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Genetics and Breeding

Usability of metadata analysis of goat genetic resources among five countries from Africa, Asia and Europe: Metadata analysis of goat genetic


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Abstract. Goats play a variety of roles all around the globe due to their capability to acclimatize different environmental conditions quite quickly since they have been regarded as one of the first sets of animals domesticated by the human. Even though domestic goats harbor precious genetic materials, research funding among developing countries is a major drawback for thorough study on them. Therefore, microsatellite markers seem to be affordable and informative. Genotypic data from different goat breeds across five countries (Nigeria, South Africa, Pakistan, France and Spain) was generated using eleven microsatellite markers for a comparative study in order to evaluate the usefulness of the available data for genetic characterization and identify the shortcomings of meta-analyses for combined data. The mean number of alleles (MNA) per population range from 6.44±2.83 alleles for Spanish to 10.25±0.96 for Pakistani goats, with an overall mean of 13.53±7.28. Observed heterozygosity (Ho) ranges from 0.61±0.02 to 0.83±0.01 for Spanish goats and Pakistani goats, respectively with an overall mean of 0.65. Ho of the markers used ranged from 0.569 (INRA5) to 0.793 (MM12). Highest and least polymorphic information content (PIC) was observed in loci MM12 (0.925) and MAF209 (0.489), respectively. All the populations showed significant change from Hardy-Weinberg equilibrium (P>0.05) indicating a low level of inbreeding. The genetic distance of each country's goat populations ranged from 0.151 to 4.245. The highest genetic distance was observed in loci MM12 (0.925) and MAF209 (0.489), respectively. All the populations showed significant change from Hardy-Weinberg equilibrium with an overall mean of 0.65. Ho of the markers used ranged from 0.569 (INRA5) to 0.793 (MM12). Highest and least polymorphic information content (PIC) was observed in loci MM12 (0.925) and MAF209 (0.489), respectively. All the populations showed significant change from Hardy-Weinberg equilibrium (P>0.05) indicating a low level of inbreeding. The genetic distance of each country's goat populations ranged from 0.151 to 4.245. The highest genetic distance (4.245) was observed between Spanish and Pakistani goats while the lowest were observed between Spanish and French goats. Spanish and French goats are from a common ancestor while South African, Nigerian and Pakistani goats came from another ancestor or cluster. A lot of genetic admixture in the Nigerian ecotypes has been observed whereas France and Saudi Arabian breeds have been subjected to high amount of selection pressure.

Keywords: goat populations, microsatellite markers, genetic characterization, population structure

Introduction

Archaeological evidence suggests that goats were one of the earliest animal species to be domesticated by humans in the mountainous area of Western Asia (Shrestha and Fahmy, 2005) around 10000 years ago (Dubeuf and Boyazoglu, 2009; Groeneveld et al., 2010). This domestication process resulted in a wide distribution of domestic goats with more than 500 recognized breeds all over the world (FAO, 2008; Aziz, 2010). Goats have played a variety of roles such as agricultural, economical, cultural, sociological and even religious throughout human civilization (Joshi et al., 2004; Castel et al., 2010). Small goats (Capra hircus) are considered to be the most prolific ruminant under a wide range of climatic conditions (Yadav and Yadav, 2008; Afroz et al., 2010), and currently play an important role in terms of food and household security worldwide, due to their adaptability, resistance to diseases and ability to survive under low input production systems (Joshi et al., 2004; Fajemilehin and Salako, 2008; Serrano et al., 2009; Castel et al., 2010). Goat production has been pivotal in improving the living standard of poor livestock keepers, by reducing poverty and increasing food security through sustainable agriculture, through the provision of a range of useful products such as meat, milk and by-products (hide and skin, hair) (Okpeku et al., 2011).

Over many centuries, goats have been subjected to natural and artificial selection resulting in a variety of unique indigenous breeds that need to be conserved for future utilization (Adebambo, 2004; Hanotte and Jianlin, 2006). Goat populations in several countries have often been classified according to their phenotypic attributes such as coat color, ear length and body conformation or size. Some of the breeds have been named according to their geographical region or related communities (Blench, 1999; Lawal-Adebowale, 2012). Most of these rural types have not been classified on a phenotypic or genetic level.

In developed countries some goat breeds have been subjected to formal selection programs and animal recording (e.g. France - Ramsay et al., 2000; Baker and Gray, 2004; Lopes et al., 2012, 2013). Despite these efforts in some countries, goats seem to have lagged behind with regards to genetic research and improvement (Lanari et al., 2003; Galal, 2005; Pandey et al., 2006). The studies
which have tackled genetic diversity of African goats using microsatellite markers are not few but they have used different number and distinct microsatellite markers. Therefore, these studies are not able to give a clear picture about phylogenetic origin of African goat populations and genetic relationships between them (Chenyambuga et al., 2004; Hanotte and Jianlin, 2006; Agha et al., 2008; Missouhou et al., 2011; Okepku et al., 2011). Very few studies have been conducted using SNP markers for performance analyses of African goat resources (lamartino et al., 2005; Traoré et al., 2009; Mahmoudi et al., 2010; Lashmar et al., 2016), and usually sample sizes were the limiting factor due to financial constraints.

Genetic characterization of available goat resources is important as it describes and defines their genetic makeup and variation in order to design selection and conservation programs (lamartino et al., 2005; Mahmoudi et al., 2010). Developments in molecular biology have revolutionized genetic characterization of animal genetic resources (Van Marle-Köster and Nel, 2003; Barcaccia et al., 2013). As a consequence of these developments, microsatellite markers have proved to be a usable and affordable marker for a wide range of molecular genetic studies such as evaluating population structure, analyzing population differentiation and the reconstruction of phylogenetic relationships among populations (Li et al., 2002; Baumung et al., 2014).

In this study, five countries from Africa, Asia and Europe contributed microsatellite genotypic data from various goat breeds for a comparative study. The aim was to evaluate the usefulness of the available data for genetic characterization and to identify the challenges for using these genotypes in a meta-analysis of the combined data.

## Material and methods

Genotypic data generated using microsatellite markers were provided for a comparative analysis by research groups involved in goat characterization from Nigeria, South Africa, Pakistan, France and Spain. The details of the samples collected and the sampling location were tabulated in Table 1.

The rest of the microsatellite markers used to generate the data are listed on the ISAG/FAO recommended goat panel for genetic characterization and diversity studies (Rischkowsky and Pilling, 2007; FAO, 2011). The number of markers varied from only three markers in Saudi Arabian goats to eleven markers in Nigerian Goats, with nine markers shared (BM1818, CSRD247, MM12, OarFCB49, SRCSRPS, INRA063, MAF209, ILSTS011, ETH10, INRA5 and SRCRSP5) across all the countries for the combined analyses (Table 2). Since the shared number of markers was so low in Pakistan and Saudi Arabia, their goat breeds were not included in the final meta-analyses.

Each separate data set was analyzed using GENALEX 6.5 (Peakall and Smouse, 2012) and Microsatellite Toolkit version 3.1 (Park, 2001) to determine descriptive parameters of genetic diversity, including MNA (Mean Number of Allele), number of effective alleles (NEA), \( H_e \) (Observed Heterozygosity) and expected heterozygosity (\( H_o \)) according to Nei (1987). Genetic differentiation based on Wright’s F Statistics between the types within a country was estimated using FSTAT 2.9.3.2 (Goudet, 2002) and confirmed with Arlequin. Genetic distances among populations were estimated using standard genetic distance (Ds) of Nei (1978; Weir and Cockerham, 1984).

Table 1. Details of goat samples data sourced from five different countries

<table>
<thead>
<tr>
<th>Country</th>
<th>Longitude and Latitude</th>
<th>Breed(s)</th>
<th>Sample size</th>
<th>Microsatellites</th>
</tr>
</thead>
<tbody>
<tr>
<td>France</td>
<td>48º 52´ N, 2º 23´ N</td>
<td>Saanen</td>
<td>36</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>41º 53´ N, 12º 27´ N</td>
<td>Alpine</td>
<td>37</td>
<td>10</td>
</tr>
<tr>
<td>Nigeria</td>
<td>6º 36´ N, 3º 21´ E</td>
<td>Red Sokoto/Maradi</td>
<td>47</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td></td>
<td>West African Dwarf</td>
<td>67</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sahel</td>
<td>47</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Lehri</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Local hairy</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td>Pakistan</td>
<td>33º 36´ N, 73º 04´ E</td>
<td>Barbari</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Beetal</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Damani</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pahari</td>
<td>9</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Teddy</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Kamori</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Khurasani</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Nachi</td>
<td>18</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Jattal</td>
<td>25</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>DDP</td>
<td>25</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Boer</td>
<td>46</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Kalahari</td>
<td>47</td>
<td>11</td>
</tr>
<tr>
<td>South Africa</td>
<td>25º 43´ S, 28º 10´ E</td>
<td>MG</td>
<td>40</td>
<td>9</td>
</tr>
<tr>
<td>Spain</td>
<td>37º 03´ N, 3º 36´ W</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*DDP- Dera Din Panah; MG- Murcia-Granada*
### Table 2. Microsatellite markers shared between the countries and respective breeds/populations for combined analyses

<table>
<thead>
<tr>
<th>Population</th>
<th>Sample size</th>
<th>Microsatellites markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>MG</td>
<td>40</td>
<td>X X X X X X X X X X</td>
</tr>
<tr>
<td>Maradi</td>
<td>47</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>WAD</td>
<td>67</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Sahel</td>
<td>47</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Saanen</td>
<td>36</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Alpine</td>
<td>37</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Boer goat</td>
<td>46</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Kalahari</td>
<td>47</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Lehri</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Local hairy</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Barbari</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Beetal</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Damani</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Pahari</td>
<td>9</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Teddy</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Kamori</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Khurasani</td>
<td>20</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Nachi</td>
<td>18</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Jattal</td>
<td>25</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>DDP</td>
<td>25</td>
<td>X X X X X X X X X X X</td>
</tr>
<tr>
<td>Ardi</td>
<td>44</td>
<td>X X X X X X X X X X X</td>
</tr>
</tbody>
</table>

*MG- Murcia-Granada; WAD- West African Dwarf; DDP- Dera Din Panah

The combined analyses consist of data from Nigeria, France, Spain and South Africa based on the nine to eleven markers present in the respective breeds. The analyses for descriptive statistics were repeated for the parameters mentioned above. A population structure analysis was performed using STRUCTURE 2.3.4 (Pritchard et al., 2000., Falush et al., 2003) to determine the true number of populations (K), by using Bayesian-based assignment principles. The model used for the simulation assumes admixture in the ancestry, and therefore assumes correlated allele frequencies. The model assumed the probability of the number of populations (Ln Pr lXlK/) to be 2 ≤ K ≤ 8. Five independent runs were performed for each K, and the probability value for each K was averaged over the runs. The runs were carried out with a burn-in period of 100000 steps, followed by 500000 Markov chain Monte Carlo (MCMC) iterations.

### Results

Analyses of the data by countries are presented in Table 3. The mean number of alleles (MNA) per population ranged from 6.44±2.83 alleles for Spain to 10.3±0.96 for Pakistani goats, and an overall mean of 13.6±7.23 (Table 3). The number of effective alleles (NEA) contributing to the population ranged from 3.23±0.98 for South Africa to 7.51±1.60 for Pakistani goats. The mean Shannon index (I) for these five populations showed 1.90±0.70 with the highest value for Pakistani goat population and the lowest for South Africa, whereas overall F was 0.08 with the highest value for Saudi Arabia Ardi population. Ho values ranged from 0.61±0.02 to 0.83±0.01 for Spanish and Pakistani goats, respectively (Table 3). A deviation from HWE test, which was performed at each locus on the overall goat population, revealed significant departure from HWE (P<0.05).
All the goat populations showed limited inbreeding, with inbreeding coefficients ($F_{IS}$) values that were low and positive. The deviation from HWE test, which was performed at each locus on the overall goat population revealed a significant departure from HWE ($P>0.05$) (Table 4). The tested microsatellite markers showed low levels ($p>0.05$) of $F$ with low positive values for 10 loci with only one locus (INRA5) having a negative value. However, the average values obtained are not reliable as some loci were only used in four populations, and will not give an accurate reflection of the parameters. As a sample, SRCRSP5 was only used in 4 populations, while ILSTS011 was applied in all the populations’ analyses. The values obtained from these two loci are very similar for the first parameters in Table 4, but differ significantly for $F_{IS}$ and $F_{IT}$ estimation. This is due to the limited use of SRCRSP5 in the total population and indicates the bias that will be part of the meta-analyses if the loci are not included at a similar rate across populations.

The mean $F_{IS}$ value (0.334) demonstrates that only about 33.4% of the total genetic variation was attributable to differentiation between populations and 66.6% was due to intrapopulation differentiation.

The global $F_{IS}$ is 0.333, while in this study $F_{IT}$ ranged from 0.113 shown by OarFCB48 to 0.749 by SRCRSP5, which indicates different degrees of genetic differentiation.

The genetic distance in each country goat populations based on Nei (1978) have been observed from 0.151 and 4.245 (Table 5). The highest genetic distance (4.245) was observed between Spanish and Pakistani goats and the lowest was observed between Spanish and French ones. The genetic relationship dendrogram (Figure 1) showed that the Spanish and French goats are from a common ancestor (the same cluster) while South African, Nigerian and Pakistani goats came from another ancestor or cluster.

### Table 4. Diversity indices for microsatellite markers commonly used in this analysis from the five countries

<table>
<thead>
<tr>
<th>Country</th>
<th>$H_o$</th>
<th>$H_s$</th>
<th>$H_t$</th>
<th>PIC</th>
<th>$F_{IS}$</th>
<th>$F_{IT}$</th>
<th>$F_{IS}$</th>
<th>Nm</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bm1818</td>
<td>0.720</td>
<td>0.792</td>
<td>0.875</td>
<td>0.901</td>
<td>0.084</td>
<td>0.176</td>
<td>0.100</td>
<td>2.243</td>
</tr>
<tr>
<td>CSRD247</td>
<td>0.689</td>
<td>0.702</td>
<td>0.793</td>
<td>0.777</td>
<td>0.011</td>
<td>0.364</td>
<td>0.357</td>
<td>0.450</td>
</tr>
<tr>
<td>MM12</td>
<td>0.793</td>
<td>0.845</td>
<td>0.915</td>
<td>0.925</td>
<td>0.053</td>
<td>0.130</td>
<td>0.081</td>
<td>2.832</td>
</tr>
<tr>
<td>OarFCB48</td>
<td>0.782</td>
<td>0.803</td>
<td>0.883</td>
<td>0.902</td>
<td>0.020</td>
<td>0.113</td>
<td>0.095</td>
<td>2.381</td>
</tr>
<tr>
<td>SRCRSP8</td>
<td>0.660</td>
<td>0.724</td>
<td>0.832</td>
<td>0.808</td>
<td>0.081</td>
<td>0.408</td>
<td>0.356</td>
<td>0.453</td>
</tr>
<tr>
<td>INRA63</td>
<td>0.587</td>
<td>0.679</td>
<td>0.699</td>
<td>0.645</td>
<td>0.128</td>
<td>0.418</td>
<td>0.332</td>
<td>0.503</td>
</tr>
<tr>
<td>MAF209</td>
<td>0.330</td>
<td>0.367</td>
<td>0.482</td>
<td>0.489</td>
<td>0.096</td>
<td>0.605</td>
<td>0.563</td>
<td>0.194</td>
</tr>
<tr>
<td>ILSTS011</td>
<td>0.659</td>
<td>0.758</td>
<td>0.848</td>
<td>0.875</td>
<td>0.124</td>
<td>0.221</td>
<td>0.111</td>
<td>1.998</td>
</tr>
<tr>
<td>ETH10</td>
<td>0.607</td>
<td>0.634</td>
<td>0.655</td>
<td>0.587</td>
<td>0.035</td>
<td>0.376</td>
<td>0.353</td>
<td>0.458</td>
</tr>
<tr>
<td>INRA5</td>
<td>0.569</td>
<td>0.544</td>
<td>0.567</td>
<td>0.505</td>
<td>-0.052</td>
<td>0.595</td>
<td>0.615</td>
<td>0.156</td>
</tr>
<tr>
<td>SRCRSP5</td>
<td>0.604</td>
<td>0.692</td>
<td>0.773</td>
<td>0.785</td>
<td>0.120</td>
<td>0.749</td>
<td>0.715</td>
<td>0.100</td>
</tr>
<tr>
<td>Overall</td>
<td>0.636</td>
<td>0.685</td>
<td>0.757</td>
<td>0.746</td>
<td>0.064</td>
<td>0.378</td>
<td>0.334</td>
<td>1.070</td>
</tr>
</tbody>
</table>

*Ho = mean observed heterozygosities; Hs = mean gene diversities within population; Ht = Gene diversities overall; PIC = Polymorphic Information Content; $F_{IS}$ = Inbreeding Coefficient; $F_{IT}$ = Global deficit of heterozygote; $F_{IS}$ = Differentiation among sub-populations; Nm = gene flow/ number of migrant alleles
Figure 2 shows the population structure of the combined analyses for four countries with nine markers in common where eight populations can be distinguished. Populations are all Nigerian ecotypes, these are followed by France, South African and Spain ecotypes. Nigerian ecotypes showed high amount of different admixture whereas South African and Spanish showed highly homogenous admixture.

**Discussion**

Mean number of alleles is 13.6±7.23 for the tested populations which is higher than the value obtained (8.1) for the Croatian spotted goat (Mahmoudi et al., 2009) and the Markhoz goat (Ramljak et al., 2011), Egyptian and Saudi goat breeds (8.5) (Mahrous et al., 2013) and Egyptian and Italian goat breeds (6.5) (Agha et al., 2008) and Pakistani goat breeds (3.2 in Damani and 4.6 in Nachi) (Hussain et al., 2013). Whereas Indian indigenous goat breeds such as Kutchi, Gohilwari, Mehsana, Zalawadi, Gohilwari and Surti showed close value to our study. However, a mean number of alleles depends on sample size and number of observed alleles. When the sample size is increased, the presence of unique alleles within populations, which occurs in low frequencies, tends to increase. The number of alleles scored for each marker is a good indicator for the future usefulness of the marker in genetic diversity studies. Number of effective alleles usually increases with the increase in heterozygosity. Therefore, alleles with low frequencies contribute very little to the effective number of alleles. The high values obtained for the PAK population is probably an overestimation due to the limited number of markers used. These values compare favorably with diversity studies conducted in a number of goat populations by Croatian spotted goat (Mahmoudi et al., 2009) the Markhoz goat (Ramljak et al., 2011) and Egyptian and Saudi goat breeds (Mahrous et al., 2013).

In population diversity studies, Shannon index is the most widely used which considers the abundance and evenness of the species studied. The mean Shannon index for overall populations was 1.90±0.70 suggesting the species richness is on the higher side therefore, the conservation strategies for these goat populations would be an ideal option. Lower Shannon index values were reported in Jamunapari (1.07±0.51) (Gour et al., 2006) and Marwari (1.30) (Kumar et al., 2005) goats of India. On the other hand, Gohilwari (1.60±0.69) (Kumar et al., 2009) and Mehsana (1.91±0.64) (Aggarwal et al., 2007) goats showed higher values. This level of inbreeding may be as a result of moderate level of mating between closely related individuals (Mahrous et al., 2013). Low inbreeding values were also reported within 45 rare breeds of 15 European and Middle East countries (Canon et al., 2006).

Similar values for expected heterozygosity were observed in Gohilwadi (0.67), Surti (0.64) (Fatima et al., 2008), Damani (0.56) and Nachi (0.63) goat (Hussain et al., 2013), Swiss goat breeds (0.66) (Glowatzki-Mullis et al., 2008), Marwari (0.63) (Kumar et al., 2005), Australian Saanen (0.62) (Kim et al., 2002) and Kalahari Red goats (0.63) (Kotze et al., 2004). An overall Ho mean of 0.65 was obtained, which is lower than that of the Croatian spotted breed (0.76) (Jelena et al., 2011), Spanish Guadarrama (0.78) (Serrano et al., 2009) and Damani (0.73) (Hussain et al., 2013), but higher than Sub-Saharan breeds (0.58) (Muema et al., 2009), Korian goats (0.36) (Kim et al., 2002), Nachi of Pakistan (0.51) (Hussain et al., 2013) and Jamunapari of India (0.42) (Gour et al., 2006). Observed heterozygosity values were lower than the Hs values for all the populations and yet still show high genetic variability, which might be due to low selection pressure, large population size and immigration.
of new genetic materials (Mahrous et al., 2013). The value obtained for the Pakistani goats from this study is, however, most probably an overestimation, due to the small number of markers. Higher genetic variability is due to low selection pressure, large population size, insertion of new genetic material through immigration of new gene and the instability of the population at the majority of the microsatellite loci studied. Most of these indices, i.e., heterozygosity measures, allele frequencies, number of alleles and PIC clearly show that these goat populations have considerable amount of genetic polymorphism that could be used in conservation programs and for sustainable livestock raising. According to Hartl (1989), per pair Fst value equals to 0.05 is indicative of moderate differentiation between populations. The pair Fst values reported in the present investigation in all tested loci was higher than 0.05, which may indicate a high differentiation between populations under investigation. A situation which could be expected of populations geospatially separated while undergoing local selection.

Our results are intermediate between observed Heterozygosity levels varying between 0.64 and 0.61, but it should be noted for the countries with nine to one markers indicating a moderate level of diversity. Estimates from studies on Croatian spotted breed (0.76) (Jelena et al., 2011), Spanish Guadarrama (0.78) (Serrano et al., 2009) were similar to this study. Lower values have been reported for Sub-Saharan breeds (0.56) (Muema et al., 2009), Korian goats (0.36) (Kim et al., 2002) and Jamunapari of India (0.42) (Gour et al., 2006), but it should be noted that studies are not directly comparable due to number of markers, choice of markers and samples sizes. This may be due to the high geographic distance between the areas in the investigated countries. The Nm value ranges from 0.10 for locus SRCRSP5 to 2.832 for MM12 locus. This is an indication that migration has a great effect on genetic differentiation reduction between these isolated populations. This is an indication that migration has a great effect on genetic differentiation reduction between populations (Laval et al., 2000).

All the goat populations showed limited inbreeding, with Fis values that were low and positive. Low inbreeding values were also reported within 45 rare breeds of 15 European and Middle East countries (Canon et al., 2006). As Ollivier and Foulley (2005) concluded, low level of inbreeding (<0.10) can be a result of lower levels of mating between closely related individuals in field conditions. A positive value of Fis indicates that there is an increased percentage of homozygote, and population may be inbred, the larger the percentage, the greater the extent of inbreeding. The negative value for Fis indicates that there are more heterozygote individuals than expected; this might happen for the first few generations after two previously isolated populations become one. Only about 33.4% of the total genetic variation was attributable to differentiation between populations and 66.6% was due to within population differentiation. According to Hartl (1989), per pair Fst value equals to 0.05 is indicative of moderate differentiation between populations. The pair Fst values reported in the present investigation in all tested loci was higher than 0.05, which may indicate a high differentiation between populations under investigation. The global Fst is 0.33, while in this study Fst ranged from 0.11 shown by OarFCB48 to 0.75 by SRCRSP5 which indicates different degrees of genetic differentiation. Generally animal species Fst ranges from 0 to 0.2 whereas plants show higher values. This may be due to the high geographic distance between the areas in the investigated countries. The Nm value ranged from 0.10 for SRCRSP5 to 2.8 for MM12 locus with a mean of 1.07, which reflects the high gene flow between these isolated populations. This is an indication that migration has a great effect on genetic differentiation reduction between populations (Laval et al., 2000).

The average values obtained for fixation indices come to reformulate the real image since some loci were only used in four populations, and will not give an accurate reflection. As a case in point, SRCRSP5 was only used in four populations, while ILSTS01 was applied in all the populations' analyses. The values obtained from these two loci are very similar for the first parameters in Table 3, but differ significantly for Fst and Fis estimation. This is due to the limited use of SRCRSP5 in the total population and indicates the bias that will be part of a meta-analysis if the loci are not included at a similar rate across populations.

The cluster analysis from Nei's dendrogram confirmed the closeness of Spanish and French goat populations, both clustered independently from Nigerian, South African and Pakistani goat populations at 14.7, 28.5 and 194.7 genetic distance. It is interesting to note that a lot of admixture has been displayed by four Nigerian ecotypes, whereas South African and Spanish breeds showed homogenous admixture. Thus, Nigerian ecotypes face higher selection pressure to be confirmed by Fis value when compared to other breeds evaluated in this study. This displays that genetic diversity of breeds is directly linked to the areas of origin, suggesting that breeds which have diverged recently have a closer relationship than breeds which diverged long time back (Maudet et al., 2002). Low levels of population structure in various animal-production systems is an attribute of non-random mating systems, selection by features of economic importance, and the intensive use of reproductive technologies (Serrano et al., 2009). Overall, structure and phylogenetic analysis displays a complex genetic structure of goat populations prevailing in these countries, where different management systems and reproductive techniques have been employed.

**Conclusion**

The goat populations from the five different countries showed higher after intrapopulation variations which are contributed by few numbers of effective alleles. The set of microsatellites used in this study are a very useful and good tool for genetic characterization of Nigeria, South Africa, Pakistan, France and Spain goats and the study of their genetic structure. The highest and lowest genetic diversity was shown by Pakistani and Spanish goats, respectively. Spanish and French goat populations have a very close genetic distance, whereas compared to them Pakistani counterparts possess high genetic distances. The information elucidated through the present study would be useful for the formulation of effective conservation strategies and meeting the demands of a future breeding programme.

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G. Zhelyazkov

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I. Valchev, N. Groseva, D. Kanakov, Ts. Hristov, L. Lazarov, R. Biinev

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K. Georgieva, G. Zhelyazkov, Y. Staykov, D. Georgiev

PRODUCTION SYSTEMS

Yield and seed quality of some soybean (Glycine max. L) varieties, cultivated in Osmaniye region, Turkey
F.F. Aşik, R. Yildiz

Productivity and yield stability at late treatment of durum wheat (Triticum durum Desf.) with antibroadleaved herbicides.
I. Influence at treatment during 1st stem node stage
Gr. Delchev, D. Delchev

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O. Basal, A. Szabó

Soil structure after treatment with different operation modes of spading machine
Y. Stoyanov, K. Trendafilov, N. Delchev, G. Tihanov
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Z. Petrova, M. Nankova

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B.N. Ndukwu, D.N. Osujieke, C.M. Ahukaemere, P.E. Imadojemu

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R. Georgiev, K. Peychev, V. Dimova, D. Georgiev

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