ASSOCIATION OF RED CELL X-PROTEIN, NADH-DIAPHORASE 1, MALIC ENZYME AND SERUM ARYLESTERASE PHENOTYPES WITH ECONOMIC TRAITS IN SHEEP

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Summary

The red cell X-protein, NADH-diaphorase 1, malic enzyme and serum arylesterase phenotypes of 50 Thai Longtail and 53 Cameroon X Thai Longtail (F_1) crossbred sheep were determined by horizontal starch gel electrophoresis. None of the economic traits was influenced by DIA1, ME and EsA phenotypes. However, XP phenotypes showed a highly significant association with body weight, body height, heart girth and back girth, with mean values of XP+ve phenotype greater than XP-ve. The XP^+ allele was associated with greater body weight, body height, heart girth and back girth.
(Key Words : Biochemical Marker, *Ovis aries*, Economic Traits, Starch Gel Electrophoresis)

Introduction

Existence of electrophoretically determined molecular variants has been reported for Tucker's red cell X-protein (XP), red cell NADH diaphorase 1 (DIA1), red cell malic enzyme (ME) and serum arylesterase (EsA) systems of sheep. Inheritance studies have revealed genetic control through at least two codominant alleles (Viz. $DIA1^F$, $DIA1^S$, ME^F, ME^S) for each of the DIA1 and ME systems (Tucker and Crowley, 1978; Yaman and Tucker, 1981) whereas two complete dominant allele (Viz. XP^+, XP^-; EsA^A, EsA^a) for XP and EsA systems (Tucker et al., 1967).

Although extensive investigations regarding these aspects in cattle and goat have been reported in literature, little is known with respect to sheep. The current status has recently been reported by Rizzi et al. (1989) on the relationship between some biochemical markers and milk production traits using 222 Sardinain ewes from one flock.

In this paper, the relationships among XP, DIAI, ME and EsA phenotypes and several economic traits in Thai Longtail and F_1 group of Cameroon X Thai Longtail crossbred are described.

Materials and Methods

Animal

Blood sampling was carried out on healthy males and females from the sheep farm of Institute of Advanced Studies, University of Malaya. This consisted of 50 Thai Longtail (12 ♂ and 38 ♀) and 53 Cameroon X Thai Longtail (21 ♂ and 32 ♀) sired by 3 Cameroon sires. All the animals were maintained under similar environmental conditions and management practices. Blood samples were taken from these animals in December 1993 and stored at $-20°C$ until examined by electrophoresis. The animals sampled were weighed fortnightly to the nearest hundredth of a kilogram. Body weight at 90 days of age was used for the analyses. Since the individual animals were not weighed at exactly 90 days of age, the body weight at these age were interpolated using the weights prior to and after this particular age with the assumption that the body weight gain during this period was linear. Body conformation traits were measured monthly from the date of birth. The data of body conformation at age of 3 month were chosen for the analyses. These measurements are defined in figure 1 and described below:

Body Height (1) — Ventral distance from the highest point of the withers between the shoulders to the ground.

Body Length (2) — Distance along the median line from the anterior of the spinous process on the first thoracic

vertebra to the posterior part of the spine.

Heart girth (3)   — Circumference posterior to the forelegs.

Back girth (4)   — Circumference just anterior to the hindlegs.
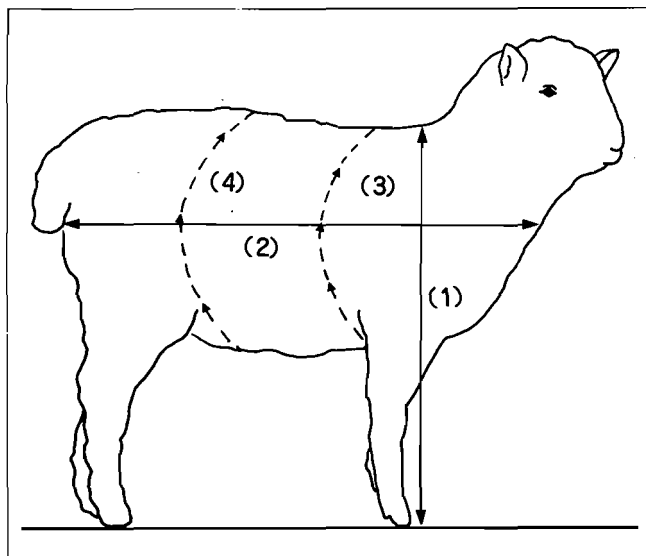

Figure 1. Body conformation measurements.
(1)-Body height
(2)-Body length
(3)-Heart girth
(4)-Back girth

Phenotyping

The samples were classified using horizontal electrophoresis in starch gel. Starch from Sigma (S-4501) was used at a concentration of 11%. The following electrophoretic procedures were used: XP and EsA

(Tucker et al., 1967), DIA1 (Cepica and Stratil, 1978) and ME (Yaman and Tucker, 1981).

Data analysis

The phenotypes were compared with respect to body weight and body conformation measurements by Student t-test analysis. Pooled variance t-test was used if the between-population variances were equal and unequal variance t-test if the between-population variances were not equal. Since the economic traits data were obtained from two breeds and from both sexes, comparisons were initially made between the breeds and the sexes.

Results

Amongst the 103 sheep examined, three phenotypes each (DIA1-SS, DIA1-FS, DIA1-FF; ME-SS, ME-FS, ME-FF) were observed in DIA1 and ME systems and two phenotypes (XP+ve, XP−ve; EsA+ve, EsA−ve) in XP and EsA. The analysis of body weight, body height, heart girth and back girth showed that there was no significant differences neither between breeds not between sex (table 1). Hence the data for the two breeds from both sexes were pooled together for the association analysis. However, for the body length, significant difference (p < 0.05) was seen between breeds (table 1) and therefore the association between genetic markers and body length were analyzed separately for the two breeds.

Table 2 showed the t values of the comparison among genetic markers for body weight, body height, heart girth and back girth. Significant differences were only found between XP+ve and XP−ve phenotypes in all the four traits with XP+ve means being greater than the means for XP−ve. The detail results of the association between body length and various phenotype combinations are given in table 3. No significant association was observed.

TABLE 1. COMPARISON BETWEEN BREED (THAI LONGTAIL AND CAMEROON X LONGTAIL) AND BETWEEN SEX (MALE AND FEMALE) FOR BODY WEIGHT AND CONFORMATION TRAITS (MEAN ± STANDARD ERROR: NO. OF OBSERVATIONS IN BRACKETS)

Measurement	Between breed comparison			Between sex comparison		
	Mean 1	Mean 2	t-value	Mean m	Mean f	t-value
Body weight	14.4±0.5(50)	13.6±0.3(53)	1.34	14.3±0.5(33)	13.8±0.3(70)	0.90
Body height	49.2±0.6(50)	48.2±0.3(53)	1.57	49.3±0.5(33)	48.1±0.4(70)	1.83
Body length	50.5±0.8(50)	48.0±0.6(53)	2.34*	49.2±0.8(33)	48.7±0.7(70)	0.47
Heart girth	55.7±1.2(50)	55.4±0.5(53)	0.25	55.4±1.0(33)	55.6±0.6(70)	0.13
Back girth	53.7±1.4	54.6±0.9	0.54	55.5±1.4	53.5±0.9	1.26

Mean 1-Thai Longtail, mean 2-Cameroon x Longtail, mean m-Male, mean f-Female.
* Significant at 5% level.

TABLE 2. COMPARISON BETWEEN GENETIC MARKERS FOR BODY WEIGHT AND CONFORMATION TRAITS IN 3 MONTHS OLD SHEEP (MEAN ± STANDARD ERROR: NO. OF OBSERVATIONS IN BRACKETS)

Phenotype comparison (1-2)	Body weight (kg)			Body height (cm)			Heart girth (cm)			Back girth (cm)		
	Mean 1	Mean 2	t-value	Mean 1	Mean 2	t-value	Mean 1	Mean 2	t-value	Mean 1	Mean 2	t-value
XP+ve − XP-ve	14.7± 0.3(64)	12.7± 0.4(39)	3.86***	49.0± 0.4(64)	47.6± 0.5(33)	2.28*	56.7± 0.7(64)	53.2± 0.6(33)	3.76***	56.0± 1.0(64)	50.6± 1.0(33)	3.47**
DIA1-FF − DIA1-FS	13.3± 0.6(26)	14.1± 0.3(53)	1.23	48.2± 0.7(25)	48.5± 0.4(48)	0.38	53.8± 0.8(25)	56.0± 0.8(48)	1.64	51.9± 1.4(25)	54.6± 1.0(48)	1.41
DIA1-FF − DIA1-SS	13.3± 0.6(26)	14.4± 0.6(24)	1.21	48.2± 0.7(25)	49.0± 0.8(24)	0.70	53.8± 0.8(25)	55.8± 1.1(24)	1.49	51.9± 1.4(25)	55.6± 1.9(24)	1.54
DIA1-FS − DIA1-SS	14.1± 0.3(53)	14.4± 0.6(24)	0.48	48.5± 0.4(48)	49.0± 0.8(24)	0.62	56.0± 0.8(48)	55.8± 1.1(24)	0.16	54.6± 1.0(48)	55.6± 1.9(24)	0.49
ME-FF − ME-FS	14.1± 0.4(36)	13.7± 0.4(47)	0.81	48.7± 0.4(35)	48.5± 0.5(43)	0.25	56.1± 0.9(35)	54.9± 0.8(43)	1.00	55.2± 1.2(35)	54.1± 1.2(43)	0.68
ME-FF − ME-SS	14.1± 0.4(36)	14.4± 0.7(20)	0.27	48.7± 0.4(35)	48.3± 0.3(19)	0.37	56.1± 0.9(35)	55.6± 1.5(19)	0.27	55.2± 1.2(35)	51.4± 2.1(19)	1.57
ME-FS − ME-SS	13.7± 0.4(47)	14.4± 0.7(20)	0.89	48.5± 0.5(43)	48.3± 0.3(19)	0.16	54.9± 0.8(43)	55.6± 1.5(19)	0.40	54.1± 1.2(43)	51.4± 2.1(19)	1.08
EsA+ve − EsA-ve	14.0± 0.5(29)	14.0± 0.3(74)	0.01	48.9± 0.6(28)	48.4± 0.4(69)	0.71	56.4± 1.0(28)	55.2± 0.6(69)	1.00	53.3± 1.6(28)	54.6± 0.9(69)	0.69

* p < 0.05. Significant at 5% level.
** p < 0.01. Significant at 1% level.
***p < 0.001. Significant at 0.1% level.

TABLE 3. COMPARISON BETWEEN GENETIC MARKERS FOR BODY LENGTH (CM) IN THAI LONGTAIL AND CAMEROON X LONGTAIL SHEEP (MEAN ± STANDARD ERROR: NO. OF OBSERVATIONS IN BRACKETS)

Phenotype comparison (1-2)	Thai Longtail			Cameroon X Longtail		
	Mean 1	Mean 2	t-value	Mean 1	Mean 2	t-value
XP+ve − XP-ve	51.1±1.0(34)	49.2±1.4(16)	1.13^{NS}	48.5±0.7(27)	46.3±1.1(20)	1.74^{NS}
DIA1F − DIA1S	48.7±2.3(10)	50.8±0.8(34)	1.09^{NS}	49.5±1.7(9)	47.2±0.9(24)	1.30^{NS}
DIA1F − DIA1FS	48.7±2.3(10)	51.8±3.9(6)	0.73^{NS}	49.5±1.7(9)	47.7±0.9(14)	0.99^{NS}
DIA1FS − DIA1S	50.8±0.8(34)	51.8±3.9(6)	0.44^{NS}	47.2±0.9(24)	47.7±0.9(14)	0.36^{NS}
MEFF − MEFS	51.5±1.6(18)	49.3±1.2(22)	1.12^{NS}	48.7±1.0(17)	46.9±0.7(22)	1.47^{NS}
MEFF − MESS	51.5±1.6(18)	51.3±1.2(10)	0.10^{NS}	48.7±1.0(17)	47.8±2.1(8)	0.29^{NS}
MEFS − MESS	49.3±1.2(22)	51.3±1.2(10)	1.01^{NS}	46.9±0.7(22)	47.8±2.1(8)	0.51^{NS}
EsA+ve − EsA-ve	50.5±0.5(18)	50.5±1.2(32)	0.02^{NS}	48.6±1.3(10)	47.6±0.7(37)	0.68^{NS}

NS-Not significant

Discussion

With this study, it was hoped that some genetic markers which are linked to economic production characters could be obtained and this may enable breeders to reduce the duration of expensive and time consuming selection programmes. However, like the results obtained by Mayo et al. (1970) and Rizzi et al. (1989), most of the associations except for XP system were not significant.

In all the above studies for an association between economic characters and biochemical markers there were no biochemical rationale among them. The only reason for expecting an association between a variant of a minor blood protein and economic trait was that a locus determining the former might just be closely linked to a second locus, influencing to a major extent, the economic character. Given the large number of linkage groups in most domestic mammals, e.g., diploid chromosome number of 54 in sheep, the probability of such linkage was pretty small to begin with and this is the main reason why most of the associations were found to be not significant.

However, XP locus was found to be the best for several economic traits. Animals with XP+ve phenotype were significantly greater than animals with XP−ve in body weight ($p < 0.001$), body height ($p < 0.05$), heart girth ($p < 0.001$) and back girth ($p < 0.01$). On the basis of the results presented here, there may be a gene or a group of genes which is on the same chromosome as the XP locus which makes a significant contribution to the characters studied.

In general, these preliminary results are sufficiently important to warrant further study for XP locus, with a larger number of individuals from a single breed, on different planes of nutrition and on population with different breeding structures.

Literature Cited

Cepica, S. and A. Stratil. 1978. Further studies on sheep polymorphic erythrocyte diaphorase. Anim. Blood Grps Biochem. Genet. 9:239-243.

Mayo, O., D. W. Cooper, R. E. Brady and C. W. Hooper. 1970. Response to partial selection on clean fleece weight in South Australian strong-wool Merino sheep. II. Association between production characters, fertility, and three genetic polymorphisms. Aust. J. Agric. Res. 21:541-547.

Rizzi, R., P. Bolla, A. Caroli, G. Pagnacco, A. Fraghi, S. Casu and F. Miglior. 1989. Blood genetic markers and production in sheep. Anim. Genet. (Suppl 1) 20:77-78.

Tucker, E. M., Y. Suzuki and C. Stormont. 1967. Three new phenotypic systems in the blood of sheep. Vox. Sang. 13:246-262.

Tucker, E. M. and C. Crowley. 1978. NADH diaphorase as a genetic marker for sheep red cell. Anim. Blood Grps Biochem. Genet. 9:161-167.

Yaman, K. and E. M. Tucker. 1981. 'Malic enzyme' polymorphism in sheep erythrocytes. Anim. Blood Grps Biochem. Genet. 12:215-218.