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BEEF CATTLE EVALUATION BY FEEDING EFFICIENCY AND GROWTH ENERGY INDICATORS BASED ON BIOINFORMATIC AND GENOMIC TECHNOLOGIES

(review)

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Abstract

Beef cattle breeding is characterized by significantly higher feed costs per unit of output compared to other livestock industries. For most species of farm animals, breeding to improve the efficiency of feed use has been difficult until recently due to the complexity of the individual assessment of this indicator. The improvement of the trait occurred indirectly, through selection for an increase in the intensity of growth and a decrease in the fat content in carcasses. In 1960-1980, Förster-Technik GmbH (Germany) developed automatic feeding stations for individual fattening to account for data on energy costs for the growth and development of animals, which made it possible to derive the feed conversion rate (FCR), which remains one of the main parameters of feed efficiency (K.R. Koots et al., 1994). FCR as a trait is not important for genetic selection due to moderate heritability (A.A. Sermyagin et al., 2020; D.N. Crews et al., 2005). In this regard, and thanks to data from feedlots, in 1963 a new alternative concept for the FCR indicator, the predicted residual feed intake (RFI), was developed. RFI is an individual characteristic of an animal, which is determined by the results of test fattening (duration from 70 to 84 days), taking into account daily feed intake and live weight gain (R.M. Koch et al., 1963). The advantage of using RFI as a measure of feed efficiency in conjunction with FCR is that selection for a negative RFI will allow for reduced feed intake without compromising growth. In addition, the predicted residual feed intake does not depend on productivity, growth and body size, making it a trait that has a clear breeding value (G. Acetoze et al., 2015; J.A. Archer et al., 2000; G.E. Carstens et al., 2002). It has been established that RFI correlates with FCR (genetic correlation coefficients vary from 0.45 to 0.85), but RFI does not depend on average daily gain (ADG) and metabolic body weight (MWT) (B.W. Kennedy et al., 1993; P.F. Artur et al., 2001). The assertion that individuals of the same body weight require different amounts of feed to achieve the same performance provides the scientific basis for assessing RFI in beef cattle. Due to the fact that RFI is hereditarily determined (heritability coefficients vary from 0.08 to 0.49), a directed search for quantitative trait loci (QTL) is conducted using the GWAS (genome-wide association study) methodology. Since the 2000s, methods have been developed and implemented for assessing the breeding value of farm animals using information on a large number of SNPs (single nucleotide polymorphism), based on the principle of linear modeling. Linear models, depending on the approach to data structuring, are divided into rrBLUP (estimation of the effect of each marker), GBLUP (estimation of breeding value based on genomic relationship), and one of the most common modern one-step estimation method ssGBLUP (genomic breeding value estimation model that takes into account genomic relationship along with pedigree). BayesA and BayesB are applicable non-linear Bayesian models. Scientific studies using genome-wide association analysis have allowed the development of genomic selection programs and the identification of a number of SNPs associated with indicators of feed efficiency. Thus, seven positional candidate genes were found which were previously associated with the efficiency of feed use and growth energy in different types of farm animals, and were recently identified in Angus cattle. The analysis of foreign studies allows us to recommend the use of the described methods both in research work and for production purposes with the prospect of including these parameters in the criteria for genomic evaluation of beef cattle of different breeds bred in Russia.

Keywords: feeding efficiency, feed conversion, predicted residual feed intake, genomic technologies, genome-wide association search, GWAS, beef cattle, pig breeding

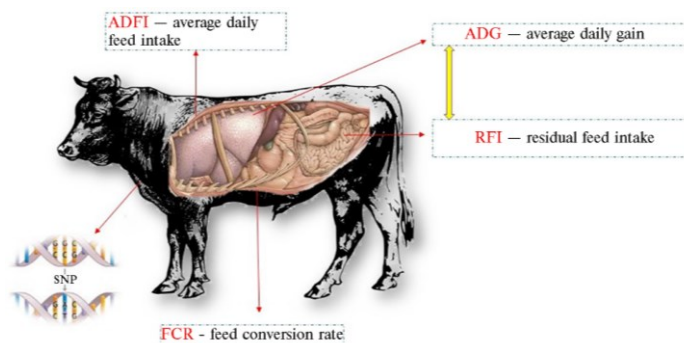
Improving feed conversion is a topical issue in livestock breeding programs, as increased feeding efficiency affects the economic efficiency of the industry as a whole. The problem is especially relevant for beef cattle breeding, where the cost of feed per unit of production is much higher than in other livestock industries. The feed cost per 1 kg weight gain in beef cattle averages 6.0 kg/kg, while in pig and poultry farming it is 2.5 and 1.9 kg/kg, respectively. Despite significant progress in genetics and herd management technologies (animal feeding, keeping, health and welfare), feed costs account for 60-65% of the beef cost, and at some stages of beef production can exceed 80% of the total costs [1].

Although feed efficiency has improved significantly over the past 40 years, further progress is expected [2]. It is estimated that due to 10% improving feed efficiency, annual savings in the US beef industry could exceed \$1 billion [3]. For most species of farm animals, breeding to improve feed efficiency has been difficult until recently, since this trait is difficult to evaluate individually. Basically, the improvement of the trait occurred indirectly, through selection for increased growth intensity and reduced fat content in carcasses. However, the effectiveness of such selection was relatively low. The problem was solved thanks to the development and implementation of automatic feeding stations that allow accurate individual accounting of feed intake [4].

The review analyzes methodological approaches to improving the efficiency of feed use in beef cattle breeding.

Automatic feed stations and feed efficiency indicators. Traditionally, evaluation of feed efficiency is based on feed conversion rate (FCR) as an economically significant indicator. FCR is the ratio of given feed weight (dry matter) over animal weight gain in a certain period of time. Animals with a low FCR value consume less feed per 1 kg weight gain, while animals with a higher FCR consume more. FCR strongly depends on the amount of feed consumed and the average daily weight gain of each animal. In 1960-1980, Förster-Technik GmbH (Germany) developed automated feedlots for individual fattening to study energy production and use in animals. Currently, there are several types of such systems in the market. These units provide various automation levels and were developed in stages [5]. At the first stage of automation ("mixing—portioning—pushing out" level), the built-in mobile equipment allowed filling the stationary mixer with silo from silo tanks. The advantage of this option is that a group of animals can be fed automatically several times a day, but filling the mixer still remains time consuming. At the second stage of automation, stations were developed in which the mixer is automatically filled, then the feed undergoes mixing—portioning—(pushing out). This type of station ensures that all animals are fed in groups several times a day, and the time when the farmer must fill the mixer and feed the animals is no longer fixed. The third stage provides for automation at the stages of unloading and transportation—filling the mixer—mixing—portioning—ejection. In systems of this type, fully automated feeding has so far been carried out only using tower or deep silos, but such systems are relatively expensive in design and power consumption.

Currently, approved and improved automated feeding technologies for cattle allow one to control feed quality and consumption, the growth rate, feeding behavior, and feed efficiency, which is especially important, since the development of animals can vary significantly. In meat cattle, different time and growth dynamics require cattle breeding not only for meat yield and quality, but also for feed conversion and predicted residual feed consumption (Fig.).



Feed efficiency indicators (ADFI, ADG, RFI, FCR) as selective significant traits in improving the productive qualities of beef cattle. Based on the phenotypic description by ADFI, ADG, RFI, FCR and the search for SNP (single nucleotide polymorphism), associations of genomic variants with these traits are searched for involvement in breeding programs.

FCR correlates with total energy intake, growth rate and body weight [6]. Genetic selection for feed conversion and average daily gain can be problematic as more attention is usually paid to traits with greater variability [7]. The genetic correlation to FCR is positive, that is, selection for feed conversion should lead to faster growth of beef cattle. Thereof, the animals will have a large final metabolic mass and will be more demanding on the keeping conditions. Selection for FCR alone is likely to be less effective in the long run. The consequence of selection for a decrease in feed conversion may be an increase in weight at weaning, upon reaching one year of age and an increase in costs due to an increase in the need of animals for nutrients [2, 8, 9]. Since the feed supply adequacy affects the profitability of the enterprise, it becomes essential to evaluate the efficiency of feed use which is often based on indirect estimates [10, 11].

K.R. Koots et al. [12] reported a negative weighted genetic correlation between feed conversion rate, growth rate and animal size. The values of the correlation coefficients indicate that selection for a decrease in FCR increases the efficiency of feed use and leads to acceleration of animal growth and maturity. Although feed conversion is a moderately inherited trait [4], it is not important as a parameter used to genetically improve feed efficiency rates [13].

An alternative feed efficiency parameter widely assessed in various farm animals, including beef cattle, is residual feed intake (RFI). RFI is an individual characteristic of an animal, which is determined during trial fattening for 70 to 84 days with daily allowance for feed intake and body weight gain. The RFI concept was introduced in 1963 by R.M. Koch et al. [14, 15] and has recently become the preferred parameter for measuring feed efficiency. This measure is unique because, unlike FCR, it separates feed intake into two different components, the feed intake for actual performance and predicted residual feed intake. RFI is a multifactorial and complex characteristic of beef cattle, the variability of this indicator is due to the interaction of many biological processes, which, in turn, are influenced by the physiological state and timely implementation of veterinary and preventive measures.

An advantage of RFI as a measure of feed efficiency in combination with FCR is that selection for a negative RFI will allow for reduced feed intake without compromising growth and physiological maturity of the animal [16, 17]. CRS with negative RFI values are more efficient than those with positive RFI. An economic analysis of genetic improvement schemes that include RFI testing of individuals has shown significant economic benefits compared to methods that do not include testing for this trait. In addition, negative RFI-based selection has the added benefit of reducing greenhouse gas emissions from cattle. Residual feed intake is considered an integral part of basic metabolic processes. The factor ensuring the profitability of livestock enterprises is the cost of feeding. Since the animal productivity indicator is not used when calculating the RFI value, this approach is considered

promising for planning this expenditure (11, 14, 16). Along with moderate heritability, RFI is independent of productivity, height, and body size, making it an ideal trait to involve in breeding for forage efficiency [18-20].

D.P. Berry et al. [11] reported on the impact of the genetic component to the RFI value. The authors point out that a reliable calculation of RFI requires additional estimates of the impact of genotype-environment interactions on variability in feed efficiency. In mathematical modeling, it is necessary to consider the genetic background quantitative traits (for example, meat quality) under the influence of the environment, as well as animal health indicators under specific growing conditions. Many studies have shown that metabolic body weight and feeding behavior [21], intestinal absorption of nutrients [22], mitochondrial function [23] and appetite regulation [24] are genetically dependent. Since fattening qualities depends on cattle nutrition, health and the stage of rearing, the efficiency of feed use cannot be considered in isolation from the applied technological system. RFI is a moderately inherited trait [11], so it is important to evaluate the expected consequences when breeding for RFI. In addition, there is still insufficient information on the relationship between the RFI value and pastoral productivity, which is important for beef production. Publications on the relationship between RFI values in mother cows and their offspring, combined with moderate repeatability and heritability of the trait, suggest that selection for negative RFI as part of the multiple selection index is possible, cumulative and promising [1, 25].

In pig breeding, the efficiency of feed utilization serves as a useful trait in animal raising and breeding herd formation. In a review article, H. Gilbert et al. [26] summarized the results of a breeding experiment on residual feed intake (RFI) in nine generations of young Large White pigs. After nine generations, divergent selection for predicted residual feed intake resulted in very significant ($p < 0.001$) differences in RFI (-165 g/day vs. $+300$ g/day) and average daily feed intake (-270 g/day). Negative values were observed for growth rate (-12.8 g/day, $p < 0.05$) and carcass composition (fat thickness $+0.9$ mm, $p = 0.57$; lean meat content 2.64% , $p < 0.001$) with a marked decrease in the feed conversion ratio (-0.32 kg feed/kg body weigh gain, $p < 0.001$). Reduced pH limit and meat color ($p < 0.001$) and little effect on meat organoleptic quality were characteristic of RFI negative pigs. Changes in meat quality were associated with disorders of muscle metabolism. L. Fu et al. [27] conducted genome-wide association studies (GWAS) for feed efficiency parameters in Landrace pigs and found eight common QTL (quantitative trait loci) regions, of which three regions related to ADFI and RFI traits overlapped. Gene ontology analysis identified six candidate genes (*PRELID2*, *GPER1*, *PDX1*, *TEX2*, *PLCL2*, and *ICAM2*) corresponding to traits associated with feed efficiency. These genes are involved in the synthesis and breakdown of fats, lipid transport, and insulin metabolism.

Interrelation of forage use efficiency signs. Examination of feed efficiency found significant individual differences in feed intake that were both lower and higher vs. predicted from body weight and average daily weight gain. The assertion that individuals of the same body weight require quite different amounts of feed to achieve the same performance provides the basis for assessing RFI in beef cattle [27]. Breeding for RFI is prospective due to phenotypic independence of this index from the average daily weigh gain while the parameters used to calculate this index are hereditarily dependent with the heritability coefficients in different livestock populations from 0.08 to 0.49 [29-31].

Table 1 submeets data on the genetic relationship between feeding efficiency parameters and predicted residual feed intake in beef cattle. Residual feed intake correlates with FCR, genetic correlation coefficients vary from 0.45 to 0.85 [32]. This means that selection for improved RFI will lead to direct improvement

in FCR [33, 36, 37]. There is a positive correlation between RFI and feed intake, indicating that more effective cattle with lower RFI consume less feed. Residual feed intake is phenotypically independent from the average daily gain (ADG) and metabolic body weight (MWT) used in calculation. B.W. Kennedy et al. [7] argue the genotypic independence of such a relationship. P.F. Arthur et al. [6] showed that the genetic influence on weaning weight and weight at one year of age is divided into maternal, paternal, and individual effects of the animal. The genetic relationship between FCR and ADG is negative and moderate in most studies [6, 32]. Individuals selected for lower FCR will produce offspring with a high final body weight, resulting in high costs to maintain the breeding herd.

1. Genetic relationship (correlation coefficients) of fattening indicators with RFI in bulls of various breeds ($r \pm SE$)

Trait	Breed						
	Angus [6]	Charolais [19]	Hereford [17]	crossbred ₁ [32]	crossbred ₂ [33]	Wagyu [34, 35]	crossbred ₃ [37]
Animal number <i>n</i>	1180	792	540	2284	1481	740	464
ADG, g	-0,04±0,08	-0,10±0,13	0,09±0,29	0,01	0,09±0,20	0,25±0,16	0,46±0,45
MWT, kg	-0,06±0,08		0,22±0,29	-0,17	-0,20±0,16	0,16±0,13	0,27±0,33
FCR, kg/kg	0,66±0,05	0,85±0,05	0,70±0,22	0,69	0,41±0,32	0,64±0,10	0,62±0,09
BW ₁ , kg	-0,45±0,22		0,34±0,34				
BW ₀ , kg	-0,26±0,14	0,32±0,10	0,15±0,28	0,81	0,43±0,15	0,19±0,15	
Feed intake, g	0,66±0,05	0,79±0,04	0,64±0,16			0,78±0,06	0,73±0,18

Note. Crossbred₁ means hybrids of Charolais, Limousine, Simmental, Hereford and Angus breeds, crossbred₂ means hybrids of Brahmin cattle and Santa Gertrudis], crossbred₃ means hybrids of Alberta, Angus, Charolais; ADG — average daily gain, MWT — metabolic body weight, FCR — feed conversion rate, BW₁ — initial body weight, BW₀ — final body weight,

Currently, genetic selection aims at improving the efficiency of feed use and profitability in beef cattle breeding. R.R. Westhuizen et al. [38] assessed genetic variation and covariance between weaning weight, reproductive performance, performance traits and feed efficiency. Metrics included residual feed intake (RFI), feed conversion rate (FCR), average daily body weight gain (ADG), weaning weight (WW), height at withers (SHD), scrotal circumference (SCR) and profitability during test feeding of young bychkov. Significant genetic correlations for WW were established with SHD ($r_g = 0.50$) and with ADG ($r_g = 0.28$). The heritability coefficient for FCR was 0.34, for RFI it was 0.31 with a genetic correlation between traits $r_g = 0.75$. The estimated genetic correlation of profitability (rand-value) with FCR and RFI was $r_g = -0.92$ and $r_g = -0.59$, respectively [38].

Traditional animal genetic improvement programs include selection for total body weight gain during the fattening period as the main trait and can reduce the profitability of fattening beef cattle [39]. This is because in bulls selected for weight gain alone, the average daily feed intake increases at the same time. Therefore, in order to achieve the desired profitability and genetic improvement of economically useful animal traits, breeding programs must involve a complex of indicators that characterize both the efficiency of feed use and fattening qualities.

Loci of quantitative traits. The intensive development of molecular genetic methods in the first quarter of the 21st century opens up new opportunities for accelerating progress in animal breeding, including increasing the efficiency of feed use.

DNA technology was first used in commercial beef farming in the 1990s. However, most economically useful traits in animals are polygenic in nature, that is, they are determined by the action of a large number of genes, called quantitative trait loci (QTL) [40]. Most QTLs have only minor effects on economic utility, and the likelihood of detecting their effect is highly dependent on sample size [41]. However, the use of some genes in animal breeding remains relevant. Thus, research is being conducted on the search for and implementation of DNA markers

calpastatin (CAST) and calpain (CLPN) associated with the tenderness of cattle meat into breeding programs.

In the early 2000s, approaches were proposed to ensure the introduction of genomic evaluation methods into animal breeding [42]. Subsequently, there were opportunities for the development of more advanced procedures for assessing the breeding value of animals using information on a large number of SNPs (single nucleotide polymorphism). This includes the linear models rrBLUP (assessment of the effect of each marker), GBLUP (estimation of breeding value by genome) and the one-step estimation method ssGBLUP (one of the best to date; allows ones to get an improved genomic estimate of breeding value, taking into account both genome and pedigree data), as well as BayesA and BayesB non-linear Bayes methods.

For the first time, genomic evaluation has been recognized as official for Holstein cattle in the United States since January 2009. From 2009 to 2013, the procedure was introduced in 12 additional countries. Currently, genomic selection is becoming a traditional practice in dairy cattle breeding both abroad [43] and in the Russian Federation [44]. The use of genomic assessment in dairy cattle breeding has made it possible to increase the accuracy of the prediction of the breeding value of young animals by 15-25% and begin their more intensive use, thereby reducing the interval between generations and accelerating progress in breeding.

In beef cattle breeding, the increase in the selection response due to the introduction of genomic selection is estimated at 29-58%, depending on the trait [45]. The lack of a phenotypic correlation between RFI and average daily body weight gains and the heritability of RFI has made this indicator the preferred measure for identifying biological mechanisms of feed efficiency for genomic breeding purposes [7, 31, 46].

For feed consumption and efficiency traits, accurate QTL mapping was performed using 2194 markers on 24 autosomes of beef cattle [47]. In the experiment, Angus and Charolais bulls from 20 populations were examined. A total of 4 QTLs exceeded the significance threshold for genome-wide associations at $p < 0.001$, 3 at $p < 0.01$, 17 at $p < 0.05$, and 30 could be considered suggestive. Nineteen chromosomes contained QTLs significant for RFI. The results of QTL for RFI obtained in many studies were generally similar, the positions were also similar but sometimes differed in significance. For FCR and DMI, fewer QTLs were found compared to RFI, 12 and 4, respectively. Some chromosomes contained QTLs for FCR but not for RFI, while all QTLs for DMI were on chromosomes where they were also found for RFI. The most significant QTL for RFI was located on BTA3 (82 cM; $p = 7.60 \times 10^{-5}$), for FCR on BTA24 (59 cM; $p = 0.0002$), and for DMI on BTA7 (54 cM; $p = 1.38 \times 10^{-5}$). The RFI QTLs with the closest mapping results to previous studies were on BTA1, BTA7, BTA18 and BTA19 [48]. The identified trait loci provide a starting point for identifying genes that influence feed intake and efficiency in marker-assisted breeding [49].

J.D. Nkrumah et al. [37] obtained information on the genotype of 20 hybrid bulls (Angus, Charolais and Alberta) with at least 400 offspring, 100 microsatellite markers and 355 SNPs. Traits analyzed included feedlot ADG, daily DMI, feed intake to body weight gain F:G (reciprocal of G:F gain efficiency) and RFI. Putative QTLs for ADG ($p < 0.05$) were found on BTA5 (130 cM), BTA6 (42 cM), BTA7 (84 cM), BTA11 (20 cM), BTA14 (74 cM), BTA16 (22 cM), BTA17 (9 cM), BTA18 (46 cM), BTA19 (53 cM) and BTA28 (23 cM). For DMI, putative QTLs that exceeded the threshold $p < 0.05$ were found on BTA1 (93 cM), BTA3 (123 cM), BTA15 (31 cM), BTA17 (81 cM), BTA18 (49 cM), BTA20 (56 cM) and BTA26 (69 cM). E.L. Sherman et al. [47] found associations of SNPs on BTA2, BTA5, BTA10, BTA20 and BTA29 with DMI, RFI and FCR. This

study shows that the detected SNPs can affect biological mechanisms of feed efficiency other than control of feed intake and weight gain. The resulting SNPs can be used in breeding [50].

The Animal QTLdb database (<https://www.ani-malgenome.org/cgi-bin/QTLdb/SS/search>) was created to accommodate publicly available QTL data for cattle, chickens and pigs. In 2007, tools were developed to map QTLs to various genome features such as bacterial artificial chromosome end sequences, SNPs, and oligonucleotide array elements. In addition to Animal QTLdb, a virtual comparison map (VCmap) is used to map QTLs across species, which was jointly developed by Iowa State University and the Medical College of Wisconsin (<http://www.animalgenome.org/VCmap>). The methodology for extracting and analyzing QTL data has been improved, and significant progress has been made over the past few years. The QTL database has now been expanded to include two more species (sheep and rainbow trout), providing additional opportunities for comparative mapping. The information provided is constantly updated. The number of publications that mention Animal QTLdb (1498 citations recorded as of August 2022) confirms its popularity [51-53]. Obtaining more detailed information about changes in quantitative traits and improving the terminological apparatus of gene ontology increase the accuracy of QTL annotation. As sets of genes become available for microarray expression analysis and high-density SNP arrays for genome-wide association studies (GWAS) have been created, QTL analysis is no longer the only way to establish relationships between genes and traits, and involving SNPs in genome-wide association studies is inevitable. This concept requires a meta-analysis of large amounts of experimental data accumulated rapidly.

Genome-wide association study of feed efficiency. Considering the economic importance of developing and implementing genomic breeding programs aimed at improving feed efficiency and growth energy, research teams in various countries have started genome-wide association studies [54-57] using DNA chips of medium density (Bovine SNP50 BeadChip, Illumina Inc., USA) [58, 60] and high density (Bovine HD Bead Chip, Illumina Inc., USA) [59, 61]. The results allow researchers to clarify the methodological aspects of the development of genomic breeding programs for beef cattle and to identify a number of positional and functional SNPs associated with feed efficiency and fattening performance.

C.M. Seabury et al. [59] performed a GWAS analysis for average daily body weight gain (ADG), dry matter intake (DMI), metabolic body weight (MWT), and residual feed intake (RFI) using natural and imputed genotypes (Illumina 778K) for 3887 animals of three American beef cattle populations (Angus, Hereford, Simangus) and values of heritability coefficients based on genotypes for SNP markers. According to the calculated proportion of additive genetic variance, which can be explained by the effect of markers (PVE 1%), and the nominal p-value threshold ($p \leq 5e-05$), QTLs with medium or high effect were found in three populations for all studied traits. Identical or closely located (± 0.2 Mb) SNPs associated with ADG, DMI, MWT, and RFI scores co-supported the potential for pleiotropic QTLs or closely spaced mutations for several traits within and between analyzed populations. Marker-based heritability rates for all traits ranged from 0.18 to 0.60 in genomic analysis using the Illumina 778K HD chip and from 0.17 to 0.57 using the Illumina Bovine SNP50 chip. Identification of QTLs detected with the Illumina Bovine SNP50 chip has yielded mixed results. It is likely that the use of a low-density chip was not sufficient to detect significant QTLs in the populations studied, and appropriate breeding or screening programs should be based on the analysis of polymorphisms (imputed or directly detected) on higher-density chips.

M.H. Santana et al. [62] aimed to identify SNPs associated with DMI and RFI in Nellore cattle using medium density (Illumina® BovineSNP50 v2 Bead-Chip), high density (Illumina® BovineHD BeadChip) panels and their combination to search for possible candidate genes with known function. The authors identified three SNPs for DMI that exceeded the threshold of significance in the Bonferroni multiple comparison test, and two SNPs for RFI.

Using the Illumina 778K chip, seven QTLs with a significant effect were found in Angus cattle, distributed over seven autosomes. Most positional candidate genes located in or near the detected QTL (*XIRP2*, *HSPB8*, *TOX/TRNACGCA*, *DDB1*, *DAK*, *ADPRHL1*, *CDC-16*) have previously been associated with feed efficiency and growth vigor in other animal species (broilers, poultry, pigs) [63, 64] and obesity in humans [65, 66]. These genes are also involved in the resumption of the human cell cycle after the S-phase checkpoint [67-70]. Moreover, one positional candidate gene (*DAK*) is involved in the biosynthesis of riboflavin-4',5'-phosphate [65] which acts as an electron acceptor in the oxidative metabolism of carbohydrates, amino acids and fatty acids and can donate electrons to the electron transport chain [69, 70]. Riboflavin is essential for energy production, which is required for growth and development of the body [65, 66, 69, 70].

2. Characterization of the main SNPs (single nucleotide polymorphism) of each chromosome in significant associations with RFI (residual feed intake) in beef cattle populations

Breed	Position (Chr_Mb)	-log ₁₀ p-value	Candidate gene	Functions	References
Angus	2_30	5.51	<i>XIRP2</i>	Feed efficiency and growth (cattle)	[63]
	17_58	4.77	<i>HSPB8</i>	Signs of obesity (human)	[64]
	14_27	4.56	<i>TOX/TRNAC-GCA</i>	Signs of obesity (human)	[65]
	29_40	4.55	<i>DDB1/DAK</i>	Cell cycle, nutritional efficiency and growth (human, chicken, duck, pigs)	[65, 66, 71]
	12_91	4.39	<i>ADPRHL1/CDC-16</i>	Feed efficiency and growth (chicken, pigs)	[67, 68, 72]
Hereford	6_113	6.51	<i>RAB28</i>	Signs of obesity (human)	[73]
	20_49	3.65	<i>STC2</i>	Role in obesity (human), growth suppression and development of bones, muscles (mouse)	[75]
	6_47	1.70	<i>NCAPG</i>	Associated with carcass and body weight (cattle)	[74]
	1_72	4.34	<i>DLG1</i>	Glucose uptake (human)	[73]

In Hereford cattle, genome-wide RFI analysis using the Illumina 778K DNA chip showed the presence of four high effect QTLs distributed over four autosomes (6_113 Mb, 19_54 Mb, 3_29 Mb, 1_72 Mb) (Table 2). Evaluation of positional candidate genes (*STC2*, *RAB28*, *DLG1*) revealed associations with human obesity, adipogenic differentiation, type I diabetes, and rheumatoid arthritis, and suppression of bone and muscle growth and development in mice. The *NCAPG* gene associated with the development of body weight in cattle was previously proposed by K. Setoguchi et al. [74] for molecular test systems as a candidate.

3. Major SNPs of each chromosome in significant associations with RFI, DMI, ADG, and MWT in a multi-breed beef cattle population

Trait	BTA	Position, bp	SNP	p-value	Candidate gene
RFI	1	121 176 492	rs109479784	8.27E-06	<i>SNORA70</i>
	2	28 511 594	rs379241952	9.69E-07	<i>B3GALT1</i>
	3	6 835 555	rs110523019	1.74E-07	<i>DDR2</i>
	4	89 834 757	rs42645457	6.12E-06	<i>GPR37</i>
	5	9 075 556	rs446215391	6.77E-07	<i>SYT1</i>
	12	54 262 083	rs382972340	8.21E-06	<i>U6</i>
	13	35 856 785	rs382536070	6.60E-06	<i>LYZL1</i>
	16	13 105 979	Chr16:13105979	8.38E-06	<i>RGS2</i>
	23	48 775 591	rs382491772	8.90E-06	<i>F13A1</i>

DMI	1	25 084 372	rs211318336	8.30E-06	<i>U2</i>	
	2	112 157 337	rs109570141	1.96E-06	<i>U6atac</i>	
	4	3 153 240	rs472695088	2.80E-06	<i>SNORA31</i>	
	6	39 105 359	rs207689046	2.77E-25	<i>LCORL</i>	
	10	31 282 009	rs109256612	7.06E-06	<i>DPH6</i>	
	12	54 262 083	rs382972340	1.03E-06	<i>U6</i>	
	13	19 004 111	rs384869645	5.56E-06	<i>PARD3</i>	
	14	24 973 953	rs110092040	1.12E-08	<i>MOS</i>	
	16	78 179 941	rs380573663	3.66E-06	<i>CRB1</i>	
	20	4 791 751	rs43357086	4.33E-09	<i>5S_rRNA</i>	
	22	30 879 104	rs211404023	3.71E-06	<i>5S_rRNA</i>	
	ADG	4	112 725 016	Chr4:112725016	3.79E-06	<i>CUL1</i>
		5	106 247 266	rs137822220	8.25E-07	<i>CCND2</i>
		6	39 113 335	rs110987922	3.28E-07	<i>LCORL</i>
		7	93 244 933	rs109901274	8.44E-08	<i>ARRDC3</i>
		14	25 006 125	rs134215421	4.82E-13	<i>PLAG1</i>
		20	4 916 731	rs42661323	3.65E-09	<i>STC2</i>
		24	15 100 338	rs111029508	5.47E-06	<i>snoU54</i>
		25	40 587 255	rs448890458	5.31E-06	<i>CARD11</i>
		28	45 058 986	rs469759962	9.68E-06	<i>TMEM72</i>
		29	41 512 334	rs137389740	3.74E-06	<i>SCGB1A1</i>
	MWT	1	118 345 325	rs210255011	3.85E-06	<i>ERICH6</i>
5		106 266 665	rs110358394	3.20E-07	<i>CCND2</i>	
6		39 111 019	Chr6:39111019	1.59E-04	<i>LCORL</i>	
7		93 244 933	rs109901274	9.61E-09	<i>ARRDC3</i>	
11		68 821 419	rs446606774	7.92E-07	<i>GALNT14</i>	
14		25 006 125	rs134215421	2.08E-28	<i>PLAG1</i>	
20		4 563 925	rs41934045	6.12E-21	<i>ERGIC1</i>	
21		21 679 784	rs209660822	8.25E-06	<i>AP3S2</i>	
26	8 545 128	rs133223744	3.27E-06	<i>AICF</i>		

Note. DMI is dry matter intake, RFI is predicted residual feed intake, ADG is average daily body weight gain, MWT is metabolic body weight. Compiled based on the data presented in the article by F. Zhang et al. (75).

F. Zhang et al. [75] showed 12 out of 16 significant SNPs for RFI, with 3 genes located within the SNP (Table 3). Genome-wide SNPs for DMI were located on 11 chromosomes, and the *LCORL* gene was identified in SNP rs207689046. Genome-wide SNPs on multiple chromosomes have also been found to be associated with ADG and MWT. Of the 12 SNPs that accounted for more than 0.30 of the phenotype variance for average daily gain, three SNPs are located near or linked to the gene, the rs110987922 is located at 121223 bp from the *LCORL* gene, the rs134215421 is located at 1166 bp and is linked to the *PLAG1* gene. In terms of metabolic body weight, 6 out of 10 genes were located within the SNP, and one gene was identified in the nearby region. SNP rs39111019 (BTA6, 118907 bp, linked to the *LCORL* gene) accounted for 5.80% of the phenotypic variance.

In general, the results of the GWAS analysis show that the vast majority of the identified patterns are population-dependent. Due to genetic (linkage disequilibrium) and phenotypic differences, it becomes necessary to conduct a GWAS for each breed or livestock population for which a genomic breeding program needs to be developed.

Thus, this review on the efficiency of feed use, including feed conversion, indicates the relevance of the topic in the countries that are leaders in meat animal husbandry. When evaluating this index, it is necessary to take into account a complex of technological, biological and economic factors, therefore, the mathematical apparatus, including models used in the practice of animal husbandry, becomes more complicated. Obviously, in Russia, the problem of feed efficiency must be given attention. The phenotypic and genotypic parameters considered in this review will be used in a set of criteria for the beef cattle genome assessment in Russia.

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