

## Contribution of genomic data in defining the breed composition of dual-purpose cattle

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### Abstract:

Animal heterosis is key in obtaining more productive animals and better adapted to the tropics. However, inadequate genetic management leads to the obtaining of mosaics of breeds that includes the loss of the productive potential of the herd. The objective of this study was to define the breed composition of dual-purpose crossbred cattle in the piedmont plains, department of Meta-Colombia. A total of 126 crossbred (CRO) individuals from six herds were evaluated by a phenotypic (APP) and a genotypic (GBA) approach. For GBA, the control breeds associated with *Bos taurus taurus* and *Bos taurus indicus* were included, for this they were genotyped with a GeneSeek GGP-LD chip of 26K of SNP and analyzed by principal component analysis (PCA) and Bayesian probabilistic assignment of ADMIXTURE. The breed groups generated by APP varied with respect to GBA. Molecular analysis detected seven ( $k=7$ ) genetic groups in the breed composition of the study animals. The three breeds with the highest participation in the breed composition of crossbred individuals were: Holstein, Gyr, Brahman with 23.4, 21.4, and 21 % respectively, while the remaining, Blanco Orejinegro, Brown Swiss, Normande and Jersey did not exceed 13 %. Unlike APP, the GBA approach effectively allowed the identification of the breed composition of crossbred cattle and provided key

information for the development of mating programs that seek to improve productive indicators, and in turn tend to the adaptation of animals, an essential requirement for dual-purpose bovine systems.

**Key words:** Genotyping, Crossbred, Variability, Genetics.

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## Introduction

The dual-purpose bovine system in Colombia accounts for approximately 35 % (8.2 million head) of the total bovine population<sup>(1)</sup>. Similar to other regions of Latin America, this system is based on obtaining animals from the crossing of breeds with some degree of productive advantage in a particular environment, and that confers greater productivity<sup>(2)</sup>.

Contrary to what is obtained under subtropical conditions, bovine production systems, in general in tropical regions, have not achieved the expected success<sup>(3)</sup> and as a resource to improve production, the selection of local and exotic breeds of the genera *Bos taurus taurus*, *Bos taurus indicus* and crosses between them is carried out<sup>(4)</sup> to make efficient use of heterosis, paternal or maternal as used, and to increase the efficiency of beef or milk production systems<sup>(5)</sup>.

However, not all crosses can confer the expected advantages and the incorrect application of zootechnical guidelines can accelerate the presence of adaptation and production problems. It is necessary to consider the implications of a multibreed herd, where its breed composition is partially known or completely unknown, and where non-additive genetic effects delineate the expression of the animal phenotype<sup>(6)</sup>.

In this regard, the situation in Colombia requires special attention because in addition to a predominant tropical condition, the use of a wide range of breeds and crosses, the lack of productive records and the indiscriminate use of breeders without knowledge of the origin or management result in an erroneous perception of animals that are more productive and better adapted to the conditions where they are exploited<sup>(4,6)</sup>.

In this case, the availability of information on the genealogical structure or co-ancestry between individuals allows managing diversity and having control over inbreeding<sup>(7)</sup> and the use of molecular markers, particularly SNP (Single Nucleotide Polymorphism), has

demonstrated the effectiveness of genomic analysis in determining the breed composition in beef<sup>(8)</sup> and milk<sup>(9)</sup> crossbred herds with deficient genealogical information.

In fact, the contribution of molecular analyses has made it possible to identify whether the origin of *B. taurus taurus* or *B. taurus indicus* of chromosomal sequence of cattle may have effects on characteristics of productive interest<sup>(10)</sup>.

Therefore, the objective of this study was to quantify the contribution of genomic information in determining the breed composition of crossbred cattle of the dual-purpose system predominant in the Colombian Piedmonte Llanero region, as a support tool in the definition of management and selection strategies in crossbred herds of the region.

## **Material and methods**

### **Location**

This study was carried out in animals present in six herds of three dairy routes in the subregion of Piedemonte Llanero in the department of Meta-Colombia. This subregion is characterized by temperatures ranging between 23 and 30 °C, relative humidity between 76 and 78 % and altitudes at sea level between 300 and 700 m asl<sup>(11)</sup>.

The crossbred (CRO) herds in each defined municipality were named by acronyms as follows: ACA: herd of the municipality of Acacías, CLN: herd of the municipality of Castilla La Nueva, CUM: herd of the municipality of Cumaryl, MES: herd of the municipality of Mesetas, SJA: herd of the municipality of San Juan de Arama and VLL: herd of the municipality of Villavicencio.

### **Phenotypic assessment**

Initially, in each selected herd (conformed by an average of 70 animals), the productive information was consolidated through a basic survey to identify the productive criteria and objectives of use of the breeds present. Subsequently, the breed classification of a group of representative animals was carried out, of which heifers and cows of up to third calving were included. For this purpose, about 21 animals per herd were selected, for a total of 126 animals, to generate a classification by their *Apparent phenotypic predominance* –APP<sup>(12)</sup>, where the wide range of crosses between the breeds of origin *B. taurus taurus* and *B. taurus indicus*, used in the herds of the dual-purpose production system. APP classify the animals as follows: animals with predominance *B. taurus taurus*

(PREDTAU): without hump, without dewlap and without umbilical fold, short and hairy ears, spotted hair or not, black, red and brown skin, horned or not. Animals with predominance *B. taurus indicus* (PREDCEB): with hump, dewlap and highly developed umbilical fold, long and hairless ears, solid, gray, black, ash or red color. With intermediate predominance *B. taurus taurus* x *B. taurus indicus* (PREDINTER): with hump, dewlap and umbilical fold, long and slightly hairy ears, rarely spotted, almost always with horns.

## Genotypic breed assignment

The genotypic breed assignment-GBA was obtained from genotypic information from 126 animals (21 per herd), previously selected (by APP) and sampled under the recommendations of a reduced extreme sampling<sup>(13)</sup>, thus ensuring the comparison between APP and GBA database. For molecular assessment, a blood sample was collected from each animal by puncture in the coccygeal vein and transported to Molecular Genetics Laboratory at Tibaitatá Research Center of AGROSAVIA for subsequent genotyping. DNA extraction was performed using the commercial UltraClean ® Blood DNA Isolation kit (MoBio Laboratories Inc.) and the genotyping of single nucleotide polymorphisms (SNPs) distributed in the bovine genome was performed with the GeneSeek® GGP-LD chip of 26K SNPs under the recommendations of the manufacturer.

## Database cleansing and statistical analysis

The information derived from the phenotypic evaluation allowed generating frequency table based on breed components observed in the evaluated herds. The molecular information was prepared for population analysis in order to identify genetic groups. Therefore, initially, SNP markers with unknown position and those located on sex chromosomes were excluded. Likewise, SNPs that were not detected in more than 5 % of the individuals, SNPs that deviated from the Hardy-Weinberg equilibrium ( $P<0.01$ ) and SNPs that presented an MAF <0.01 were excluded from the analysis. After carrying out the cleansing, 24,266 SNPs of the 126 samples were used, with which the genetic analyses were carried out.

With the molecular information, the genetic structure of the CRO population was initially determined through principal component analysis (PCA), that is, from the genotypic data the genetic relationships between individuals were evaluated and possible agglomerations were sought with respect to genetic groups established in APP and the control breeds used in GBA. For this purpose, PRCOMP command of STATS library for R<sup>(14)</sup> was used. To

identify the genetic relationships and possible introgression events, the probabilistic assignment of individuals to genetic groups was used, for this, the maximum likelihood algorithm was used, which, based on models, estimates the ancestry and calculates the probability of the observed genotypes using ancestry proportions and population allele frequencies of the population, algorithm implemented in ADMIXTURE<sup>(15)</sup>. To determine the presence of k genetic groups in the population, from k= 2 to k= 10 genetic groups were analyzed, and the most probable k value was identified by the lowest error value in the cross-validation software with the default options of the program, and the author's recommendations<sup>(15)</sup>.

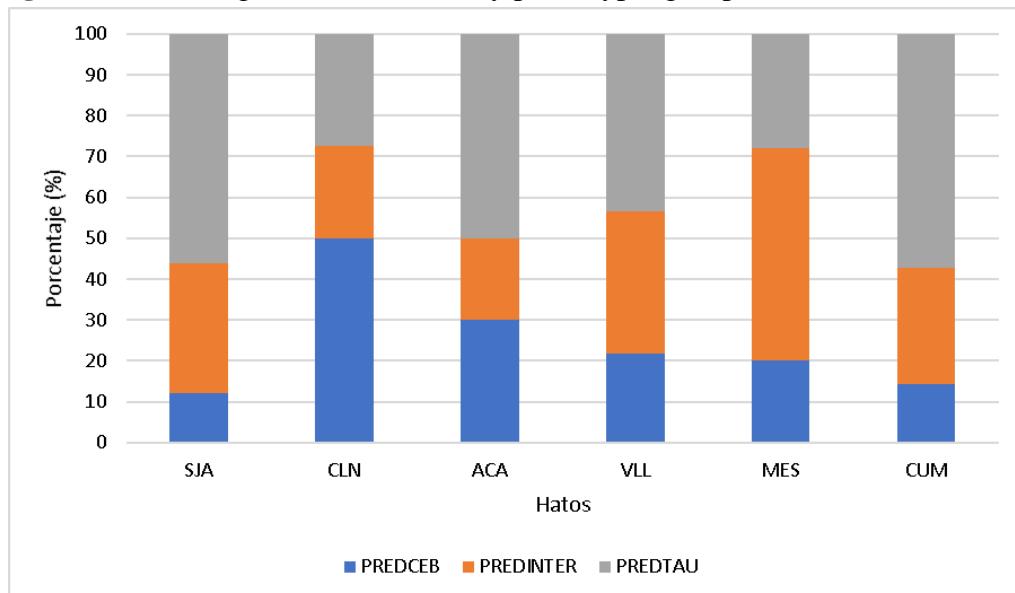
Finally, by the algorithm described above<sup>(15)</sup>, allele frequencies of SNPs in crossbred population (CRO, n= 126) were compared with respect to the control breeds, where an approximate number of 20 samples was used, looking for symmetry with the number of samples taken per herd (21 samples). To do this, a database of SNPs of the seven control breeds was used, provided by Molecular Genetics Laboratory at Tibaitatá Research Center of AGROSAVIA and corresponded to the breeds: Brahman (BRA, n=18), Holstein (HOL, n=29), Blanco Orejinegro (BON, n=19), Gyr (GYR, n=18), Brown Swiss (BRO, n=20), Jersey (JER, n= 20) and Normande (NOR, n=20), for considering their apparent use in the formation of the crossbreeding of cattle of the dual-purpose system and thus establish the genetic groups with greater precision.

## Results

### Phenotypic assessment

From information provided by producers, it was found that predominant breed groups were crosses with Gyr (22.45 %), Zebu (18.36 %), Holstein (16.32 %), Brown Swiss (10.20 %), Normande (4.76 %) and Jersey (4.08 %). In most cases, the producers responded that the apparent breed composition of their herds was due to the breed of breeding bull used in recent mating years. The remaining 23.80 % of the crosses refer to individuals with possible Creole and undefined breed groups.

On the other hand, in the CRO herds with the APP approach, 34 % of the animals were classified as PREDCEB, 37 % as PREDTAU and the remaining 29 % as PREDINTER. At the level of the herds, the proportions of the groups by phenotype were variable among themselves, although a slight similarity was observed between SJA and CUM (Figure 1), which, despite being in distant regions, show similar genetic compositions due to their management and productive orientation.

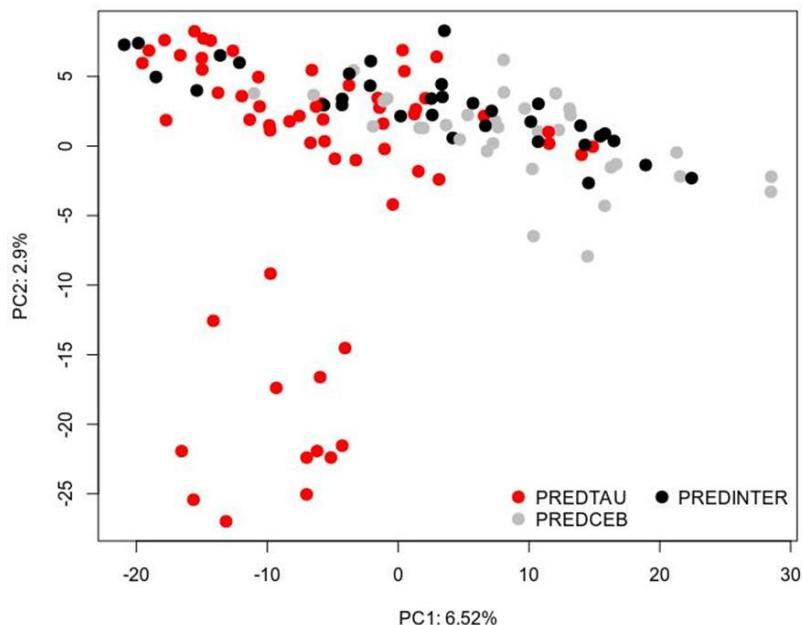
**Figure 1:** Percentage of contribution by phenotypic groups in the evaluated herds

PREDCEB= animals with predominance *Bos taurus indicus*, PREDTAU= animals with predominance *Bos taurus taurus*, PREDINTER= animals with intermediate predominance *Bos taurus taurus* x *Bos taurus indicus*, ACA= herd of the municipality of Acacías, CLN= herd of the municipality of Castilla La Nueva, CUM= herd of the municipality of Cumaral, MES= herd of the municipality of Mesetas, SJA= herd of the municipality of San Juan de Arama and VLL= herd of the municipality of Villavicencio.

### Genotypic breed assignment

First, with the genotypic information, the genetic relationship between the samples was established by principal component analysis for the three genetic groups PREDTAU, PREDINTER and PREDCEB (Figure 2). The first principal component (PC1) explained 6.52 % of the total variance, associated with the differentiation of the genetic components *Bos taurus taurus* and *Bos taurus indicus*. The groups by APP proposed PREDTAU, PREDCEB and PREDINTER did not show the expected genetic separation for the CRO population and on the contrary, all individuals in the groups were dispersed throughout the first component. On the other hand, the second principal component explained 2.9 % of the variation, where a group of individuals assessed by APP as PREDTAU separated from the differentiation axis observed in PC1 (Figure 2). In the PCA graphs, a high dispersion was observed in animals with phenotype *Bos taurus taurus* and *Bos taurus indicus*, which may be associated with a genetic variability of the populations greater than the phenotypic variation. However, the spatial projection of the animals differentiated by PC2 is an indicator of how the allele frequencies distinguish animals with predominance of a phenotype, which makes it mandatory to use control breeds for their better definition.

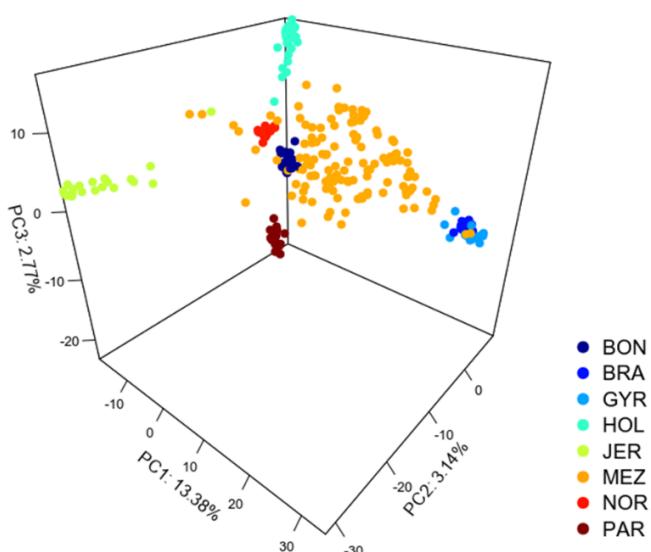
**Figure 2:** Principal component analysis (PCA) among individuals for dual-purpose crossbred cattle and their apparent phenotypic predominance (APP)



PREDCEB= animals with predominance *Bos taurus indicus*, PREDTAU= animals with predominance *Bos taurus taurus*, PREDINTER= animals with intermediate predominance *Bos taurus taurus x Bos taurus indicus*.

In order to establish possible breeds that conform the genetic group of the CRO group, seven control breeds were included and their relationship was assessed by PCA (Figure 3).

**Figure 3:** Principal component analysis (PCA) with the inclusion of control breed groups in the dual-purpose crossbred (CRO) cattle population



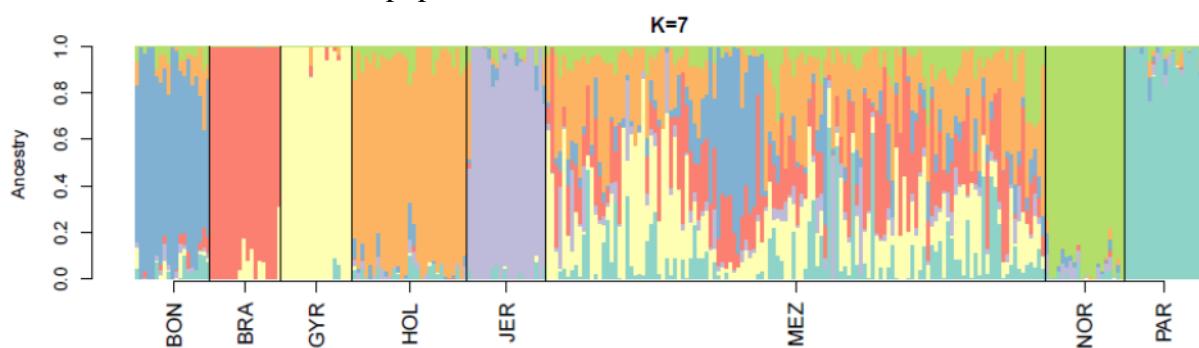
BON= Blanco Orejinegro, BRA= Brahman, GYR= Gyr, HOL= Holstein, JER= Jersey, NOR= Normande, PAR= Brown Swiss (BRO), MEZ= crossbred (CRO).

The PC1 explained 13.38 % of total variation associated with the differentiation between animals of the group of breeds *B. taurus indicus* (BRA and GYR) located on the right side and group of breeds *B. taurus taurus* (HOL, JER, BRO, BON and NOR) located on the left side (Figure 3). In fact, the spatial projection of crossbred individuals presents a broad spectrum between these two groups of breeds as initially observed in the APP.

The second principal component PC2 explained 3.14 % of variation. It is evident that the group of breeds *B. taurus taurus* presents greater variability than group *B. taurus indicus*, it is highlighted that the breed JER shows the greatest separation between breeds *B. taurus taurus* and only a small group of CRO animals would appear in the spectrum towards this breed (Figure 3). The third component-PC3, 2.77 % of the variation was explained by this component, HOL and BRO breeds are shown as the most distant groups from each other and in the spectrum, it covers a part of crossbred animals of this study and animals of BON and NOR breeds.

The second approach to define existing genetic groups used Bayesian probabilistic assignment implemented in ADMIXTURE, where it was determined that the smallest error in cross-validation corresponded to 7 ( $k=7$ ) genetic groups, taking this value as adequate to explain genetic composition in the CRO population of this study, associated with genetic groups BRA, GYR, BON, HOL, BRO, JER and NOR (Figure 4), here, each individual is represented by a vertical line, and the colors represent the fraction of assignment to each genetic group.

**Figure 4:** Population structure of genotypes of the dual-purpose crossbred (CRO) population and control breeds



BON= Blanco Orejinegro, BRA= Brahman, GYR= Gyr, HOL= Holstein, JER= Jersey, NOR= Normande, PAR= Brown Swiss (BRO), MEZ= Crossbred (CRO).

The HOL, GYR and BRA breeds had the highest breed proportion in the CRO population. The ADMIXTURE analysis made it possible to determine more clearly the breed composition of the study herd compared to the PCA analyses. However, certain herds exceptionally showed abundant breed compositions for certain breeds, such as BON.

Table 1 shows breed composition by herd, based on information generated from the ADMIXTURE analysis. The contribution of HOL, GYR and BRA breeds to composition of CRO was found to be 23.47 %, 21.43 % and 21.05 % respectively. Other breeds such as BON (12.41 %) and BRO (10.15 %) contributed to a lesser extent, and the NOR and JER breeds showed the lowest contribution of all control breeds with 6.51 and 4.96 % respectively. HOL, GYR and BRA breeds were predominant in the phenotypic and molecular observations of CRO population, but the estimation of their contribution to the gene pool of crossbred population improved considerably when molecular analyses were used.

**Table 1:** Percentages of breed conformation of dual-purpose crossbred (CRO) cattle with respect to control breeds

Herd*	BRO	GYR	JER	BRA	BON	HOL	NOR
ACA	10.99	23.41	2.84	16.65	6.33	32.18	7.59
CLN	9.70	36.07	4.08	14.39	3.58	28.05	4.13
CUM	19.12	15.52	10.04	18.96	8.54	22.38	5.42
MES	12.93	18.14	3.36	28.92	5.62	25.05	5.98
SJA	7.03	22.58	5.94	18.12	6.29	28.02	12.01
VLL	3.04	14.58	2.87	25.76	41.07	9.41	3.29
Overall total	10.15	21.43	4.96	21.05	12.41	23.47	6.51

BRO= Brown Swiss, GYR= Gyr, JER= Jersey; BRA= Brahman, BON= Blanco Orejinegro, HOL= Holstein, NOR= Normande.

\*Herd: ACA= crossbred herd of the municipality of Acacías, CLN= crossbred herd of the municipality of Castilla La Nueva, CUM= crossbred herd of the municipality of Cumaral, MES= crossbred herd of the municipality of Mesetas, SJA= crossbred herd of the municipality of San Juan de Arama, VLL= crossbred herd of the municipality of Villavicencio

Similarly, the use of molecular markers allowed quantifying the proportion of other breeds whose contribution by phenotype is less predictable. For example, the high presence of the Colombian Creole breed BON was identified in VLL (41.07 %); presence of the BRO breed in CUM (19.12 %), MES (12.93 %) and ACA (10.99 %), while NOR stood out in SJA (12.01 %) and JER in CUM (10.04 %) as shown in Table 1.

### Apparent phenotypic predominance (APP) vs Genotypic breed assignment (GBA)

When the three genetic groups generated by the apparent phenotypic predominance-APP (PREDTAU, PREDCEB and PREDINTER) were compared with the breed compositions generated by the genotypic breed assignment-GBA, it was found that the animals assigned to the PREDTAU group (37 % of the study population) presented a wide

variation of their breed composition obtained by GBA. The breed groups used as controls in GBA, in the breeds, they ranged from a minimum of 0.1 % to a maximum of 80 %, the highest assignment value was found in the BON breed, followed by BRO and HOL, however, the GYR breed also showed a considerable proportion (Table 2).

**Table 2:** Maximum individual genotypic breed assignment (GBA), with respect to the breed groups assigned by apparent phenotypic predominance (%)

APP groups*	BRO	GYR	JER	BRA	BON	HOL	NOR
PREDCEB	35.78	84.27	34.57	71.66	18.34	53.34	14.26
PREDINTER	44.42	60.41	15.39	58.34	88.07	56.09	34.84
PREDTAU	65.16	65.40	53.46	52.73	80.01	64.86	33.49

BON= Blanco Orejinegro, GYR= Gyr, NOR= Normande, BRA= Brahman, JER= Jersey, HOL= Holstein, BRO= Brown Swiss.

\*APP= apparent phenotypic predominance, PREDCEB= with predominance *Bos taurus indicus*, PREDTAU= with predominance *Bos taurus taurus*, PREDINTER= with intermediate predominance *Bos taurus taurus x Bos taurus indicus*.

For their part, animals cataloged in PREDCEB (34 % of the study population) showed a variability in breed composition, mainly for the breeds related to the *Bos taurus indicus* group, with values ranging from a minimum of 0.1 % to a maximum of 84.2 %, the maximum assignments in the GYR and BRA breed stood out, and even the considerable assignment found for HOL stands out (Table 2).

For animals grouped in PREDINTER (29 % of the study population), whose predominant breed assignment presents greater difficulty, they showed great variability for both *Bos taurus indicus* breeds and *Bos taurus taurus* breeds according to GBA. Breed assignment values ranged from 0.1 % to 88 % for BON and HOL breeds and relevant assignment values in GYR and BRA breeds (Table 2). In this way, the discrepancies between the phenotypic and genotypic assignment of individuals were evident.

## Discussion

### Phenotypic assessment

The information derived from visits to farms and provided by producers gives an idea of constant environmental, health and economic situations that transform day by day the livestock farming in Colombia. In CRO, the abundant proportion found of breeds historically associated with milk production (e.g. Holstein and Brown Swiss) and more recently Gyr breed recognized for its capacity for milk production, rusticity and fertility

throughout tropical and subtropical areas<sup>(16)</sup> are directly associated with the finding of more productive animals with adaptation to the environment.

As has been established, a proportion greater than 50 % of *B. taurus taurus*, especially by Holstein, Brown Swiss and Jersey dairy breeds, is associated with higher milk production and a lower reproductive response in tropical environments, while a higher proportion of *B. taurus indicus*, especially of Brahman and Gyr breeds, is associated with a higher adaptation and higher reproductive rates than *B. taurus taurus*, without ignoring the factors clearly related to animal management<sup>(17,18)</sup>. Under this premise, producers have promoted the crossbreeding of animals, but without an orientation of animal resource management, without technical criteria and sometimes without knowledge of the breed purity of breeders<sup>(19)</sup>. As a result of these practices, in this study, it was observed that the total ignorance of crossbreeding can reach up to a 23.8 % of the animals in their herds.

Groups generated by APP showed some symmetry between the PREDTAU, PREDCEB and PREDINTER groups, only a slight deviation was observed in PREDTAU (+3 %). This makes evident the intention of the producer to maintain the breed proportions between the genetic groups established by APP, to better use the hybrid vigor between the most common breeds *B. taurus taurus* and *B. taurus indicus* for milk production and at the same time of beef in a traditional dual-purpose system. The APP approach was an initial approach to the understanding of the various crosses of defined breeds<sup>(12)</sup>, and obeys breed characterization protocols, which provide information to genotypic analyses based on molecular markers<sup>(20)</sup>.

The wide range of crosses and the predominance of the phenotype *B. taurus indicus* found in CRO is well argued in the constant search to complement the components of higher milk production generally given by dairy breeds of genus *B. taurus taurus*, such as Holstein, Brown Swiss, among others, and take advantage of the adaptation of animals *B. taurus indicus* or existing creoles of herds of the dual-purpose system in the Orinoquia<sup>(21)</sup>.

Principal component analysis shows the high genetic variability of the population and that it reduces the correspondence with the proposed APP groups. This translates into a wide margin of error when designing the mating strategy, where more accurate genotypic or genealogical information of the ancestors that conform each individual, and therefore in each herd, is required<sup>(22)</sup>.

Similarly, the principal component analysis with control breeds showed the high degree of crossbreeding between *B. taurus taurus* and *B. taurus indicus*. The considerable number of control breeds used in this study show the complex genetic relationship in dual-purpose herds in the study region and may be an indicator of what happens in the genetic management of dual-purpose herds in Colombia. Other studies present the same characteristic, such as those reported for crossbred herds in East Africa, where the studied population showed a similar spectrum of crossbreeding between *Bos taurus taurus* and *Bos taurus indicus* but without the presence of the Gyr breed<sup>(23)</sup>.

## Genotypic breed designation

The relatively low definition of population structure obtained by principal components for CRO population clearly evidences crossbreeding events. These results are due to genealogical monitoring, limited use of records and crossings without clear orientation. In fact, a relationship in the cline of individuals is observed in projection of PC1 (Figures 2). Allele frequency of CRO animals is expected to be intermediate with respect to animals *Bos taurus taurus* and *Bos taurus indicus*<sup>(10)</sup>. However, production systems tend to form crossed animals without control of breed proportions, guided to the search a greater degree of adaptation to the environmental conditions of the region, reproductive efficiency and milk production<sup>(18,19)</sup>.

When known genetic groups were included in the analyses (Figure 3), it was possible to project the genetic structure of populations and it allowed establishing the composition of CRO, with the location at the extremes of genetic groups *B. taurus taurus* being evident, made up of breeds: HOL, JER, BRO, NOR and BON and genetic group *B. taurus indicus* made up of the breeds: GYR, BRA, since the production system is focused on looking for better cataloged animal for milk and beef production. The wide variability observed in principal component analyses (PC1; Figure 3) coincides with the distribution observed in studies with dual-purpose crossbred herds in Africa<sup>(23)</sup>.

The abundant proportion of the breeds HOL, GYR and BRA found in the study population through ADMIXTURE analyses evidences to use of breeding bulls of origin *B. taurus taurus* with greater affinity for milk production (Holstein) and of origin *B. taurus indicus* (Brahman and Gyr) with affinity for beef and milk production<sup>(24)</sup>. However, there are herds with particular cases where the contribution *B. taurus taurus* can come from other breeds of European origin such as Brown Swiss, Normande, Jersey and Creole breeds such Blanco Orejinegro, even despite their apparent lower tolerance to the warm tropics, certain local breeds can meet the hybridization needs with *B. taurus indicus* breeds<sup>(25)</sup>.

The predominant breed proportions may vary by herd, region or country, depending on the availability of breeders (seminal material and live animals), orientation and herd base<sup>(8)</sup> as evidenced by studies in crossbred herds in East Africa, where the largest composition of herds was given by Holstein, Friesian (Tanzania and Ethiopia) and Ayrshire (Kenya) breeds, while the Nelore breed was common to all three countries<sup>(23)</sup>.

Diversity in the management of dual-purpose cattle herds in Colombia has generally been associated with extensive management, with limited record of productive information of animals, which has further undermined problems to establish biotypes or crosses that provide greater heterosis and therefore the best productive performance<sup>(24,26)</sup>, in this sense, genotypic approaches are decisive to know the breed composition and to cement bases for understanding of productive and adaptive performance of herd.

## Proposed phenotypic grouping (PPG) vs Genotypic breed assignment (GBA)

The proposed phenotypic grouping (PPG) partially helped the breed designation of 71 % of the animals in the PREDTAU and PREDCEB groups, therefore, it could be used as a guiding tool in the management of crossings or a strategy for genetic improvement<sup>(27)</sup>. However, the orientation of the 29 % of animals classified as PREDINTER is complex, requiring the animals to have a defined phenotype *B. taurus taurus* and *B. taurus indicus*.

The wide range observed in PREDTAU (0.1 to 80 %), PREDCEB (0.1 to 84.2 %) and PREDINTER (0.1 to 88 %) for the individual breed assignment made visible how the GBA approach favors the correct definition of breed composition, even when detecting a considerable proportion for the Gyr breed (65.4 %) in PREDTAU, a group where the proportion of breeds *B. taurus indicus* is presumed to be minimal, or HOL (53.3 %) in PREDCEB, where a minimum portion of *B. taurus taurus* breeds is expected. On the other hand, the portion that presents the greatest difficulty, such as PREDINTER, revealed that both genetic groups *B. taurus taurus* (BON and HOL) and *B. taurus indicus* (GYR and BRA) reached maximum values greater than 50 %. As suggested by studies in Brangus animals and in terminal crosses between Angus, Charolais and Hereford, the genotypic approach contributed precision to correct definition of maximum composition for the Angus breed<sup>(22)</sup> and terminal crosses<sup>(28)</sup>.

Consideration of an APP classification requires that animals exhibit the phenotypic traits of breeds, or that they show a phenotypic structure with combined traits. However, although individuals present a similar phenotype, it is possible to find allele differences associated with other characteristics of interest, such as carcass yield, milk production, beef and milk quality<sup>(29)</sup>. A wide divergence between the APP and GBA methods was observed when they were compared with each other, a wide and varied range of genetic contribution (determined by GBA) of various breeds was found (0.1 % to 88.9 %), which exposes the erroneous interpretations to which the management of a herd has been submerged when this is limited to the perspective of their appearance, contrary to what happens in hybridizations oriented by genealogical information, as is the case of animals for beef production, seeking balance in genetic compositions and better exploiting hybrid vigor<sup>(22)</sup>. Likewise, it is known that not all phenotypic changes can be attributed to genetic changes. Some differences in hair color can be attributed to non-genetic factors such as age, intensity of solar radiation or by the combination of genetic and non-genetic factors<sup>(28)</sup>. This is the reason why it is possible to observe differences in phenotypic and genotypic correspondence, and it is here that genotypic evaluations gain great value for their contribution in the accuracy of determinations and an additional tool for orientation of mating schemes more in line with reality<sup>(22,25)</sup> and that contribute to improving productive indicators by cutting time to achieve the objectives of the producer, by allowing the latter to early identify and select animals whose breed composition diverges

from the established goals, in other words, making the productive system more profitable<sup>(22)</sup>. The definition of breeds that contribute the most to composition of crossbreeding in each herd gives an idea of orientation it has received, therefore, it is the faithful indicator of productive indicators in a herd whose focus include milk and beef production<sup>(23)</sup>.

Previous reports suggest that genotypic predictions have allowed effectively correcting erroneous assignments based on genealogical information of crossbred cattle<sup>(9)</sup>. On the other hand, genotypic breed assignment incorporates elements of demography of populations and allows defining management and conservation strategies both in terms of population<sup>(30)</sup> and in management of allele frequencies for genes of productive interest associated with growth, carcass quality, milk quality, reproduction and adaptation to the tropics<sup>(9,25)</sup>.

## Conclusions and implications

The knowledge of the producers and the APP approach (PREDTAU, PREDCEB and PREDINTER) contributed to partially elucidate the breed composition of a crossbred herd of dual-purpose cattle and on the genetic management that a herd has in search of a balance between the genetic groups *B. taurus taurus* and *B. taurus indicus*. However, a wide range of errors was observed under this methodology, so a portion of herd could be misassigned in a certain group and trigger the well-known crossbreeding without orientation. The GBA approach allowed to effectively identifying 7 genetic groups in conformation of CRO herds, thus clearly allowing strengthening conventional methods based on phenotypic assessments, such as APP, to define breed composition of dual-purpose crossbred cattle. The GBA has the capacity to guarantee a wide accuracy in predictions of individual and herd breed composition, with which it could contribute in a safe and profitable way to development of directed mating or crossing strategies that guarantee better use of hybrid vigor with a balance between and that consider their adaptation, recognizing the tropical conditions where this production system is developed, such as the Piedemonte.

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