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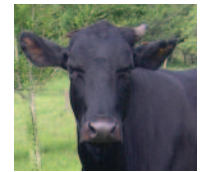
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Opportunities and challenges from the use of genomic selection for beef cattle breeding in Latin America



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Implications

- Beef cattle production in Latin America is very important worldwide. The region accounts for 29% of the world's cattle population and beef production.
- Genomics allows the estimation of breeding values for young animals from DNA samples through the use of panels of single nucleotide polymorphisms (a type of DNA genetic marker). This information is used to increase the accuracy of estimated breeding values. More accurate estimates for young animals should increase the rates of improvement for economically important traits.
- To implement these evaluations, the effects of single nucleotide polymorphisms on the traits need to be estimated in a training population. The cost of running a training population depends on the number and types of measured traits and also on the number of phenotypes and genotypes.
- Several beef cattle populations in Latin America undergo traditional genetic programs for genetic evaluation. Opportunities exist for increasing the improvement rates by using genomic selection.
- Not all populations are suitable for short-term implementation of the methodology owing to the small numbers of sires with genetic evaluations and small numbers of progeny per sire. Another short-term consideration is cost, although genotyping costs are decreasing.
- Longer term reasons to consider using genomic selection are to increase the competitive position of a breed in the market, to select for a larger number of traits more closely related to the economic performance of the animals in specific environments, and to detect the genes associated with variations in productivity so that genetic improvement can become more efficient.

Key words: beef cattle, breeding program, genome-wide association study, Latin America, selection, single nucleotide polymorphism

Beef Cattle Production in Latin America

In 2009, Latin American countries had approximately 401 million cattle (29% of the world's total cattle population) and produced 8.2 million tonnes of beef, equivalent to 29% of the world's total production (FAO, 2011). Beef in Latin American countries is produced under widely differing climates (ranging from tropical to temperate), resources available (vegetation, food), types of markets, and genetic backgrounds of the animals. The main production systems are classified as beef and dual-purpose cattle. The genetic backgrounds of animals vary from purebred European (*Bos taurus taurus*) or Zebu (*Bos taurus indicus*) to crossbreeds (Figures 1 and 2). Beef production systems may also be characterized by their management intensification levels as grazing only, grazing with food supplementation, and feedlot production.

The main beef-producing countries are Brazil (51.6% of the total Latin American beef production), Argentina (18.5%), Mexico (9.4%), and Colombia (5.1%). Other countries contributing more than 1% of the total regional production are Uruguay, Venezuela, Paraguay, Bolivia, Ecuador, and Chile (Table 1). Latin America is a region of the world that can significantly increase its production in response to beef demand.

Brazil has a mature beef cattle industry based on grass-fed cattle, in which feeding *B. taurus indicus* cattle, especially the Nellore breed, is a common practice. Over the last 8 years, beef production in Brazil has become one of the most important activities for employment and wealth creation. Foot-and-mouth disease issues are still a factor limiting the increase in Latin American beef exports (Ferraz and de Felício, 2010; Domingues Millen et al., 2011). Only a few Latin American countries, including Chile and Mexico, have the status of being free of this disease without vaccination. In most countries, the disease is controlled using a combination of free areas without vaccination and areas with vaccination.

Other countries with a strong *B. taurus indicus* background in their beef cattle populations are those with large tropical areas dedicated to beef cattle production, such as Colombia, Venezuela, and Paraguay. Beef production in Argentina, Chile, Uruguay, and some portions of Brazil and



Figure 1. European × Zebu crossbred cattle from Mexico.

Mexico is based mainly around the production of *B. taurus taurus* cattle (Peel et al., 2010; Arelovich et al., 2011; Domingues Millen et al., 2011).

The Mexican beef cattle industry consists of 2 nearly separate market components. Beef producers in the northern part of Mexico have largely focused on the production of calves for export to the United States (Galyean et al., 2011). European beef genetics have been widely used in the region, beginning with importations of Hereford cattle and continuing with today's popularity of Angus and Brangus along with several continental breeds, such as Charolais and Simmental. The central and southern regions of Mexico have historically produced grass-fed beef for the national market as well as dual-purpose dairy-Zebu crossbred cattle to produce milk and beef (Peel et al., 2010).

Currently, breeding programs for the genetic evaluation of beef cattle in Latin America are based on statistical analyses in which performance and pedigree information are integrated. These analyses are based on a mixed model methodology, in particular the animal model statistical approach using best linear unbiased prediction methods to obtain estimated breeding values (EBV) for economically important traits.

This methodology for obtaining EBV has been set up in Argentina, Brazil, Colombia, Mexico, Uruguay, Venezuela, and other countries. It has been established for specific purebred populations and also for some crossbred populations, such as multibreed populations with a dual purpose (beef and milk) in the Latin American humid tropics, which involve animals crossbred between *B. taurus taurus* and *B. taurus indicus* and composite breeds. Most programs focus on evaluating growth and reproductive traits, although a few have included longevity (stayability), heifer pregnancy, conformation, and carcass and meat quality traits.

Genomic Selection

The development of dense arrays (SNP chips) for detection of thousands of single nucleotide polymorphisms, also known as SNP (DNA sequence variation within the strand), has allowed genome-wide association studies

(GWAS) for economically important livestock species (Meuwissen et al., 2001; Chan et al., 2009; Goddard and Hayes, 2009; Schmitt et al., 2010).

The objective of these studies has different implications according to the species of interest. In dairy cattle, it has been used to identify markers that will improve the accuracy of the breeding value estimates of traits associated with milk production, milk components, cow health, and cow conformation (Pryce et al., 2010). In beef cattle, the objective is to increase the accuracy of the genetic predictions for growth, carcass, reproduction, and health traits (Kuehn et al., 2011).

Genome-wide association studies in dairy cattle have been completed for several traits and types of traits in different regions of the world. Australia has taken the lead in identifying genomic regions associated with milk production (Bolormaa et al., 2010; Pryce et al., 2010), and several studies have been completed in the United States and Canada (Wiggans et al., 2009; Cole et al., 2011). This has also been done in China (Jiang et al., 2010). VanRaden (2008) used the information generated in GWAS to increase the accuracy of the EBV of young dairy sires for milk production traits in the United States through genomic selection (GS). This procedure is helping to increase the yearling rates of genetic progress in dairy cattle considerably (Calus, 2010; Goddard et al., 2010).

Studies have been conducted in beef cattle to identify genomic regions associated with growth and feed efficiency (Snelling et al., 2010, 2011). Information from GWAS has been used to attempt to predict genetic values from a population based on the information of another population (Kuehn et al., 2011). Information from GWAS is now being used to ascertain the genetic components of reproduction and health in beef cattle. The GS methodology allows prediction of the breeding value of young animals or animals without their own information, based on GWAS performed on training populations, to estimate marker effects (Goddard et al., 2010).

Genomic selection can be explained as a 2-step process. The first step consists of the estimation of marker effects in a training population containing animals with phenotypic (measurement of economically important traits) and genotypic information (information on the SNP for

Table 1. Meat production and population of cattle in Latin American countries in 2009¹

Country	Production, tonnes	%	Population, animals
Brazil	9,395,000	51.6	205,292,000
Argentina	3,378,000	18.5	50,750,000
Mexico	1,704,990	9.4	32,000,000
Colombia	936,302	5.1	27,359,300
Uruguay	491,213	2.7	12,490,000
Venezuela (Bolivarian Republic of)	480,000	2.6	16,900,000
Paraguay	315,200	1.7	11,643,400
Bolivia (Plurinational State of)	254,579	1.4	8,079,580
Ecuador	244,800	1.3	5,194,730
Chile	209,853	1.2	3,900,000
Peru	164,704	0.9	5,459,440
Nicaragua	107,587	0.6	3,600,000
Dominican Republic	99,000	0.5	2,652,600
Costa Rica	92,693	0.5	1,287,100
Guatemala	75,000	0.4	3,061,000
Panama	74,558	0.4	1,614,100
Cuba	65,000	0.4	3,892,800
Honduras	63,909	0.4	2,697,580
Haiti	41,000	0.2	1,455,000
El Salvador	31,097	0.2	1,342,510
Total	18,224,485	100.0	400,671,140

¹Source: Faostat (FAO, 2011).

each animal). The second step consists of obtaining the SNP genotypes for the animals in the test population and estimating their genomic breeding values (GBV) by summing the marker effects of the SNP estimated from the training population.

The predicted theoretical accuracy of GBV when using only genomic information is very high and may be close to 100%. The current accuracy is lower, and in practice, there are advantages of combining genomic and traditional genetic evaluations (EBV) into a genomic-assisted EBV. Research is ongoing to increase the accuracy of genomic evaluations and optimize the use of genomic information and phenotypes in accurate predictions of breeding values (Goddard et al., 2010).

Beef Cattle Breeding in Latin America

Genetic evaluation systems currently ongoing for selected beef breeds in several Latin American countries are discussed.

Bos taurus taurus Breeds

Angus is the most popular breed for beef production in the United States. There are several genetic evaluation systems for this breed in Latin America. In Argentina, the Asociación Argentina de Angus (<http://www.angus.org.ar>) has had an agreement with the Instituto Nacional de Tecnología Agropecuaria since 1989. In 2011, the Asociación issued the 21st Sire Summary, with 5,125 bulls evaluated for growth traits, height, and scrotal circumference. The data set had more than 362,000 records from 404 farms. Some of these bulls were genetically evaluated for carcass and meat quality traits and for gestation length. Some bulls were also evaluated for meat tenderness by using 4 DNA markers (calpastatin2959, calpastatin UoG, calpain316, and calpain4751). In Brazil, the Programa de

Melhoramento de Bovinos de Carne (PROMEBO; <http://www.promebo.com.br>) is a breeder's organization that is associated with Melhoramento Genético Animal (GenSys; <http://www.gensys.com.br>) to run genetic evaluations for several beef breeds. In the last Sire Summary, a data set with almost 200,000 records and approximately 3,500 bulls was analyzed for growth traits, visual appraisal traits, size, scrotal circumference, ultrasound rib-eye area, and backfat thickness. In Uruguay, a genetic evaluation program is in place for Angus that includes meat quality traits. In Mexico, the genetic evaluation for Angus has been performed since 2007 by the Universidad Autónoma Chapingo for growth traits and scrotal circumference (CONARGEN, 2010).

The genetic evaluation of Braunvieh is held in Brazil by the Animal Breeding and Biotechnology Group at the College of Animal Sciences and Food Engineering of the University of São Paulo (GMAB; <http://www.usp.br/gmab>). The 2009 evaluation considered more than 29,000 records and 370 bulls.

Charolais is an important breed in South America. In Brazil, PROMEBO handles the genetic evaluations for the breed. In the 2010 Sire Summary, approximately 20,000 records and 900 bulls were evaluated for growth, visual appraisal traits, and scrotal circumference. In Mexico, the Charolais-Charbray Association has been producing genetic evaluations for both breeds with Investigaciones Forestales Agrícolas y Pecuarias (INIFAP) since 2002. Traits evaluated include growth, size, and scrotal circumference. The 2010 Sire Summary included data from approximately 100,000 records and 3,590 bulls.

Devon is a breed that is decreasing in importance in South America, especially in Brazil. Only PROMEBO still holds genetic evaluations for this breed. The 2010 Sire Summary analyzed more than 30,000 records and approximately 600 bulls. Traits included in the evaluations were growth, visual appraisal, and scrotal circumference.

Genetic evaluations for the Hereford are done in Argentina, Brazil, Uruguay, and Mexico. In Brazil, 3 independent genetic evaluations are performed, which consider growth and visual appraisal traits in addition to scrotal circumference. The PROMEBO 2010 Sire Summary analysis included approximately 180,000 records and 2,500 bulls. In the 2011 Sire Summary (<http://www.gensys.com.br/>), Conexão Delta G (<http://www.deltag.com.br>), which is evaluated by GenSys, analyzed more than 400,000 records from the joint analysis of Hereford and Braford breeds. Reproductive, growth, and carcass traits, in addition to visual appraisal traits, were considered in the analysis. In addition, Geneplus/Embrapa, together (<http://geneplus.com.br/>) with the Brazilian Association of Hereford and Braford (<http://www.abhb.com.br/>), is initiating a program called PampaPlus (<http://www.pampaplus.com.br/>) to generate genetic evaluations. The Mexican Hereford Association (<http://herefordmexicana.com/>) undergoes a genetic evaluation program that includes only growth traits.

In Brazil, the genetic evaluation of Simmental is done jointly with Simbrah (a 5/8 Simmental, 3/8 Zebu composite breed) by São Paulo State University and the Federal University of Espírito Santo. The 13th Sire Summary (<http://www.simentalsimbrasil.org.br>) issued EBV for growth traits from 38,106 Simmental and 7,634 Simbrah animals, with pedigree information from more than 77,000 animals. In Mexico, the genetic evaluation is completed by INIFAP. The Simmental-Simbrah Association of Mexico (<http://www.simentalsimbrah.com.mx>) issued expected progeny differences from growth traits, stayability, frame score, and scrotal circumference from a pedigree of 147,216 animals.



Figure 2. European × Zebu crossbred calves in Mexico.

In Mexico, the Brown Swiss breed undergoes genetic evaluations for growth traits and scrotal circumference by the Universidad Autónoma Chapingo.

Limousin is a breed that is increasing in importance in Mexico, and INIFAP performs genetic evaluations for growth traits for animals of that breed. The 2011 Sire Summary analyzed more than 19,000 records and approximately 600 bulls for growth traits.

***Bos taurus indicus* Breeds**

Nellore is the most numerous breed raised in Brazil, with more than 80% of the contribution to the Brazilian herd of close to 200 million cattle. The breed is well adapted to tropical conditions. It is also being raised in Northern Argentina, Paraguay, Bolivia, Colombia, and Venezuela. Several Nellore genetic evaluations are being held in Brazil, using data from Brazil, Paraguay, and Colombia. Different groups [Zebu Breeders Association, Agro-Pecuária CFM Ltda/GMAB, Agropecuária Santa Bárbara, Associação Nacional de Criadores e Pesquisadores (ANCP; <http://www.ancp.org.br/>), Condomínio Agropecuário Irmãos Penteado Cardoso/Fazenda Mundo Novo/GMAB (<http://www.fazendamundonovo.com>), Conexão Delta, Geneplus/Embrapa, Programa de Avaliação e Identificação de Novos Touros (<http://www.crvlafoa.com.br/paint.asp>)] analyze in total more than 2 million records and 10,000 bulls in their data set. Characteristics considered in their evaluations are growth, reproductive, carcass, and meat quality traits. These evaluation programs are well structured, and they provide breeders with high-quality evaluations and many scientific research results. Agro-Pecuária CFM Ltda, ANCP, and Conexão Delta G/Agropecuária Jacarezinho, in partnership with 2 international companies (Meril and Pfizer) and a Brazilian company (Genoa Biotecnologia), are involved in the use of DNA markers in their genetic evaluations of Nelore cattle. More than 15,000 records on reproductive, growth, ultrasound

measurements, docility, parasite resistance, and beef quality have already been used in studies validating the use of genetic markers.

Important markers for *B. taurus taurus* are fixed in *B. taurus indicus* or do not show a significant effect. Studies done by Agro-Pecuária CFM Ltda/GMAB and ANCP indicate increases in the accuracy of breeding value estimates of more than 60% when young replacement bulls are genotyped with a limited number of selected markers, reaching accuracies similar to those of bulls with 7 to 10 progeny.

The Guzerath breed is evaluated by 2 organizations: ANCP and the Zebu Breeders Association. The ANCP began its program in 1999 and has a data bank with almost 43,000 records in the pedigree and more than 15,000 animals with records. Growth, reproductive, and ultrasound traits are evaluated.

The Brahman is an important breed in several Latin American countries. Genetic evaluations are done in Argentina by the Breeding and Genetics Group of the Agronomy College, University of Buenos Aires. The evaluation includes growth and ultrasound traits. In Brazil, the Brahman breed is growing in importance. Genetic evaluation of the Brahman is conducted by ANCP, which analyzes reproductive, growth, and ultrasound carcass traits and visual appraisal traits. Colombia, Mexico, and Venezuela also have genetic evaluation programs for the Brahman.

***Bos taurus taurus* × *Bos taurus indicus* Composite Breeds**

Genetic evaluations of the Braford breed are conducted in Argentina, Brazil, and Mexico. In Argentina, the program is held in the Breeding and Genetics Group of the Agronomy College, University of Buenos Aires. In the 2011 Sire Summary, more than 161,000 animals from Argentina, Paraguay, and Uruguay were analyzed. In Brazil, the breed is genetically evaluated together with the Hereford by PROMEBO/GenSys. The 2010 Sire Summary analyzed approximately 6,000 animals and approxi-

mately 200 bulls for growth, visual appraisal, and size traits. In Mexico, the genetic evaluation for growth traits is performed by the Universidad Autónoma Chapingo.

Genetic evaluations are provided in Argentina for the Brangus by the Asociación Argentina de Brangus (<http://www.brangus.org.ar>) in cooperation with the Breeding and Genetics Group of the Agronomy College, University of Buenos Aires. In the 2011 Sire Summary, a total of 155 farms from Argentina, Bolivia, Colombia, Paraguay, and Uruguay were included in the analysis. The data bank has 205,356 animals, born between 1950 and 2010. Multitrait animal models are used to estimate the EBV of animals. Adjustments for heterosis and maternal heterosis are also included. In Brazil, private Brangus breeding programs began to be evaluated in the 1990s, but only the programs initiated by Natura (<http://www.gapgenetica.com.br>) and PROMEBO are currently functioning. In the 2011 Natura Sire Summary, more than 500,000 animals from approximately 4,500 bulls were used. This evaluation included data from farms in Brazil and Paraguay. The PROMEBO program analyzed approximately 14,000 records and 570 bulls. In Mexico, genetic evaluations for Brangus and Red Brangus are performed by the Universidad Autónoma de Chihuahua.

The Canchim is a 5/8 Charolais × 3/8 Zebu synthetic breed developed in Brazil that is being genetically evaluated by Embrapa Sudeste (<http://www.cppse.embrapa.br>). The 2010 Sire Summary analyzed more than 100,000 records on growth traits from Brazil and Uruguay.

The Montana Tropical (Figure 3) is a composite breed developed since 1994 by CFM-Leachmann Agropecuária (<http://www.compostomontana.com.br/>). Using the concept of grouping breeds by their biological types into 4 groups (N = *B. taurus indicus* breeds; A = *B. taurus taurus* adapted to a tropical environment; B = *B. taurus taurus* of British origin; and C = *B. taurus taurus* breeds of Continental European origin), that program, which is genetically evaluated by GMAB, considered more than 329,000 records on growth, reproductive, and visual appraisal traits in the 2011 Sire Summary and has begun ultrasound measurements in the last 3 years. More than 520,000 animals were in the pedigree of this evaluation.

The Santa Gertrudis is a 5/8 Red Poll × 3/8 Zebu composite breed raised mainly in Argentina, Uruguay, and Brazil. The Brazilian genetic evaluation is done by GMAB. The last Sire Summary available included approximately 40,000 measures of growth traits and scrotal circumference. In total, more than 63,000 animals were included in the pedigree.

Other Breeds

The Caracu is a local Brazilian breed of Iberian Peninsula origin. Embrapa/Geneplus/Instituto Agronômico do Paraná (<http://www.iapar.br>) generates a genetic evaluation annually. In the last Sire Summary available (2009), growth and scrotal circumference data were evaluated. Approximately 72,000 animals had phenotypic information, and 83,000 animals with pedigrees were included in the analysis (http://www.cnpqc.embrapa.br/~locs/sumario/caracu/car_dados.htm), corresponding to 2,129 bulls.

The Romosinuano breed is a Colombian beef breed also of Iberian Peninsula origin. This breed can be found in Costa Rica and Venezuela. Other important local Colombian breeds are Blanco Orejinegro, Costeño with Horns, and San Martinero. Limited genetic evaluation efforts have been done in these breeds.

Opportunities and Limitations for the Use of Genomic Selection Programs

Beef production in Latin America is very important and has great potential for growth. Despite the general difficulties encountered in developing well-funded, long-term genetic evaluation programs in Latin America for beef cattle, some examples of success are emerging. Genetic evaluations are very well established and developed in several breeds, such as the Nellore, Angus, Hereford, Braford, and Brangus. In these breeds, important advances should come with nontraditional breeding programs using GS. Significant increases in the accuracy of selection are expected with the use of more dense panels of DNA markers because the results of studies using fewer than 200 markers have revealed increases of more than 60% in the accuracy of breeding value estimates.



Figure 3. Montana bulls in Brazil.

Success in the use of highly dense commercial DNA markers (SNP chips) will depend on several factors:

- Chips need to be developed by scientists and companies that are appropriate for *B. taurus indicus* crossbred and composite cattle populations, with large validation trials with local animals if multibreed chips prove inefficient.
- Because even local South American *B. taurus taurus* breeds are genetically separated from the main European and North American cattle breeds and their environments are also not similar, relevant differences are expected in the effects of DNA markers in South American cattle. This would be an expression of genotype \times environment interactions.
- The cost of genotyping is a major issue. Selection for milk is very different from selection for beef, and the value of selected replacement beef bulls, which are normally used in natural mating in more than 90% of the herds, is very different from that of dairy bulls used in artificial insemination. Hence, genotyping for beef bulls and heifers has not been affordable with the technology prices in 2011.

In the short term, in Latin American countries with relatively small populations under genetic evaluation, the utilization of GWAS would be limited. This is due to the lack of suitable phenotypic data and the data structure (i.e., the large number of progeny of each sire) required to obtain accurate estimates of the SNP associations that, in turn, constitute the accuracy of the GBV of animals without records. For example, the Simmental-Simbrah population is one of the largest under genetic evaluation in Mexico; however, in the 2010 genetic evaluation for these breeds, only 115,077 animals were evaluated, which included 5,159 bulls but only 703 Simmental and 387 Simbrah with more than 10 progeny each. From these numbers, only 210 Simmental and 153 Simbrah bulls had accuracies greater than 0.80 for some traits. Under these conditions, the number of animals needed to have a reference population to achieve adequate accuracies (0.70 or greater) for estimated GBV for growth traits is larger than the actual number in practically all the beef cattle breeds in Mexico.

Beef production efficiency is affected by a large number of traits (Bullock and Pollak, 2009; Garrick and Golden, 2009). Therefore, the measurement of only a few traits, or the exclusion of key trait groups (i.e., meat quality traits) from a breeding program may be a factor that limits efficient estimation of the breeding value of animals. The traits measured may include growth, reproduction (age at first calving, pregnancy rates of heifers, bull fertility traits), conformation, meat yield and quality, survival, and health. In developing countries, it has been difficult to implement traditional genetic improvement programs because they are logistically complex, considering that they require recording pedigree and phenotypic information on thousands to millions of animals for key traits.

In the long term, GS might be more practical than traditional selection in these countries for some beef cattle populations. The development of a prediction equation would still require recording the performance of many animals, but pedigree would not be required and implementation would require only a DNA sample from each selection candidate and the laboratory facilities to genotype SNP and compute GBV. As genotyping costs decline and methods develop for imputing the genotypes of nongenotyped SNP from a smaller number of genotyped SNP chips, it will be easier to implement this technology.

Genomic information from SNP chips may be used not only to obtain genomic predictions of polygenic values for quantitative traits, but also to determine the genetic relationships between animals with no or incomplete pedigree information. This will assist in developing genetic evaluations for populations with incomplete pedigree information or even, in extreme cases, in the absence of pedigree information. The lack of pedigree is an important factor affecting the possibility of doing genetic evaluations in many Latin American beef cattle populations. Genomic information will allow the breed composition of animals to be determined at the individual level, which represents a possibility for increasing the accuracy of estimations of the purebred or crossbred breeding values in composite breed or crossbred populations. Another advantage of genomic evaluations is the possibility of evaluating commercial populations for traits with low heritability or traits that would be too expensive to evaluate in such populations, by using prediction equations developed in training populations. Therefore, if the SNP set and equation have good predictive ability, it would be possible to have genetic evaluations of large populations of animals based on only their DNA information without having phenotypic information. That situation is different from the one for the recorded animals in animal populations currently undergoing GS, in which the genomic information will usually add to the phenotypic data, making their value comparatively lower.

In the long term, it would be possible using GWAS to advance knowledge of the genomic basis of economically important traits for beef cattle. It would also be possible to establish differences in breed composition and genomic differences between breeds developed and used in this region of the world compared with breeds used in other regions. It would allow the identification of genes or groups of genes with the potential to enhance some characteristics, or to inhibit them if desired.

Literature Cited

- Arelovich, H. M., R. D. Bravo, and M. F. Martínez. 2011. Development, characteristics, and trends for beef cattle production in Argentina. *Anim. Front.* 1(2):37–45. doi:10.2527/af.2011-0021.
- Bolormaa, S., J. E. Pryce, B. J. Hayes, and M. E. Goddard. 2010. Multivariate analysis of a genome-wide association study in dairy cattle. *J. Dairy Sci.* 93:3818–3833.
- Bullock, K. D., and E. J. Pollak. 2009. Beef Symposium: The evolution of beef cattle genetic evaluation. *J. Anim. Sci.* 87 (E-Suppl.):E1–E2.
- Calus, M. P. L. 2010. Genomic breeding value prediction: Methods and procedures. *Animal* 4:157–164.
- Chan, E. K. F., R. Hawken, and A. Reverter. 2009. The combined effect of SNP-marker and phenotype attributes in genome-wide association studies. *Anim. Genet.* 40:149–156.
- Cole, J. B., G. R. Wiggins, L. Ma, T. S. Sonstegard, T. J. Lawlor Jr., B. A. Cooker, C. P. Van Tassell, J. Yang, S. Wang, L. Matukumalli, and Y. Da. 2011. Genome-wide association analysis of thirty-one production, health, reproduction and body conformation traits in contemporary U.S. Holstein cows. *BMC Genomics* 12:408.
- CONARGEN (Consejo Nacional de los Recursos Genéticos Pecuarios). 2010. Guía Técnica de programas de control de producción y mejoramiento genético en Bovinos de carne. Consejo Nacional de los Recursos Genéticos Pecuarios, México, D. F. Accessed Nov. 17, 2011. <http://www.conargen.mx/documentos/guias/guiabovinoscarne.pdf>.
- Domingues Millen D., R. Dias Lauritano Pacheco, P. M. Meyer, P. H. Mazza Rodrigues, and A. De Beni Arrigoni. 2011. Current outlook and future perspectives of beef production in Brazil. *Anim. Front.* 1(2):46–52. doi:10.2527/af.2011-0017.
- FAO (Food and Agriculture Organization of the United Nations). 2011. Faostat. Accessed Oct. 2, 2011. FAO, Rome, Italy. faostat.fao.org/.

- Ferraz, J. B. S., and P. E. de Felicio. 2010. Production systems—An example from Brazil. *Meat Sci.* 84:238–243.
- Galayan, J. L., C. Ponce, and J. Schutz. 2011. The future of beef production in North America. *Anim. Front.* 1(2):29–36. doi:10.2527/af.2011-0013.
- Garrick, D. J., and B. L. Golden. 2009. Producing and using genetic evaluations in the United States beef industry of today. *J. Anim. Sci.* 87(E-Suppl.):E11–E18.
- Goddard, M. E., and B. J. Hayes. 2009. Mapping genes for complex traits in domestic animals and their use in breeding programmes. *Nat. Rev. Genet.* 10:381–391.
- Goddard, M. E., B. J. Hayes, and T. H. E. Meuwissen. 2010. Genomic selection in livestock populations. *Genet. Res. (Camb.)* 92:413–421. doi:10.1017/S0016672310000613.
- Jiang, L., J. Liu, D. Sun, P. Ma, X. Ding, Y. Yu, and Q. Zhang. 2010. Genome wide association studies for milk production traits in Chinese Holstein population. *PLoS ONE* 5:e13661.
- Kuehn, L. A., J. W. Keele, G. L. Bennett, T. G. McDanel, T. P. L. Smith, W. M. Snelling, T. S. Sonstegard, and R. M. Thallman. 2011. Predicting breed composition using breed frequencies of 50,000 markers from the US Meat Animal Research Center 2,000 Bull Project. *J. Anim. Sci.* 89:1742–1750.
- Meuwissen, T. H. E., B. J. Hayes, and M. E. Goddard. 2001. Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157:1819–1829.
- Peel, D. S., R. J. Johnson, and K. H. Mathews Jr. 2010. Cow-Calf Beef Production in Mexico. Outlook Rep. No. LDPM-196-01. US Dept. Agric., Econ. Res. Serv., Washington, DC. Accessed Nov. 17, 2011. <http://www.ers.usda.gov/Publications/LDP/2010/10Oct/LDPM19601/>.
- Pryce, J. E., S. Bolormaa, A. J. Chamberlain, P. J. Bowman, K. Savin, M. E. Goddard, and B. J. Hayes. 2010. A validated genome-wide association study in 2 dairy cattle breeds for milk production. *J. Dairy Sci.* 93:3331–3345.
- Schmitt, A. O., R. H. Bortfeldt, and G. A. Brockman. 2010. Tracking chromosomal positions of oligomers—A case study with Illumina's BovineSNP50 beadchip. *BMC Genomics* 11:80.
- Snelling, W. M., M. F. Allan, J. W. Keele, L. A. Kuehn, T. G. McDanel, T. P. L. Smith, T. S. Sonstegard, R. M. Thallman, and G. L. Bennett. 2010. Genome-wide association study of growth in crossbred beef cattle. *J. Anim. Sci.* 88:837–848.
- Snelling, W. M., M. F. Allan, J. W. Keele, L. A. Kuehn, R. M. Thallman, G. L. Bennett, C. L. Ferrell, T. G. Jenkins, H. C. Freetly, M. K. Nielsen, and K. M. Rolfe. 2011. Partial-genome evaluation of postweaning feed intake and efficiency of crossbred beef cattle. *J. Anim. Sci.* 89:1731–1741.
- VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91:4414–4423.
- Wiggans, G. R., T. S. Sonstegard, P. M. VanRaden, L. K. Matukumalli, R. D. Schnabel, J. F. Taylor, F. S. Schenkel, and C. P. van Tassell. 2009. Selection of single-nucleotide polymorphisms and quality of genotypes used in genomic evaluation of dairy cattle in the United States and Canada. *J. Dairy Sci.* 92:3431–3436.

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