01$; * – $P \leq 0.05$

4. DISCUSSION

The in-house studies confirm the results achieved by Juszczak [6], who claimed that bigger growth performance of cows is a trait positively connected with productive capabilities of the animals. An appropriate type and build of a cow boosts its production

and helps to achieve good health and longevity. A high productivity cow should have an excellent udder as well as strong legs and hooves [11]. Guliński [2] in his study claimed that beside leg and hoof evaluation, traits positively related to milk production capacity included the remaining elements of general evaluation of cows. Nogalski [8], while studying the relations between cow body dimensions and productivity of milk and fat and protein content, observed low and mostly positive coefficients of phenotype correlations.

Puchajda et al. [9] found low and mostly negative correlation coefficients between traits of milk performance and cow body dimensions. Only in the case of productivity of fat and width in the ischiadic tubers, a low but significant relation was found [9]. This was not confirmed by the presented results of the in-house studies.

According to Trela et al. [11], build and conformation scoring is an important tool in the husbandry work, as it provides additional information on an animal, its predisposition to higher productivity, longevity as well as beneficial changes in animal silhouette in every generation. According to Januś [4], body condition and daily productivity of milk were significantly influenced by the following factors: a farm, period of nutrition, level of daily productivity, stage after calving, another lactation, and genotype. Januś and Borkowska [5] showed that throughout the lactation the body condition of cows depends on the age and season of calving. First-calf cows and cows calved in the autumn-winter season were found to demonstrate a smaller loss of condition at the beginning of lactation and slower recovery in the following period [4]. Also Jankowska and Sawa [3] claimed that cow body condition is significantly influenced by the level of milk production in a farm, genotype of the animals, stage of lactation, age of the animals, and season the evaluation is made in.

The majority of available literature gives examples of positive relations between cow body condition scoring and their milk usability and the in-house studies do not correspond with these results. Waltner et al. [12] observed the highest production in the case of cows of medium fatty cover reserves at calving and the lowest at the head of extreme condition. Also Nogalski [9], while analyzing the productivity of ECM milk at standard lactation, found that cows of body condition in the range from 3.25 to 3.75 points produced most milk, fat, and protein. According to Wildman et al. [13], Body Condition Scoring (BCS) is a subjective measure of fat reserves used for assessing the correctness of nutrition and state of health of the animals [13]. Januś [4], on the basis of her studies, claims that she found the lowest condition scores < 2.0 at cows in the first month after calving, 4 plus scores were usually given to dried off cows or cows in late lactation.

At present, in Poland economic reasons as well as applied production technologies require carrying out the scoring of new traits which will enable longer and more effective use of the animals [11]. High production of milk in the country encourages breeders to work more on functional traits of cows, which influence production costs to be lower. Working on dairy cattle husbandry comprises developing production and functional traits [7]. A Productivity and Functionality (*Polish*: Produkcyjność i funkcjonalność – PF) general index has been in use since the 2007/1 assessment for dairy cattle, presented in animal catalogues and containing a conformation subindex.

5. CONCLUSIONS

1. In the in-house studies it was found that most milk and its components was obtained from cows of high type and build scores.
2. A negative relation between body condition scoring and milk performance of first-calf cows was found. The presented fact may result from too small population considered in the studies or subjective body condition scoring.
3. Studies on a relation between body condition scoring and milk performance should be extended with additional factors and repeated on a bigger population of cattle of the Kujawsko-Pomorskie province.

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UŻYTKOWOŚĆ MLECZNA A OCENA TYPU I BUDOWY ORAZ KONDYCJI KRÓW PIERWIASTEK

Streszczenie

Badania przeprowadzono na podstawie użytkowości mlecznej oraz cech związanych z typem i budową 645 krów pierwiastek z województwa kujawsko-pomorskiego. Pod uwagę wzięto również wyniki oceny 333 krów. Wyodrębniono grupę 135 krów pierwiastek, których data pierwszego wycielenia przypadała na 2007 r. Najwyższą wydajnością mleka i jego składników cechowały się krowy z najwyższymi ocenami typu i budowy. Stwierdzono istnienie ujemnej zależności między oceną kondycji a wynikami użytkowości mlecznej pierwiastek, a także wysokie, dodatnie korelacje między ogólną oceną za budowę oraz ocenami za pokrój.

Słowa kluczowe: wydajność mleka, ocena typu i budowy krów, kondycja krów

UNIWERSYTET TECHNOLOGICZNO-PRZYRODNICZY
IM. JANA I JĘDRZEJA ŚNIADECKICH
W BYDGOSZCZY
ZESZYTY NAUKOWE NR 255 – ZOOTECHNIKA 38 (2010) 39-44

DYNAMICS OF THE POPULATION OF RED FOX *Vulpes vulpes* (LINNAEUS 1758) IN THE CIECHANÓW DISTRICT OVER 2002–2006

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The research was carried out in 112 sub-districts of the Ciechanów District over 2002–2006. It involved the analysis of the fox population and distribution over five hunting seasons. It was found that the average of hunting fox in the first hunting season 2001/2002 was 1.7 pcs./1000 ha and in the last hunting season 2005/2006 – 4.3 pcs./1000 ha of the sub-district. The average fox number, on the other hand, over the research period in the first hunting season was 4.1 pcs./1000 ha and in the fifth, last hunting season 7.6 pcs./1000 ha of the sub-district. Despite the increasing hunting in respective hunting seasons, the fox population did not decrease.

Keywords: red fox, Ciechanów, population changes

1. INTRODUCTION

Fox (*Vulpes vulpes*, Linnaeus 1758) is one of the best known animals of the biggest range of occurrence, in practice, it is present in all the types of environments of the northern hemisphere, it also got acclimatized in Australia. The effect of foxes on the environment is very important, their positive effect is limited to combat small rodents and the selective-sanitary role [11]. Starting from the first half of the 1990s, the fox population increased drastically despite increasing hunting. With a dynamic increase in the number of that predator, one shall not disregard its role in the hunting ground since it can pose a threat to some species being its preys. That situation was analyzed by Kamieniarz, Bresiński [9] and Jabłoński et al. [6] as well as Kirkiłło-Stacewicz et al. [10] in different economic years. One can see clearly that in the regions where there were performed vaccinations against rabies, the fox population and hoot-out shows a growing tendency, while the small game number decreases drastically, which was confirmed by the reports by Brudnicki et al. [2]. Predatory nature of that species is the most common reason for a decrease in the population of pheasants [5] and one of the main reasons for the current regress of partridge [12]. Predatory nature of fox is also mentioned among the causes of the decreased population of roe deer [9]. By limiting the factor of fox mortality, which was rabies, the situation of that predator improved,

demonstrating an increase in its number. Juszko [7] paid attention to the need to decrease the fox population and maintaining it at a rational level as a result of hunting. Kamieniarz [9] claims that the effectiveness of the activities aiming at decreasing fox density depends on the intensity of the shoot-out, the area size, numerous seasons involving hunting.

The aim of the present paper was the analysis of data on the population and distribution of fox in the Ciechanów District in five successive economic years. The data on the numbers of hunting of the predator in respective sub-districts of the district will be a springboard for the characteristics of changes in the population abundance of that species.

2. MATERIAL AND METHODS

The analysis of the number and distribution of fox was made over five hunting seasons: 2001/2002, 2002/2003, 2003/2004, 2004/2005 and 2005/2006 in the Ciechanów District. The research material was obtained from the District Board of the Polish Hunting Association in Ciechanów. The data cover 112 sub-districts of that district and have been taken from Hunting Breeding Plans. The information collected facilitated the analysis of changes in fox population. The paper also aimed at determining the causes of those changes.

3. RESULTS

The research covered all 112 sub-districts of the Ciechanów District. In the first hunting season researched, 2001/2002, acquisition of fox was 1004 pcs. In 63 sub-districts (56.3%) fox shoot out was lower than 3 pcs./1000 ha. From 3.1 to 6 pcs./1000 ha were shot out in the area of 20 sub-districts (17.9%), 1 sub-district (0.9%) showed the shoot out ranging from 9.1 to 12 pcs./1000 ha. In the other 28 sub-districts (24.9%) no shoot-out was recorded. That situation is presented in map 1 in the fifth last hunting season researched, 2005/2006, fox acquisition in that district was 2453 pieces. In the area of 41 sub-districts (36.5%) fox shoot-out was below 3 pieces/1000 ha. From 3.1 to 6 pieces /1000 ha was shot out in the area of 51 sub-districts (45.5%); from 6.1 to 9 pieces/1000 ha against the total of 14 sub-districts (12.6%); 3 sub-districts (2.7%) demonstrated the shoot-out from 9.1 to 12 pieces/1000 ha. Over 12 pieces/1000 ha was shot out only in 2 sub-districts (1.8%). In 1 sub-district (0.9%) no shoot-out was reported. That situation is presented in map 2. The average fox acquisition for sub-districts of the Ciechanów District:

- in the 2001/2002 hunting season it was 1.7 pcs./1000 ha of the sub-district,
- in the 2005/2006 hunting season it was 4.3 pcs./1000 ha of the sub-district.

Map 1. Fox acquisition number by shoot-out in the 2001/2002 hunting season in the Ciechanów District

Mapa 1. Wielkość pozyskania lisa metodą odstrzału w sezonie łowieckim 2001/2002 na terenie okręgu ciechanowskiego

Map 2. Fox acquisition number by shoot-out in the 2005/2006 hunting season in the Ciechanów District

Mapa 2. Wielkość pozyskania lisa metodą odstrzału w sezonie łowieckim 2005/2006 na terenie okręgu ciechanowskiego

Legend – Legenda

	no data avail. – brak danych
	0 pcs. – 0 szt.
	0.1–3 pcs. – 0.1–3 szt.
	3.1–6 pcs. – 3.1–6 szt.
	6.1–9 pcs. – 6.1–9 szt.
	9.1–12 pcs. – 9.1–12 szt.
	> 12 pcs. – 12 szt.

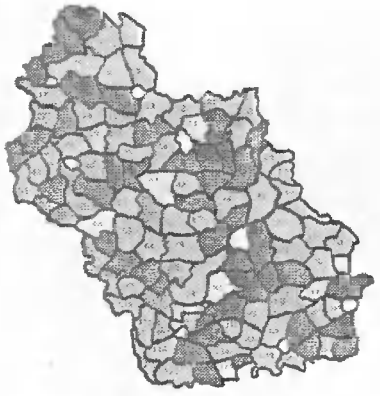
After the first hunting season, 2001/2002, the fox population in the Ciechanów District was 2355 pcs. In 33 sub-districts (29.4%) the fox population did not exceed 3 pcs/1000 ha, in 44 sub-districts (39.2%) the population ranged from 3.1 to 6 pcs/1000 ha, and 18 sub-districts (16.1%) demonstrated the population from 6.1 to 9 pcs./1000 ha. In successive 6 sub-districts (5.4%) the population ranged from 9.1 to 12.0 pcs./1000 ha. Over 12 pcs/1000 ha occurred in 2 sub-districts (1.8%). In the other 9 sub-districts (8.1%) no fox population was recorded (map no 3).

After the fifth, last hunting season, 2005/2006, the fox population in the Ciechanów District was 4340 pcs. In 4 sub-districts (3.6%) the fox population did not exceed 3 pcs./1000 ha, in 35 sub-districts (31.2%) the population ranged from 3.1–6 pcs./1000 ha, and 45 sub-districts (40.1%) showed the population of 6.1–9 pcs./1000 ha. Successive 13 sub-districts (11.7%) showed the population ranging from 9.1 to 12 pcs./1000 ha. Over 12 pcs./1000 ha of the sub-district occurred in 15 sub-districts (13.4%) (map no 4). The average fox population for sub-districts of the Ciechanów District:

- after the 2001/2003 hunting season it was 4.1 pcs./1000 ha of the sub-district,
- after the 2005/2006 hunting season it was 7.6 pcs./1000 ha of the sub-district.

Map 3. Fox population after the 2001/2002 hunting season in the Ciechanów District

Mapa 3. Stan liczebny lisa po sezonie łowieckim 2001/2002 na terenie okręgu ciechanowskiego



Map 4. Fox population after the 2005/2006 hunting season in the Ciechanów District

Mapa 4. Stan liczebny lisa po sezonie łowieckim 2005/2006 na terenie okręgu ciechanowskiego

Legend – Legenda

	no data avail. – brak danych
	0 pcs. – 0 szt.
	0.1–3 pcs. – 0.1–3 szt.
	3.1–6 pcs. – 3.1–6 szt.
	6.1–9 pcs. – 6.1–9 szt.
	9.1–12 pcs. – 9.1–12 szt.
	> 12 pcs. – 12 szt.

4. DISCUSSION

In the Ciechanów District one can observe a clear increase in the fox population and acquisition. In the 2001/ 2002 hunting season the fox population was 2355 pcs and increased up to 4340 pcs in the 2005/2006 hunting season, while in the case of shoot-out in the first season acquisition was 1004 pcs and with each year it increased and in 2005/2006 shoot-out was 2453 pcs. Fox population in the earlier years was researched by many authors, including Brudnicki et al. [2] and Skoczylas et al. [13]. Since vaccines against rabies were introduced, there has been recorded an increase in the population of that predator, the consequences of that decision and the dynamic increase in the population was reported by Kamieniarz and Bresiński [9] and Flis [3, 4]. Definite actions of hunters are the only way to bring about the desired effects which would contribute to a decrease in the fox population. In Poland foxes are hunted in a traditional way and having eliminated rabies, being the basic factor reducing the population, with no clear increase in shoot-out there are no chances for stopping the eruption of the fox population. The following possibilities are considered:

- greater activity of hunters hunting foxes,
- more frequent organization of special group fox hunting,

- introducing different forms of promoting for the performance of shoot-out,
- prolonging the hunting period and popularizing other famous but effective hunting methods, hunting with burrows, hunting young foxes at the very beginning of the hunting season, hunting in artificial burrows.

The specificity of the species is also essential. In the case of fox, we deal with a very flexible species. Besides the use of vaccines against rabies, considered to be the direct cause of increasing the fox head, the situation can be also affected:
- the skill of fox settling in open spaces,
- the use of waste left by the man.

One should consider the mechanisms which could effectively decrease the constantly growing fox population. The total shoot-outs with the other mortality factors must be higher than the increment. Knowing neither the extent of other losses nor the real increment rate, one shall plan the shoot-out at the level not lower than the spring state. The reliable stock-taking, determining all the known burrows, regular schedule of hunting with burrows, the placement of clothes soaked with vixen urine over heat period, or even the construction of artificial burrows with the use of adequate terrain conditions, all that definitely increase the number of foxes shot out [1].

5. CONCLUSIONS

1. In the research period analyzed the fox population in the Ciechanów District shows a growing trend.
2. In the five hunting seasons researched in the Ciechanów District fox acquisition is increasing considerably.
3. Despite the increasing acquisition in five hunting seasons the fox population has not got smaller.
4. The inhibition in the fox population is difficult due to high reproductive potential of that species.
5. One should aim at limiting the fox population to the extent where it plays sanitary role in nature.

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DYNAMIKA POPULACJI LISA POSPOLITEGO *Vulpes vulpes* (LINNAEUS 1758) W OKRĘGU CIECHANOWSKIM W LATACH 2002–2006

Streszczenie

Badania przeprowadzono w 112 obwodach łowieckich okręgu ciechanowskiego w latach 2002–2006. Obejmowały one analizę stanu liczebnego i rozmieszczenia lisa podczas pięciu sezonów łowieckich. Średnia pozyskania lisa w pierwszym sezonie łowieckim 2001/2002 wynosiła 1,7 szt./1000 ha, a w ostatnim – 2005/2006 – 4,3 szt./1000 ha obwodu. Średnia liczebność lisa w okresie badań w pierwszym sezonie łowieckim wynosiła natomiast – 4,1 szt./1000 ha, a w piątym, ostatnim – 7,6 szt./1000 ha obwodu. Pomimo wzrastającego pozyskania w poszczególnych sezonach łowieckich liczebność populacji lisa nie uległa zmniejszeniu.

Słowa kluczowe: lis pospolity, Ciechanów, zmiany liczebności populacji

ISSN 1899-0096