Investigations

Genetic Structure of Populations of Kazakh Whiteheaded and Hereford Cattles on the Basis of Microsatellite DNA

Adas Tileubekovna Tyngoziyeva, Talgat Nikolaevich Karymsakov and Serik Doldashevich Nurbaev

Kazakh National Agrarian University, 050010, Almaty, Abay Street, 8, Kazakhstan
Kazakh Scientific Research, Institute of Animal Breeding and Forage Production, 050035, Almaty City, Zhandosov Street, 51, Kazakhstan

Abstract: This work is aimed at determination of genetic dissimilarities between two allied cattle breeds: Kazakh Whiteheaded and Hereford. Hair follicles were analyzed, from which DNA was extracted with subsequent amplification. Identification of amplification products was performed using an ABI Prism 310 genetic analyzer. Allele 147 was detected in Kazakh Whiteheaded cattle in locus BM 2113, there was no such allele in Hereford cattle. Average number of alleles per one locus of Hereford and Kazakh Whiteheaded breeds was 11.82 and 12.27, respectively. Herewith, the number of private alleles in Kazakh Whiteheaded cattle was 10 and in Hereford cattle-11. No confidential difference in average heterozygosity was determined. Analysis of sample allele fund with regard to both considered breeds revealed the characteristics' range for both of them, thus facilitating determination of genetic dissimilarity between the two breeds.

Keywords: Kazakh and Hereford Breeds, Allele, Locus, Microsatellites, Heterozygosity

Introduction

In 1950 in Kazakhstan the first cattle breed was approved: Kazakh Whiteheaded, created on the basis of Kazakh and Kalmyk cattle by cross breeding with servicing bulls of Hereford breed imported from Uruguay and England (Dankvert, 2007; Cherekaev and Cherekaeva, 1973).

In recent decade, aiming at increase in productivity of Kazakh Whiteheaded cattle, Hereford bulls were again used, however, admixture of new blood was applied, that is, with single and double blood admixture.

Therefore, the studies were aimed at determination of genetic properties of Kazakh Whiteheaded and Hereford breeds. Selection of these breeds for studies was based on the fact that Kazakh Whiteheaded breed originated from Hereford cattle; as a consequence, the new breed inherited actually identical color type, conformation and productive properties. Since phenotypic properties of both breeds are the same, it would be interesting to clarify the aspect of genetic similarity of these two breeds.

It is well-known that significant contribution to characteristic of allele variety is made by regional populations, which were formed mainly on the basis of local cattle with its own unique allele fund and under conditions of relative geographic isolation (Tapio et al., 2010).

Necessity to maintain optimum level of genetic variances and heterozygosity in cattle population is related with the fact that these properties are directly attributed to adaptive abilities of cattle with regard to modified environmental conditions. Without required genetic variety cattle populations lose their evolutionary adaptiveness and become unstable against impacts of pathogenic flora and negative environmental influences (climatic changes, negative impact of hazardous substances (Dubinin and Mashurov, 1986; Stolpovskii, 2010).

Loss of cattle genetic variety leads to significant economic damage.

One of the methods of revealing of genetic dissimilarities between populations, evaluation of population structure is application of anonymous DNA markers-microsatellites. Microsatellites are short (100-200 base pairs) tandem segments of DNA characterized by high extent of polymorphism (Tautz, 1989; De Woody and Avis, 2000).

Numerous data on applied significance of microsatellites are published regarding evaluation of
state and dynamics of allele fund of dairy breed. However, there are few data on genetic variety of beef breed. Herewith, the microsatellite data can be applied both for evaluation of genetic variety in the breeds and between the breeds and genetic mixture of the breeds; average number of alleles (\( mna \)), observed and expected heterozygosity (\( Ho \) and \( He \)) are more widely applied calculated genetic parameters of populations for evaluation of variety in the breed. Average number of alleles per locus, on the one hand, is one of the properties of informative value of analytical system and, on the other hand, serves as a criterion of genetic variety of the studied cattle groups (Gibson et al., 2007; Zinov’eva et al., 2009; Ernst and Zinov’eva, 2008).

Analysis of locus itself as well as revealing of dominating allele variants of this locus is highly important for selection and development of monitoring procedures of genuineness of cattle breeds (Gershenzon, 1974; Sulimova, 2004; Glazko et al., 2013).

Methods

Hair follicles of 5617 animals of Kazakh Whiteheaded breed, Kazakh population and of 108 animals of Hereford breed imported from abroad were used for analysis. Biological material was sampled in 40 farms situated in various regions of Kazakhstan. Significant difference in amount of samples from the breeds was stipulated by the fact that Hereford breed was supported by at least one hundred years of purely breeding, whereas in Kazakh Whiteheaded breed - 12.27.

In Hereford breed the existence of private alleles was detected in four loci and in Kazakh Whiteheaded breed in two loci. Thus, in loci BM 2113 and ETH 3 of Hereford breed there was one private allele in each, in loci TGLA 53 and TGLA 222 and 7, respectively. Private alleles for Kazakh Whiteheaded breed were detected in loci BM 2113 and TGLA 122, their number was 2 and 8, respectively.

Analysis of the obtained data made it possible to determine that the alleles occurred in Hereford breed nearly completely exist in Kazakh Whiteheaded breed. However, in Kazakh Whiteheaded breed allele 147 was detected in locus BM 2113, which was absent in Hereford breed.

In total, in 11 loci of Hereford breed there were 35 alleles with occurrence index above 0.1 and in Kazakh Whiteheaded breed 41, respectively Table 2.

As can be seen, the gene pools of the considered breeds differed not only in spectrum but in allele occurrence frequency. Among the frequently occurred alleles the most spread was allele 103 in locus ETH 3 of both breeds (0.2685 in Hereford and 0.3314 in Kazakh Whiteheaded). It should be mentioned that occurrence frequency of allele 139 in locus BM 2113 and TGLA 222 was different for the considered breeds (0.1389 in Hereford and 0.208 in Kazakh Whiteheaded) at high confidence according to Student’s t-test (\( t = 2.9027, \) d.f. = 1, \( p > 0.05 \)).

Analysis of heterozygosity extent in loci of both breeds made it possible to detect sufficiently high level of this property in all 11 loci. The lowest heterozygosity extent was observed in locus ETH3 of Hereford breed equaling to 0.8357, the highest-in locus TGLA122of the same breed equaling to 0.9319. In Kazakh Whiteheaded breed the heterozygosity extent in all 11 loci varied from 0.8113 and 0.9211.
Table 1: Allele occurrences in 11 loci of Kazakh Whiteheaded and Hereford breeds

| Name of loci and alleles | Allele variants |
|--------------------------|-----------------|
| TGLA 227                 | 75 121 154 209 248 109 |
| BM 2113                  | 77 123 156 213 250 111 |
| TGLA 53                  | 79 125 158 215 252 113 |
| ETH 10                   | 81 127 160 217 254 115 |
| SPS 115                  | 83 129 162 219 256 117 |
| TGLA 126                 | 85 131 164 221 258 119 |
| TGLA 122                 | 87 133 166 223 260 121 |
| INRA 23                  | 89 135 168 225 262 123 |
| ETH 3                    | 91 137 170 225 262 123 |
| ETH 225                  | 93 139 172 225 262 123 |
| BM 1824                  | 95 141 174 225 262 123 |

Note: *only in Kazakh Whiteheaded population

Table 2: Number of alleles in loci with occurrence frequency above 0.1

| Locus   | Hereford  | Kazakh Whiteheaded | Hereford  | Kazakh Whiteheaded |
|---------|-----------|--------------------|-----------|--------------------|
| TGLA 227| 75 0.1435 | 75 0.1889          | BM        | 129 0.1065         |
| 2113    | 139 0.1389| 139 0.2080         |           | 225 0.2593         |
| TGLA 53 | 154 0.1898| 154 0.2339         | ETH 10    | 121 0.1574         |
| SPS 115 | 248 0.1898| 248 0.2031         | BM        | 109 0.1713         |
| TGLA 126| 143 0.1157| 143 0.1244         | INRA 23   | 198 0.2037         |
| ETH 3   | 103 0.2685| 103 0.3314         | BM 1824   | 188 0.2361         |
| ETH 225 | 148 0.2176| 148 0.2158         |           | 180 0.1944         |
Discussion

The performed molecular and genetic analysis revealed that cattle population of domestic and integrated beef breeds had dissimilarities in genetic parameters. Kazakh Whiteheaded breed has higher genetic variety in terms of allele number in comparison with Hereford breed, which probably can be attributed to gene pool merging of these two breeds of different origin. With regard to locus BM 2113, existence of 14 alleles for Kazakh Whiteheaded breed and 13 alleles for Hereford breed was detected. Hereford breed had no allele 148 in locus BM 2113. Hereford breed had private alleles in loci TGLA 122, BM2 113, ETH 3 and TGLA 53; in Kazakh Whiteheaded populations private alleles were detected in loci TGLA 122 and BM 2113, which indicated at unique essence of each breed on the basis of rare alleles of the population.

Average value of heterozygosity of the two breeds demonstrated no confidential difference between the two breeds. For Kazakh Whiteheaded breed this value was 0.8743 and for Hereford breed -0.8808, which indicates at necessity to maintain optimum level of genetic variety and heterozygosity in cattle populations.

Conclusion

The performed studies demonstrated that the obtained results and analysis of allele variety of the two breed could be applied for development of measures aimed at conservation of unique gene pools, well adopted for local natural and climatic conditions.

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Author’s Contributions

Adas Tuleibekovna Tyngoziyeva: Participated in all experiments, coordinated the data-analysis and contributed to the writing of the manuscript.

Talgat Nikolaevich Karymsakov: Coordinated the mouse work.

Serik Doldashevic Nurbayev: Designed the research plan and organized the study.

Ethics

Authors declared no conflict of interests.

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