

РЕЗЮМЕ

В статье приведены данные по изучению микробной этиологии гнойно-катарального эндометрита в ТОО «Агрофирме Акас» с применением метода ПЦР. В условиях молочных предприятиях бесплодие коров регистрируется у 20-26% поголовья и часто приводит к значительному экономическому ущербу. Среди причин бесплодия коров особое место занимают заболевания половой системы. Болезни органов половой системы регистрируются у 30-51% бесплодных коров и у 13-28% телок, а технология содержания молочных коров способствует возрастанию роли этих заболеваний в этиологии бесплодия. Основными предрасполагающими причинами для возникновения низкой оплодотворяемости являются следующие факторы: снижение резистентности организма на фоне нарушения метаболизма, а также некоторые инфекционные заболевания оказывающие косвенное воздействие посредством иммунного статуса у высокопродуктивных коров или даже прямого воздействия на оплодотворение, течение беременности и послеродового периода. Например такие как *Leptospirosis*, *Brucella* или *Neospora* вызывающие аборт и, следовательно, уменьшающие выработку молока у стад и иногда плодовитость. Исследования показали, что влагиалище в микрофлоре здоровых коров преобладает *L. sakei* и *W. koreensis*, при этом нет доминирующих бактериальных штаммов у коров с эндометритом, у которых было обнаружено увеличение количества бактерий. Это говорит о том, что нарушение микрофлоры влагиалищного микробного сообщества может способствовать возникновению эндометрита.

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EVALUATION OF POLYMORPHIC VARIANTS OF GENES OF SOMATOTROPIN CASCADE AS GENETIC MARKERS OF MEAT PRODUCTIVITY IN DOMESTIC CATTLE BREED

Abstract

It is known that growth hormone (GH-somatotropin) is the most important growth regulator in mammals. Synthesis of somatotropin and the realization of its physiological effects is a chain of successive interactions of the protein receptor (self-tropic cascade). The key links of this chain are the pituitary transcription factor-1 (bPit- 1), triggering the expression of the genes of somatotropin and prolactin, prolactin and growth hormone, regulating lactation, the growth hormone receptor (bGHR), which transmits the somatotropin humoral signal to target cells. Thus, based on the researches performed, the following data is stated below. On the first hand, specified allele frequencies for all the polymorphisms in question are comparable with the other authors' data; rare allele of other breed representatives are also rare according to the results of our research. The research works were performed within the frameworks of the scientific project of the Ministry of Education and Science of the Republic of Kazakhstan.

Keywords: DNA, somatropine cascade, polymorphism, gene, cattle.

Introduction. Nowadays, the need in modernization of beef breeding in the Republic of Kazakhstan has been arisen. In order to solve this problem, strengthening of selection of local breed is needed together with delivery of highly-productive breeds of foreign selection. This means Auliekol bovine cattle breed having stable immunity to the diseases spread on the territory of the Republic of

Kazakhstan through introduction of well-adapted to food base and climatic conditions and modern highly-productive scientific technologies.

One of these DNA technologies is MAS (marker assisted selection) enabling to accelerate the selection speed and cutting down the financial expenses for classical selection measures. MAS uses information concerning phenotypic characteristic of genetical allele responsible for digital properties (candidate genes) to assess the genetical potential of cattle productivity at the primary stages of development after selection birth [1].

Genes of somatotropin cascade are polymorphic and are attractive for MAS as genetic markers with useful properties regarding economics, great composition of their alleles has been determined from bovine cattle. However, different criteria of somatotropin cascade (bPit-1-HinFI, bPRL-RsaI and bGH-AluI) taken from different breeds contradict in the data published in a few situations about gene allele association [2].

Based on the above, the aim of this research is to study the phenotypic impact of polymorphisms of bPit-1-HinFI, bGH-AluI and bGHR-SspI genes in order to assess the future of application as a marker on meat highly-productive Auliekol bovine cattle in the selection works.

Materials and methods. Object of the research is beasts of Auliekol bovine cattle (n=296). Topic of the research: polymorphic genes of somatotropin cascade: bPit-1, bGH, bGHR. Material of the research – DNA samples selected from the blood of Auliekol cows. Karkyn LLP located in Kostanay region presented the blood samples. High-bred bovine cattle’s cards presented by the farm were used as the information source concerning the cattle productivity.

Genotype of bovine cattle was performed through PCR-RFLP method.

Polymorphism of length of restriction fragments of bPit-1-HinFI, bGH-AluI and bGHR-SspI genes was analyzed; genotype of bovine cattle for all the analyzed genes was documented and entered into the general database.

Association and genotype of meat productivity criteria was assessed during a few stages. Microsoft Excel 2010 and Statistica 6.0 (StatSoft, Inc. 1994 – 2001) programs were used for data processing [3].

Results and discussion. Assessment of comparative spread frequency of genetic alleles studied in Auliekol population (n = 284 of bovine cattle (n = 296) (Q = SQ) are presented in table 1.

Table 1 – Assessment of comparative spread frequency of genetic alleles studied in Auliekol population (n = 284 of bovine cattle (n = 296) (Q = SQ).

Polymorphism	Allele	Allele’s controlled frequencies	Allele’s comparative frequencies
bPit-1-HinFI	bPit-1-HinFIA	154	0,341±0,002
	bPit-1-HinFIB	298	0,659±0,002
bGH-AluI	bGH-AluIV	159	0,352±0,002
	bGH-AluIL	452	0,648±0,002
bGHR-SspI	bGHR-SspIF	434	0,960±0,000
	bGHR-SspIY	18	0,040±0,000

Based on the data presented on table 1, we can note that bPit-1-HinFI^A allele matches with bPit-1-HinFI polymorphism. This data corresponds to the results of Zhao et al. taken from the researches of Angus beef meat [4]. Inter alia, жұмысында bPit-1-HinFI^A allele frequency is 0.33 in his work. According to Yang et al [5], correlation of alleles among /B Nanyang cattle, Qinchuan cattle, Jiaxianhong cattle, izhen cattle, Luxi cattle and Holstein cattle is 0.444/0.556, 0.477/0.523, 0.538/0.462, 0.421/0.579, 0.523/0.477, 0.475/0.525, respectively.

bPit-1-HinFI^A allele frequency of dairy breeds is significantly lower comparing to those of beef breeds. Thus, according to Renaville et al., bPit-1-HinFI^A and bPit-1-HinFI^B allele frequencies

were 0.18 and 0.82 in the research of bovine cattle. According to our Belarusian colleagues, the said allele frequency of Holstein and black and white breeds is 0.21 and 0.23 [6].

Thus, it may be noted that bPit-1-HinFI^A allele frequency is different in different population of one breed. According to our data, spread of bGH- AluI^L and bGH-AluI^V allele frequency of growth hormone gene of Auliekol breeds is 0.648/0.352. This data matches the results of the research of black and white breeds of bovine cattle of Lithuanian population: correlation of bGH- AluI^L and bGH-AluI^V alleles is 0.7 and 0.3, respectively. This correlation of different populations of Holstein bovine cattle for bGH-AluI^L allele changes from 0.74 to 0.93 and for bGH-AluI^V allele – from 0.07 to 0.26 [2].

Frequency of bGHR-SspI^Y rare allele of bGHR-SspI polymorphism was 0.040 at Auliekol bovine cattle, according to our data. This allele frequency varies significantly according to the data of different authors. According to Fontanesy et al., bGHR-SspI^Y allele frequency of Jersey, Holstein Frisian and Simmental breeds is 0.05, 0.27 and 0.10. bGHR-SspI^F allele frequency of the said breeds is 0.95, 0.73 and 0.90 [7]. According to Viitala et al., bGHR-SspI^F and bGHR-SspI^Y allele frequencies of Finnish Ayrshire breed are 0.89 and 0.11 [8]. Thus, our data remains inside the other authors' data published earlier. Spread of bGHR-SspI^Y and bGHR-SspI^F allele frequencies of the breeds in question vary significantly from each other.

According to Hardy–Weinberg principle, matching of genotypic spread of polymorphic genes in question of somatotropin cascade expected theoretically of the Auliekol breed has been researched. Importance of the observed deviation has been assessed according to χ^2 measurement. The data taken is presented in table 2.

Table 2 – Frequent spread of polymorphic gene genotypes of somatotropin cascade of Auliekol bovine breed population.

Polymorphism	Genotype	Auliekol breed (n=286)		
		n controlled	n expected	χ^2
bPit-1-HinFI	bPit-1-HinFI ^{AA}	27	26	0,05
	bPit-1-HinFI ^{AB}	100	102	
	bPit-1-HinFI ^{BB}	99	98	
bGH-AluI	bGH-AluI ^{VV}	28	28	0,00
	bGH-AluI ^{LV}	103	103	
	bGH-AluI ^{LL}	95	95	
bGHR-SspI	bGHR-SspI ^{FF}	211	208	21,12
	bGHR-SspI ^{FY}	12	17	
	bGHR-SspI ^{YY}	3	0	

Note. When $\chi^2 \geq 3.84$, frequency of the genotypes controlled under the Hardy-Weinberg principle deviates from the frequency of the genotypes expected theoretically.

In table 2, according to bPit-1-HinFI polymorphism, χ^2 value of Auliekol bovine cattle population is 0.05. This means that profit of deviation of the controlled genotype from the equal genotype is observed.

According to bGH-AluI polymorphism, theoretically expected equal spread matches the frequency of the controlled genotypes according to Hardy-Weinberg. As well, according to bGHR-SspI polymorphism, χ^2 value is 21.12. This shows the statistical important deviation of the equal genotypic number from the controlled genotypic number. This means that there is a possible association of polymorphism with the criteria of productivity of Auliekol bovine cattle and artificial selection pressure of the populations in question.

Conclusion. Thus, based on the researches performed, the following data is stated below. On the first hand, specified allele frequencies for all the polymorphisms in question are comparable with the other authors' data; rare allele of other breed representatives are also rare according to the results of our research.

On the second hand, according to bPit-1-HinFI and bGHR-SspI polymorphism, controlled frequency of genotypes deviates from the equal frequency expected theoretically according to the Hardy-Weinberg principle. This in turn shows the existence of the artificial selection pressure

among the populations in question and the possibility of matching of these polymorphisms and bovine cattle productivity.

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ТҮЙІН

Өсу гормоны (GH - соматотропин) –сүтқоректілердің өсуінің ең маңызды реттегіші. Соматотропин синтезі және оның физиологиялық әсерлерін жүзеге асыру бірізді ақуыз-рецепторларының (соматотропинді каскад) өзара әрекеттесу тізбегі болып табылады. 1 – транскрипциясының (bPit-1) гипофизарлық факторы бұл тізбектің негізгі түйіндері болып табылады. Олар лактацияны реттейтін пролактин мен соматотропин гендерінің және мақсатты жасушаларға соматотропиннің гуморальды сигналын беретін өсу гормонының рецепторлары гендерінің экспрессиясын тудырады.

РЕЗЮМЕ

Известно, что гормон роста (GH – соматотропин) является важнейшим регулятором роста у млекопитающих. Синтез соматотропина и реализация его физиологических эффектов представляет собой цепь последовательных взаимодействий белок – рецептор (соматотропиновый каскад). Ключевыми звеньями этой цепи являются гипофизарный фактор транскрипции-1 (bPit-1), запускающий экспрессию генов соматотропина и пролактина, пролактин и гормон роста, регулирующие лактацию, рецептор гормона роста (bGHR), передающий гуморальный сигнал соматотропина к клеткам-мишеням.