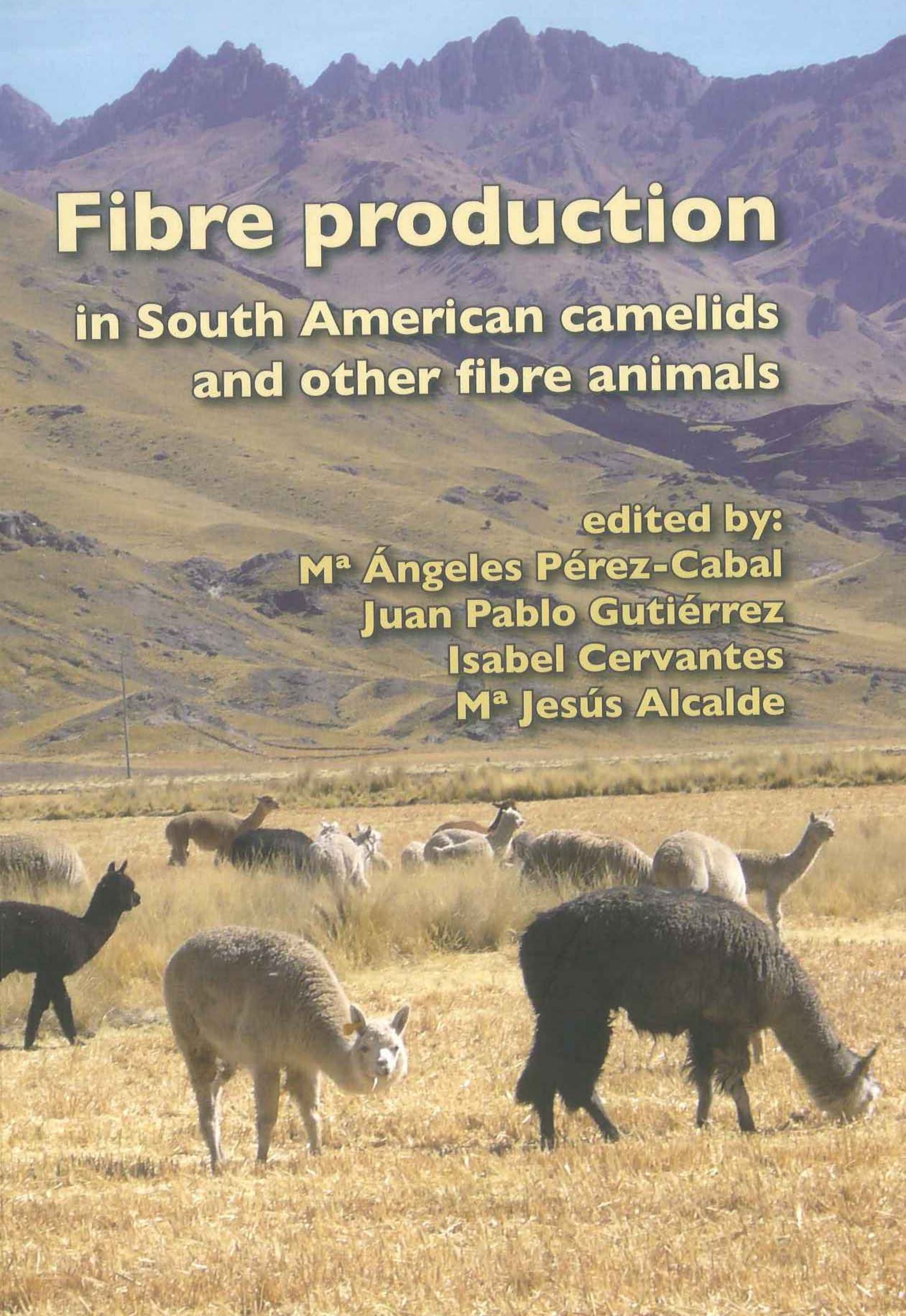

Fibre production

in South American camelids and other fibre animals

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Diversity and comparison of wool parameters in 31 different American and European ovine breeds

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Abstract

A study was designed with the aim of establishing phenotypic relationships between certain American and European autochthonous sheep breeds based on wool parameters. Data were collected from 1,143 animals from 31 sheep breeds or varieties. Nine quantitative wool characteristics – length and amount of long, short and kemp fibres, mean fibre diameter and fibres with diameter > 30 μ, and percentage after degreasing with alcohol – were investigated. A principal component analysis (PCA) was carried out with the aim of obtaining the variables exhibiting a pattern of jointly contributing to the total variation. To present data structure and relationship among population accessions, a cluster analysis and a principal coordinates analysis of all the data were conducted. For all analyses, the correlation matrix was utilised. Percentage of fibres and fineness appear as the most useful grouping criteria. The resulting dendrogram showed a 'short coarse wool sheep', a 'medium fine wool sheep' (with different percentages of short fibres that allow them to be divided into three subgroups) and a 'long medium wool sheep'. No 'short fine wool sheep' appeared. Although no phylogenetic information is generated, the results seem to establish different, but more concise groups than those traditionally considered: Merino, Entrefino, Churro and Iberian stock.

Keywords: fibre diameter, clustering analysis, phylogeny, population assignment, sheep breeds

Introduction

There is little published information about comparative wool characteristics for some of the breeds investigated. Moreover, there have been conflicting reports in the literature regarding the relationships between some American and European breeds. In this paper, we present an analysis based on breed wool characteristics with a view to obtaining a deeper insight into relationships within and between breeds.

Materials and methods

Sample collection

Data was collected from 1,143 animals belonging to thirty-one autochthonous breeds or varieties from America and Europe. For a description of the breeds, see Esteban (2003). Management for each breed was different, but each provided a good representation of the standard breed. Samples were taken from the mid-lateral part of each ewe before shearing. Sampled animals were randomly chosen from herds. Each sampled animal was more than 18 months old.

Data collection

Each wool's characteristics were determined using standard methods (see Rojas *et al.*, 2005) at the Wool Quality Laboratory at the Institute for Indigenous Studies, Universidad Autónoma de Chiapas (UNACH), in San Cristóbal de Las Casas, Chiapas (Mexico). Nine wool characteristics were investigated for each sample (Parés, 2008): fibre length (cm), percentage of each type of fibre (long-coarse fibres – outer-coat, short-fine fibres – inner-coat, and kemp), mean fibre diameter (μm), percentage of fibres > 30 μm (F30) and yield after scouring with alcohol (%). No colour or crimp parameters were obtained. Data for each wool's characteristics were analysed for their effects on breed.

Data analysis

To present data structure and relationship among population accessions, a principal component analysis (PCA) and cluster analysis were conducted. A PCA was carried out of all the quantitative data with the aim of obtaining an aggregate of variables exhibiting a pattern of jointly contributing to the total variation. The first three eigenvectors were extracted from the correlation matrix derived from the nine measurements collected. Correlation rather than a correlation matrix was used because the former measures standardised variation and is not affected by unequal variances that occur in data matrices with variables of different absolute size (López-Martín *et al.*, 2006). Character loading (i.e. component correlations) was used to determine the contribution of each variable to the first component vector. In order to organise breeds into feasible groups, a constrained method using Ward's method was utilised with data for most discriminative parameters. A principal coordinate analysis (PCoA) was finally generated from the correlation matrix. The scores of breeds for the first two components were projected. Different PAST – 'Paleontological Statistics Software Package for Education and Data Analysis' (Hammer *et al.*, 2001) programmes were utilised to perform all the analyses.

Results and discussion

Descriptive statistics for each breed are shown in Table 1. Inter-breed correlations for the entire population showed considerable variation (0.060 to 0.7129). There is significant variability among different breeds, which indicates a high response to selection.

The plot of sample means on the first two principal components axes is shown in Figure 1. Component 1, which explains 61.2% of the total sample variance, is the short fibre percentage, whereas Component 2, which explains 17.6% of the total sample variance, is the long fibre percentage and fineness. Table 2 shows the variable contributions, in terms of percentage of total variance explained, to the formation of 1-3 axes, obtained by PCA. According to the PCA, the primary source (PC1) of variation for the sample studied was the percentage of short fibres. Fibre diameter and percentage of long fibres are significant variables of PC2. Percentage of kemp fibres is the significant variable for PC3. These are then useful as grouping criteria, as indicated by some authors (Briggs, 1995; Maddever and Cottle, 1999). Scouring seems not to be an important discriminative parameter.

Using the correlation matrix of the four most discriminative parameters (percentage of each kind of fibre, fibre diameter and F30), a dendrogram was obtained utilising Ward's method (Figure 2). As the figure shows, most of the breeds are grouped into three large clusters, with one isolated breed appearing (CHB). The cluster's coefficient correlation was 0.894.

Table 1. Some descriptive wool traits for the sheep breeds studied.

Breeds	Abbr.	n	Long fibres length (cm)	Short fibres length (cm)	Kemp fibres length (cm)	Long fibres (%)	Short fibres (%)	Kemp fibres (%)	Alcoholic yield (%)	Mean diameter fibre (µ)	F30 (%)
Aranesa	ARA	18	4.1	4.1	1.2	5.85	93.17	0.96	84.2	29.5	39.4
Berberina	BER	15	2.5	2.9	0.8	0.75	98.35	0.88	81.1	26.7	23.4
Blanca Colombia	BCO	45	20.8	10.5	4.1	15.23	80.90	3.85	83.3	31.2	40.8
Castellana Negra	CAN	4	6.3	3.6	1.7	19.66	71.84	8.49	75.6	19.2	10.5
Castillonesa	CAS	15	4.3	4.7	0.7	2.49	96.59	0.91	83.5	35.3	66.8
Chiapas blanca	CHB	48	21.9	11.3	6.1	57.87	38.89	3.22	83.4	30.4	40.0
Chiapas café	CHC	51	24.9	12.0	5.5	21.25	74.93	3.81	87.8	29.6	40.0
Chiapas negra	CHN	62	19.7	11.5	8.5	27.11	70.83	2.04	83.9	25.0	27.5
Churra	CHU	25	13.7	7.6	3.2	6.55	85.21	8.23	81.0	24.5	20.5
Churra badana	CBA	74	22.6	15.6	3.5	11.07	77.44	1.48	79.1	39.7	63.6
Churra terra quente	CTQ	30	20.4	11.5	3.4	16.99	76.55	6.44	81.4	35.4	42.7
Criolla de Bolivia	CBO	82	13.5	10.6	2.1	23.12	73.56	3.30	70.3	29.7	38.3
Crioula Brasil	CBR	52	26.8	11.8	4.3	21.56	75.02	3.41	98.7	31.8	38.6
Guirra	GUI	15	7.5	6.3	2.4	3.94	92.36	3.69	74.7	27.7	19.4
Latxa Chilena	LAC	88	24.5	11.3	7.6	17.89	80.47	1.61	89.0	42.9	62.9
Linca	LIN	10	18.6	9.3	0.0	8.34	91.65	0.00	75.5	26.6	19.2
Manchega Negra	MAN	63	9.5	7.6	2.6	0.33	89.92	9.73	77.8	29.0	31.0
Mer. Grazalema	GRA	44	7.7	6.6	1.3	33.28	65.60	1.11	77.3	32.6	46.1
Mirandesa	MIR	40	17.5	12.5	2.9	5.14	83.56	11.28	86.9	30.4	40.5
Mixteca	MIX	61	5.2	3.3	1.2	11.31	87.46	1.21	71.2	23.4	15.0
Mondegueira	MON	28	17.86	8.8	3.2	16.90	75.62	7.46	74.6	38.9	56.5
Mora Colombiana	MOR	27	14.5	8.4	1.9	3.01	96.92	0.05	79.5	20.2	7.98
Navajo-Churro	NAV	29	21.2	11.8	1.8	12.49	86.92	0.57	62.9	24.2	19.5
Oaxaca	OAX	56	9.2	5.5	2.6	19.83	77.34	2.82	75.9	21.5	16.6
Ripollesa	RIP	14	5.5	5.3	1.3	0.30	96.76	2.92	85.5	28.8	29.0
Roja Mallorquina	RMA	12	12.0	9.5	2.9	10.33	83.42	6.24	76.5	27.9	27.4
Socorro	SOC	49	0.0	6.6	0.1	0.71	97.80	1.48	54.7	22.1	1.60
Tarahumara	TAH	44	12.2	8.3	4.3	13.67	82.01	4.30	73.1	26.9	25.3
Tarasconesa	TAR	18	2.5	4.4	1.1	0.00	98.83	1.16	71.4	27.3	32.3
Xisqueta	XIS	10	11.7	4.0	1.4	0.12	98.06	1.80	80.9	30.6	42.3
Zongolica	ZON	14	13.7	9.3	3.0	9.97	87.56	2.46	82.4	24.4	23.9

The results of the PCoA are shown in Figure 3. The results observed in the PCoA analysis reinforce the results observed in the dendrogram. A cluster formed by GRA, LAC, MON, CBA and CAS presents a large fibre diameter (greater than 50 microns) and a medium percentage of long fibres (X=16.3%), allowing it to be labelled 'short coarse wool sheep'. The presence of GRA in this group is not surprising, as it is said that the breed originated as a cross between the Merino and Churra, the latter being the cause of the coarse wool (Esteban, 2003).

It should be noted that CHB differed somewhat from other breeds, with more abundant long fibres (X=57.9%) which are also finer (X=30.4 µ, median=24.0 µ, highly skewed to the right); we

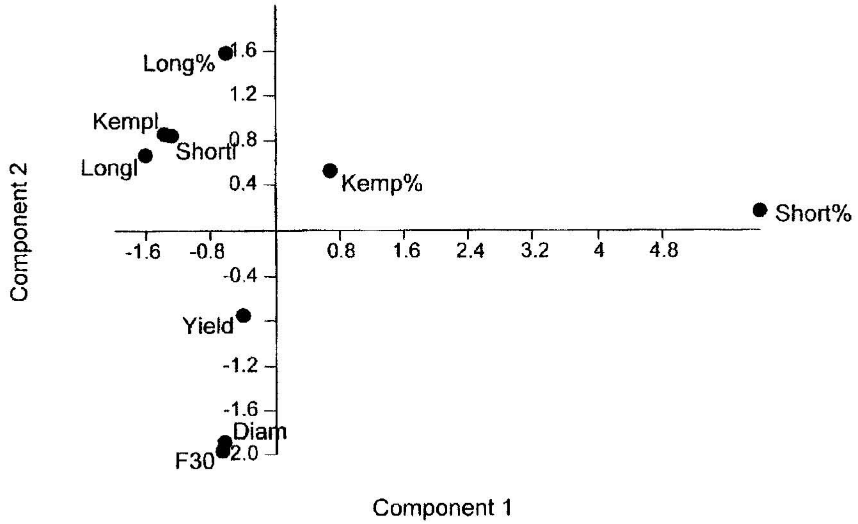

Figure 1. Plot of the sample means for nine wool parameters on the first two principal component axes.

Table 2. Variable contributions, in terms of percentage of total variance explained, to the formation of 1-3 axes, obtained by PCA.

	Axis 1	Axis 2	Axis 3
Long fibres length	-1.615	0.666	-0.129
Short fibres length	-1.297	0.840	0.554
Kemp fibres length	-1.382	0.850	-0.509
Long fibres %	-0.614	1.582[a]	-0.959
Short fibres %	5.996[a]	0.171	-0.442
Kemp fibres %	0.681	0.518	2.300[a]
Alcoholic yielding %	-0.417	-0.769	-0.970
Diameter μ	-0.661	-1.894[a]	0.172
F30%	-0.691	-1.965[a]	-0.017

[a]Highest contribution of variables (4 out of 9) to axes 1 and 2.

could classify it as a 'long fine wool sheep' with a clear double coat (57.9% long fibres vs. 38.9% short fibres). The 'short coarse wool sheep' and CHB occupy opposite sides of the dendrogram obtained. The middle groups could be classified as 'medium fine wool sheep', with a cluster formed by TAR, RIP, XIS, MAN, MIR, RMA, ARA and BER and another formed by CHC, CBR, BCO, CTQ, CBO and CHN. They are characterised by highly uniform medium fine fibres (X=29.5 μ, median=29.6 μ), but with different percentages of fibres: more abundant long fibres in the latter group (X=20.8%, 'long medium fine' group) than in the former (X=2.8%, 'short medium fine' group). According to Rojas *et al.* (2005), MIR, BCO, CTQ, NAV, CHU and CHI have similar origins. In the last group (OAX, ZON, TAH, NAV, LIN, MIX, MOR, CHU, GUI, CAN and SOC), there are breeds with values that could allow them to be classified as 'middle medium fine wool sheep' (X=23.7 μ, median=24.3 μ and 9.9% of long fibres). Interestingly, the

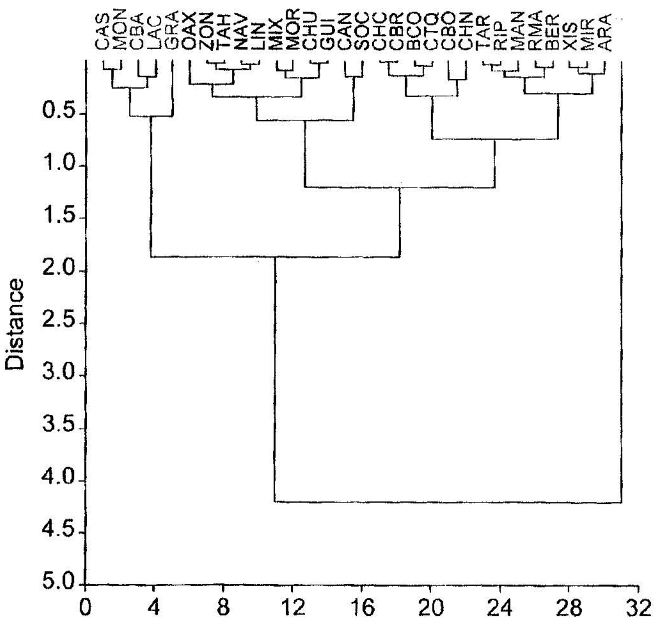

Figure 2. Constrained clustering (Ward's method) (coefficient correlation = 0.894).

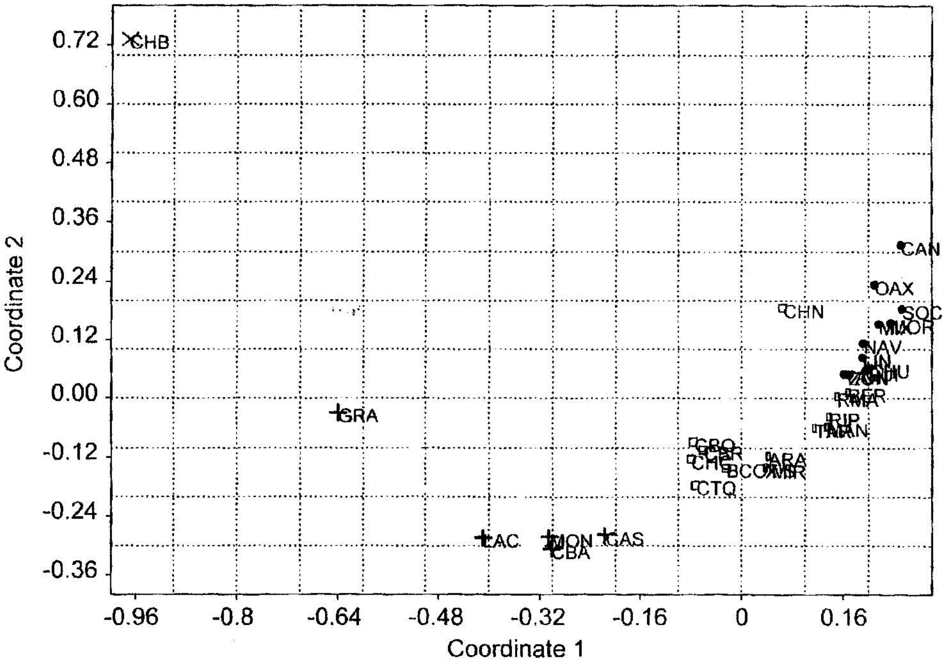

Figure 3. Two-dimensional plot of the principal coordinates from the correlation matrix.

Churra (CHU) and Latxa breeds (LAC), which belong to what is referred to as 'Latxas', were grouped into different clusters. As we have seen, LAC shows a very different pattern of fibres (low fineness and a medium percentage of long fibres). All these 'medium sheep' present a low degree of differentiation in the fleece. Although some of them are still used for traditional textile purposes in Indian villages using traditional textile processes, they do not possess a double coat, as occurs in CHB, according to the bibliography consulted (for instance, see Corzo *et al.*, 2005 for Zongolica). No 'short fine wool sheep' (with a very small fibre diameter, 20 microns or less) appeared.

Conclusion

The data reported here provide valuable insight into population and help in assessing inter-breed comparison, supporting the idea that the analysis of racial relationships is not necessarily linked to historical relationships. However, our results seem to determine different but more concise groups than those traditionally considered: Merino, Entrefino, Churro and Iberian stock.

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