Journal of Animal and Veterinary Advances 12 (23): 1681-1689, 2013
ISSN: 1680-5593
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Genetic and Phenotypic Trends of Selected Production Traits in Black and White Dairy Cattle Populations of Poland

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Abstract: Monitoring genetic trends for production and functional traits is an important element of breeding work. In the present study, researchers analyse genetic and phenotypic trends for some production traits in Polish Black and White dairy cattle population. In the analysis the information on 6454 cows born to 709 sires was used and the time span studied was 1905-2006. For all of the analysed traits, i.e., milk, butterfat and protein yields (kg) and percentage composition of milk (%) in subsequent lactations, the observed genetic trends were positive during the entire analysed period (over 100 years). The linear increase of genetic trend was not equal for each of the traits as selection intensity had been changing and more acurate evaluation methods were introduced to identify superior animals as parents for the next generation.

Key words: Dairy cattle, genetic trend, production traits, milk, protein

INTRODUCTION

Selection is the basic method of livestock genetic improvement. The measurement of selection efficiency is genetic gain also referred to as genetic trend. The expected genetic gain is not always equal the realised genetic gain, especially in cattle where generation interval is very long. The obtained genetic trend is influenced by mate selection method used by different breeding value estimation or by different selection intensity (Mayer and Musani, 2002).

In 1970's in order to speed up the rate of genetic improvement in Polish dairy cattle, the Holstein-Frisian breed was used for absorptive crossing with local black and white cattle population (Filistowicz *et al*., 1993; Karwacki *et al*., 2001).

With the unique database, dating back over 100 years, the realised genetic gain for Black and White breed dairy cattle population was estimated. The research also shows the effect of different breeding value evaluation method on the genetic progress. Other researchers investigating similar problem usually analyse the trend for the periods short enough to consider only one method of breeding value evaluation (Khorshidie *et al*., 2012). The aim of the research was the analysis of genetic and phenotypic trends for some milking traits.

MATERIALS AND METHODS

The research concerned the population of Black and White dairy cattle population, kept on one farm (1-4 herds, depending on the year) in Wielkopolska (Great Poland) region. The analysis was performed on 1905 to 2006 database. Selection and the best black and white breed sires had always been used in that population and since 1970's mainly Holstein-Frisian (of black and white variety) bulls had been used (as recommended in the national breeding programme). The analysed population comprised 6454 cows coming from 709 sires and divided into family groups. The oldest pedigree was 20 generation long.

Considering the changes in dairy cattle evaluation that had taken place over the last 100 years, the only production trait to be analysed was milk yield, together with butterfat and protein yield and taking regression and proportional adjustments (according to the formulae described by Szyszkowski *et al.* (1991a-c) into account. The adjustments allowed for recalculating the obtained lactation values for the 305 days yield. The lifetime lactation was defined as the total milk (kg) produced in all milking days during all the lactations.

The material was divided into 92 classes of genetic groups, described by the birth year. The first one

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comprised (due to small number of individuals) all the cows born by 1912 and the last class comprised cows born after 2003.

Due to the fact that the earliest documentation lacked the complete pedigree data so for the better comparison of all birth years researchers used DFREML Statistical Method (Meyer, 1993). On the basis of the information gathered the following linear model was used to assess the genetic gain in respective age-groups:

$$Y_{ijklmno} = \mu + s_i + d_j + g_k + h_l + f_m + w_n + e_{ijklmno}$$

Where:

- $Y_{ijklmno}$ = The phenotypic value observed for the trait
- μ = Population mean
- s_i = Sire random effect
- d_j = Dam random effect
- g_k = The fixed effect of genetic group of individuals born in the same year
- h_l = The fixed effect of herd-year-season (according to the production year)
- f_m = The fixed effect of h-f genes proportion
- w_n = The fixed effect of the first calving age
- $e_{ijklmno}$ = Random error

The statistical package used was DFREML (Meyer, 1993). On the basis of the estimated genetic group effects a regression line was drawn showing the genetic trend for the analysed traits. The REG procedure of SAS statistical package was used for calculation (SAS, 2010).

RESULTS AND DISCUSSION

Milk yield: In Fig. 1-4, genetic and phenotypic trends for milk yield in the first 305 days lactation and for lifetime lactation are presented. The trends are positive for each of the analysed lactations and the regression coefficient (b) ranges from 34.38-47.54. The highest regression coefficient was estimated for lifetime lactation. Despite decreasing productive lifespan the single lactation yield increased enough for the gain to be quite considerable (b = 59.4).

Until 1990 the genetic trend for milk yield was similar in subsequent years. However, for cows of 1990-1995 age groups the gain increases considerably. For the lifetime yield the trends have been negative for the last several years because some cows have been still alive and lactating. That is why these years should be ignored in the analysis.

Fat yield: Just like in case of the milk yield, the genetic trends for fat yield (kg) are also positive for 1990-1995. The general trend for this trait showed by the regression line is much higher than the one for the milk yield (Fig. 5-7).

Protein yield: Protein content in milk has been assessed only since 1953 at first in heifers and since 1964 in all the lactating cows. It was only in 1964 when the protein content started to be assessed in all the lactating cows. Figure 8-10 present the genetic trends for protein yield (kg) which turned to be much higher than for fat yield and milk yield. The higher value of genetic gain for

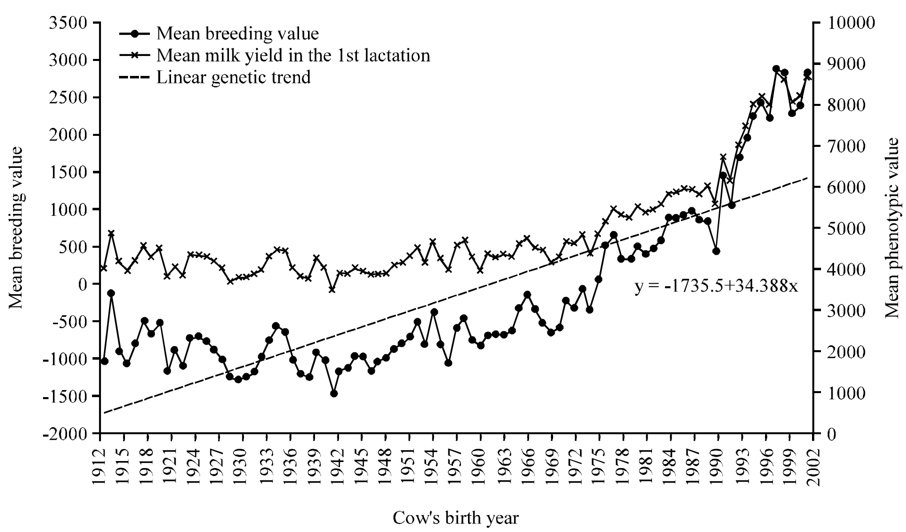

Fig. 1: Genetic and phenotypic trend for milk yield in the 1st lactation (kg)

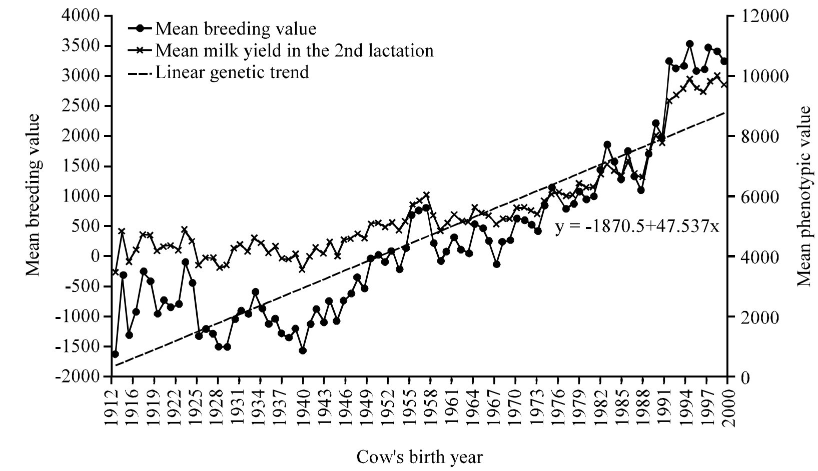

Fig. 2: Genetic and phenotypic trend for milk yield in the 2nd lactation

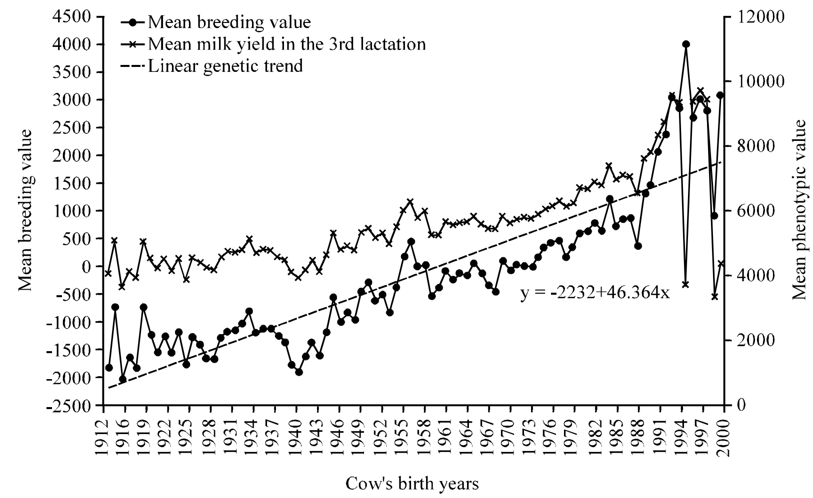

Fig. 3: Genetic and phenotypic trend for milk yield in the 3rd lactation

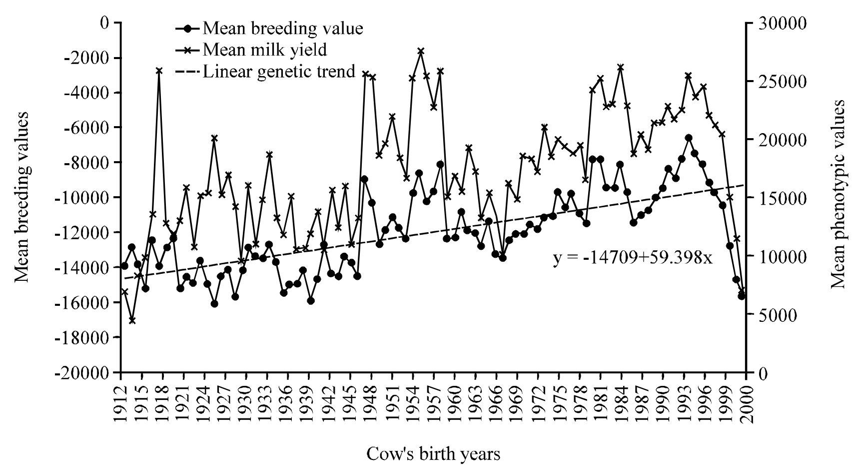

Fig. 4: Genetic and phenotypic trend for milk yield in the lifetime lactation

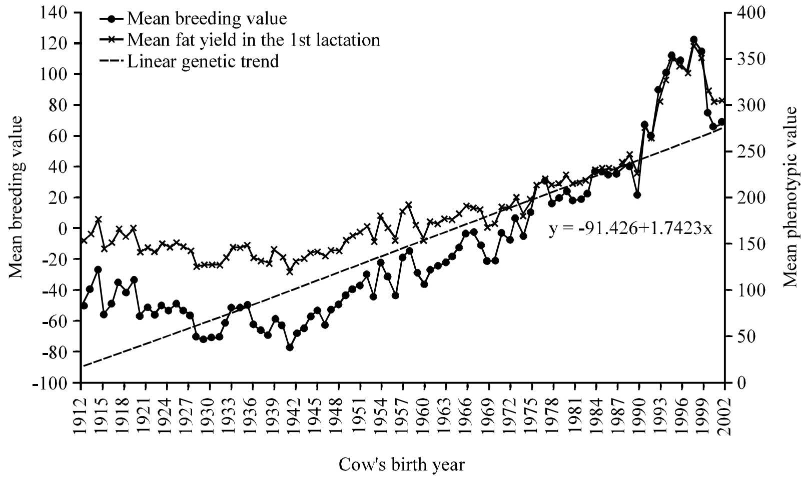

Fig. 5: Genetic and phenotypic trend for fat yield in the 1st lactation (kg)

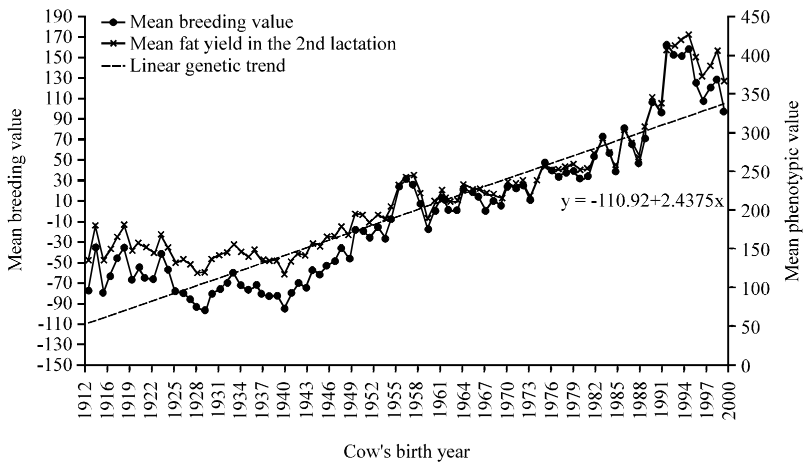

Fig. 6: Genetic and phenotypic trend for fat yield in the 2nd lactation

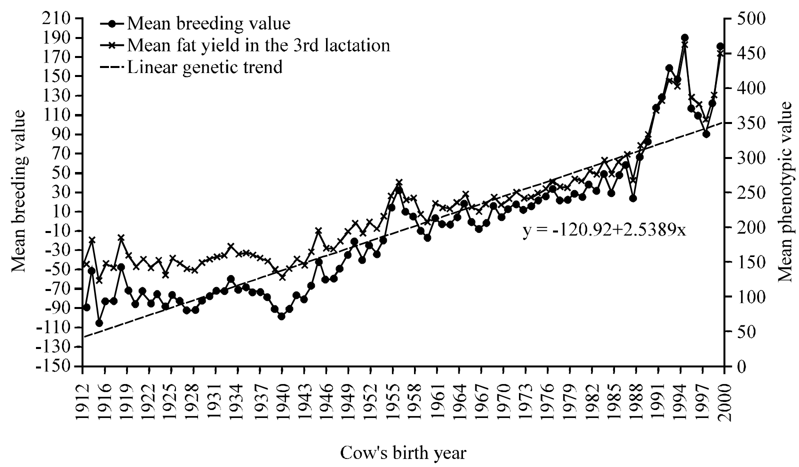

Fig. 7: Genetic and phenotypic trend for fat yield in the 3rd lactation

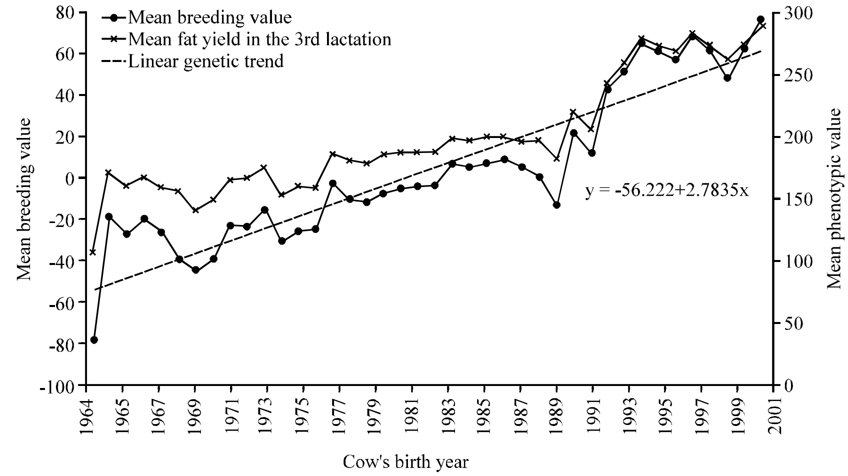

Fig. 8: Genetic and phenotypic trend for protein yield in the 1st lactation

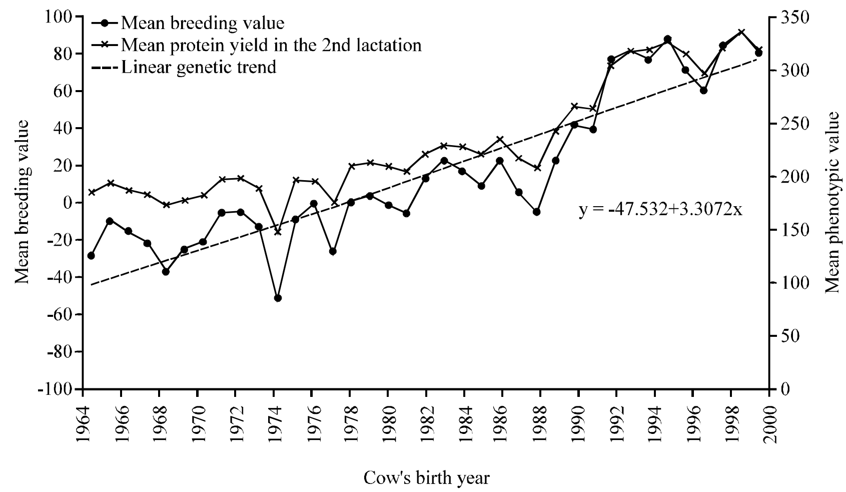

Fig. 9: Genetic and phenotypic trend for protein yield in the 2nd lactation

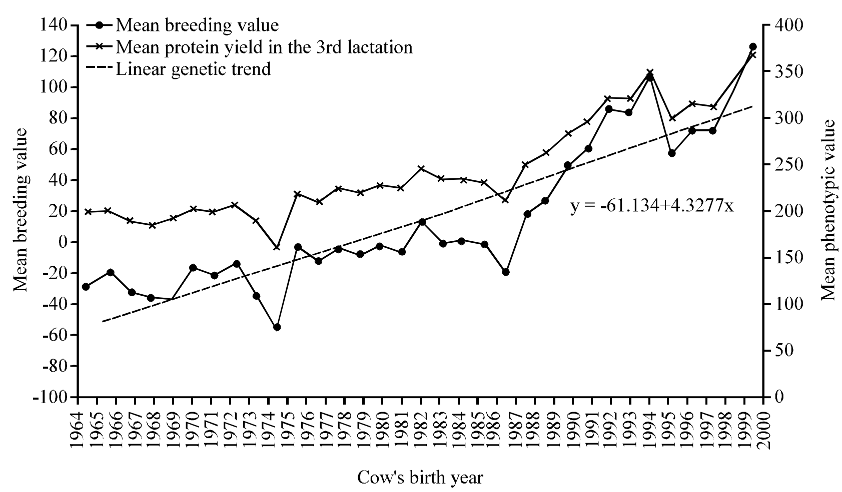

Fig. 10: Genetic and phenotypic trend for protein yield in the 3rd lactation

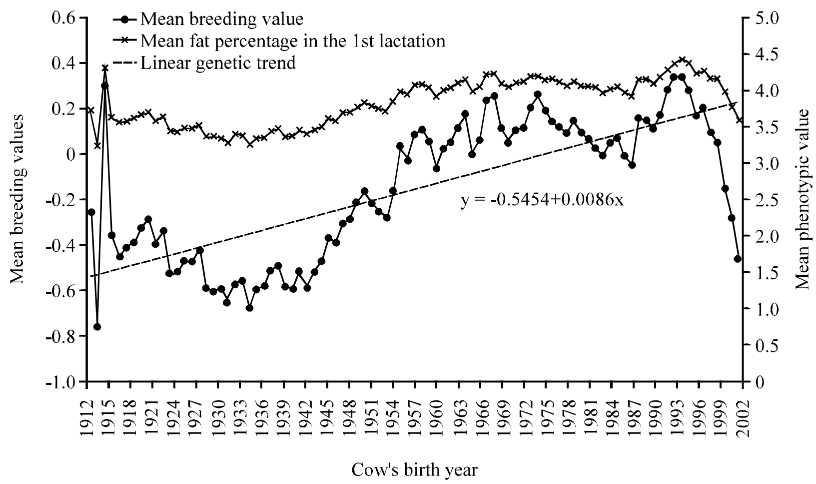

Fig. 11: Genetic and phenotypic trend for fat content in the 1st lactation (%)

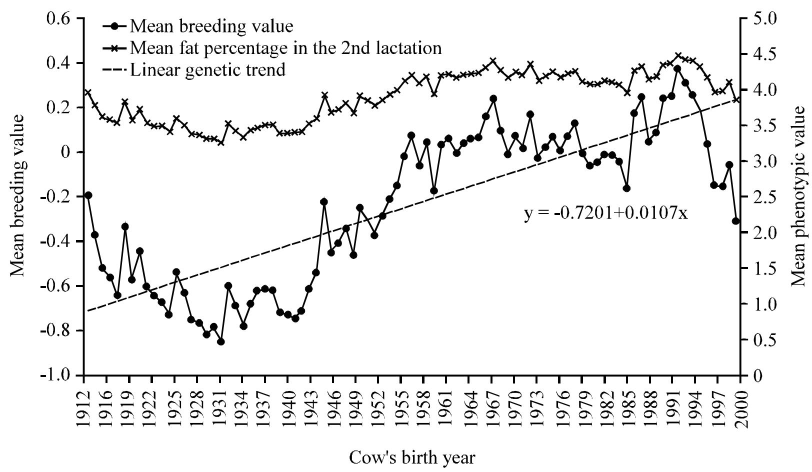

Fig. 12: Genetic and phenotypic trend for fat content in the 2nd lactation (%)

protein yield is accompanied by much higher regression coefficient values in all of the analysed lactations (b = 2.7; b = 3.3, b = 4.3).

Fat content: There has been very little genetic gain in fat percentage in milk over the subsequent years (Fig. 11-13) and the trends for lactations I-III are very similar.

Protein content: Figure 14-16 present genetic trends for the protein percentage in milk showing relative stability of this trait, especially in the 1st lactation. In the subsequent lactations a slightly increasing trend can be observed for this trait.

The analysis of the protein percentage genetic trend curve shows evident drop in the early 70's which may be connected with the breeding work, aiming at upgrading the local population with breeds of considerably higher productivity. No similar decrease had been reported for fat content.

In majority of research papers the genetic trends analysis is restricted to the time span of several years or several decades (Khorshidie *et al*., 2012; Zuc *et al*., 1994). In the present study, however with over 100 years old data set, it has been possible to investigate more thoroughly the influence of both history and breeding programme on the trend. For the analysed traits it has been proved that both breeding programme implementation and breeding value assessement methods greatly affect the genetic trend.

Untill 1939, when evaluation had been based on an animal's (or also its ancestors) own performance in subsequent years the plus and minus trait values were evidently leaping. In 1939-1945 (II World War, no

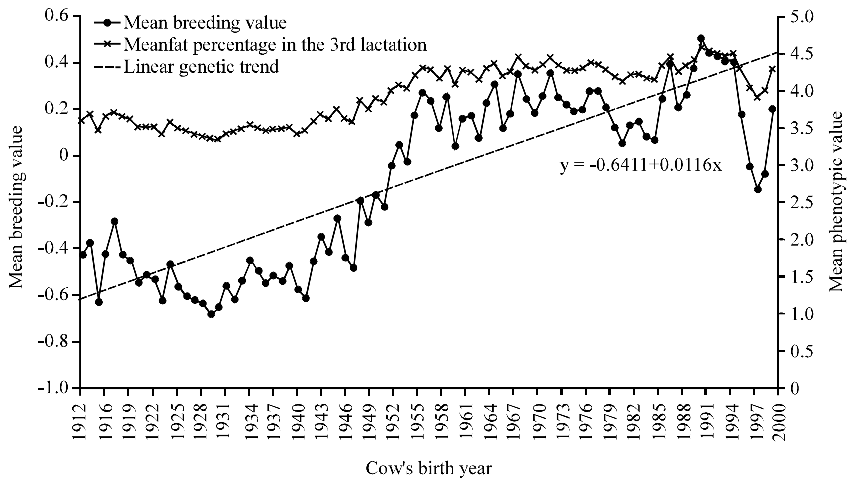

Fig. 13: Genetic and phenotypic trend for fat content in the 3rd lactation (%)

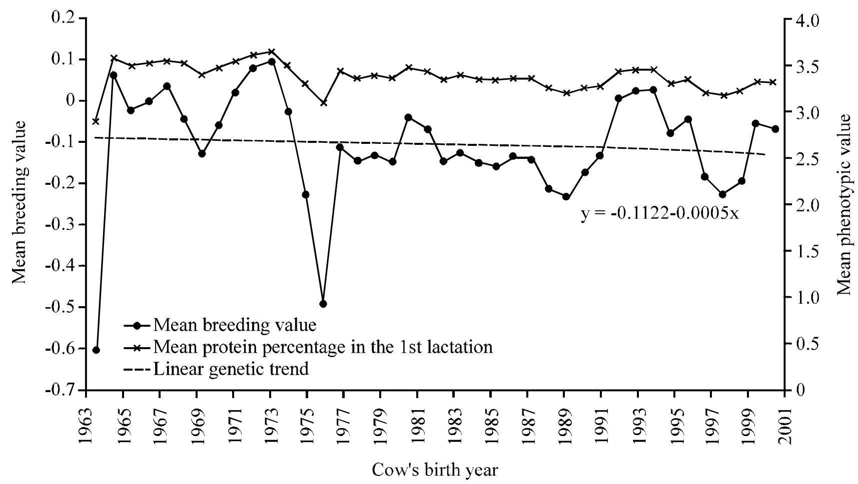

Fig. 14: Genetic and phenotypic trend for protein content in the 1st lactation (%)

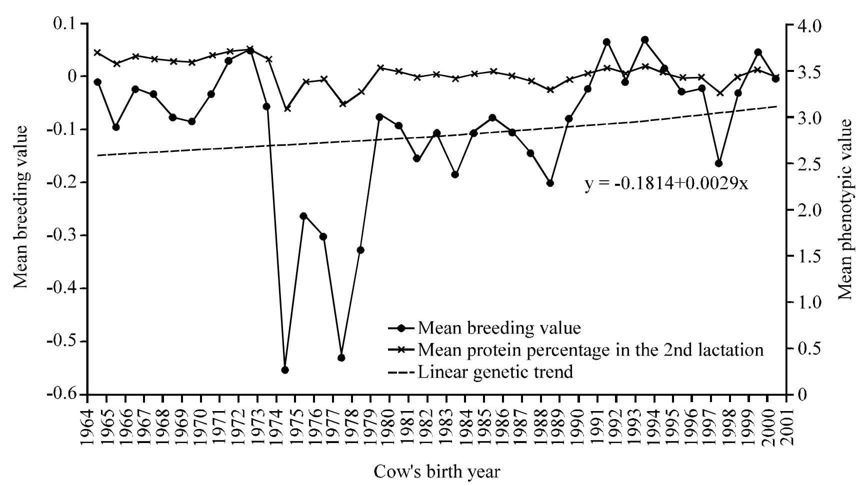

Fig. 15: Genetic and phenotypic trend for protein content in the 2nd lactation (%)

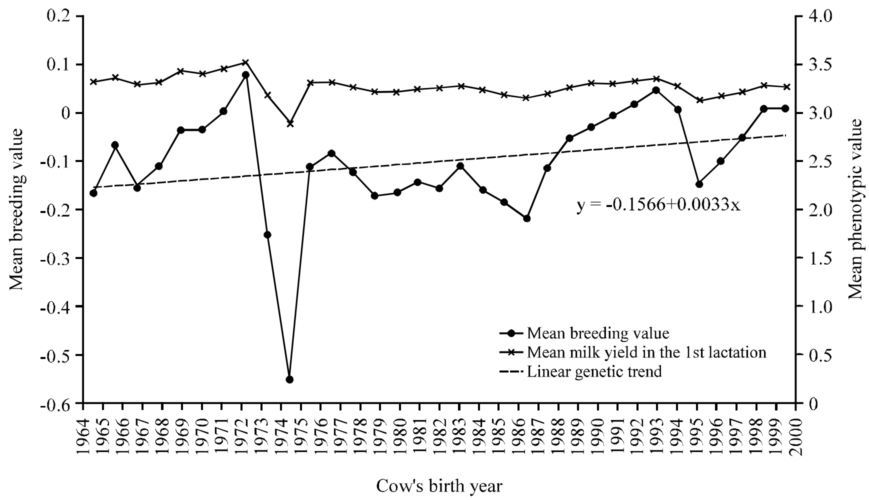

Fig. 16: Genetic and phenotypic trend for protein content in the 3rd lactation (%)

breeding work implemented) there was a sharp decrease in values of the traits under evaluation in that population. After 1945 the trend tends to rise, however there is evident variation among the age groups. In the end of 1960's when the CC (Contemporary Comparison) Method of evaluation came into use the trend was still rising but the variation among the age groups was definitely smaller, although for 1970-1992 the trend for the entire dairy cattle population of Poland has been estimated to be negative (Zukaszewicz *et al.*, 1996). Another milestone is the period between 1990 and 1995 when the Contemporary Comparison Method was substituted by BLUP and BLUP-AM. It was the time of very intense genetic progress (Sobek, 1989).

In 1990's the active population of dairy cattle in Poland was shrinking due to social and economic changes (e.g., privatisation of herds). That had certain influence on the selection intensity and the level of genetic progress. Additionally, AI and the availibility of superior breeding material allowed for the increase in genetic progress.

The research performed on entire Polish dairy cattle population in different periods of time showed various levels of genetic gain. Generally, the genetic trend was rather low but still positive. Dymnicki *et al.* (1995) reported lack of progress in milk yield and Zuc *et al.* (1994) proved the genetic trend to be negative for the first three lactations of cows born in 1973-1990.

In the examined population the linear regression coefficient of genetic trend for milk yield was equal 34.388 (for the entire period under analysis). In 1988 to 1998, according to Jagusiak (2001) that coefficient estimated value for the entire Polish dairy cattle population was 37.084 which makes the realised breeding work compatible with the assumptions of the breeding programme.

In the research concerning the entire cattle population of Poland the milk yield in different periods showed different genetic progress values. Generally, the trend was slightly positive. Dymnicki *et al.* (1995) reported null genetic gain for milk yield in 1981 to 1992 and Zuc *et al.* (1994) showed that the gain was negative in the first three lactations for cows born in 1973-1990.

The genetic trend for butterfat yield (kg) estimated for the same time span was evidently positive. However, analyses involving shorter time spans indicate that sometimes that trend was being negative (Szwaczkowski and Hagger, 1993; Zukaszewicz *et al.*, 1996).

The level of genetic progress within breeds or within populations is under an interest of many researchers. Nizamani and Berger (1996), Roman *et al.* (1999) examining the Jersey breed in 1960-1990 report on negative trends for both yield and percent composition of milk. For the Israeli-Holstein population those trends were some what contradictory in 1981-2000 as estimated by Weller and Ezra (2004). Until 1990 the genetic trend for butterfat and protein percentage was evidently negative and after 1990 (until 2000) it started increasing. For milk, butterfat and protein yield the trend was increasing during the entire analysis period. For the Iranian Holstein-Frisian population in 1991-2007, Khorshidie *et al.* (2012) found the genetic trend for milk yield 305 days lactation to be constantly increasing.

For research involving such a long time span it is worth noticing that in the initial period for almost 50 years there was no evaluation of protein percentage in milk, so no direct improvement of that trait had been conducted. After it had been included in the evaluation, the trend turned out to be very low (near zero) for subsequent years and it was slightly negative for lifetime lactation. It might seem obvious, however that once the trait was included in the evaluation, it should show definite changes.

CONCLUSION

- Breeding work conducted in the analysed herd for over 100 years resulted in positive genetic trend for all the analysed traits
- The genetic trend was not equal for each of the traits
- The linear increase of genetic trend was being altered by the changes in selection intensity and different methods of evaluating genetic progress

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