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Factor analysis for genetic evaluation of linear type traits in dual purpose breeds

R. Mantovani, I. Cerchiaro, B. Contiero

Dipartimento Scienze Zootecniche, Università di Padova, Italy

Corresponding author: Roberto Mantovani. Dipartimento Scienze Zootecniche. Viale dell'Università 16, 35020 Legnaro, Italy – Tel: +39 049 8272661 – Fax: +39 049 8272633 – Email: roberto.mantovani@unipd.it

RIASSUNTO – Analisi fattoriale nelle valutazioni genetiche per i caratteri morfologici lineari in razze a duplice attitudine. *È stata condotta l'analisi fattoriale di 23 caratteri morfologici lineari rilevati su 2800 primipare di razza Rendena. I punteggi fattoriali, ottenuti dai fattori latenti esplicativi, sono stati utilizzati per calcolare i parametri genetici dei fattori stessi e successivamente per ottenere indici genetici fattoriali (EBVF). Gli EBVF sono stati quindi confrontati con indici ottenuti dai singoli punteggi morfologici (EBVM). L'analisi di correlazione ha messo in luce che gli EBVF riflettono, sia in valore che in termini di classifiche, il legame fenotipico palesato dai singoli caratteri lineari con i fattori (Es: correlazione tra EBVM dei lineari inerenti la muscolosità ed EBVF del fattore saturato principalmente da questi caratteri compresa tra 0,86 e 0,90). Questi risultati suggeriscono il possibile uso dei fattori nelle valutazioni genetiche per i rilievi morfologici lineari, soprattutto in situazioni contraddistinte, come nel caso oggetto di studio, dalla presenza di un gran numero di caratteri valutati.*

KEY WORDS: genetic evaluation, factor analysis, linear type traits, dual purpose breeds.

INTRODUCTION – Type traits have become a selection goal in many breeder association due to the economic value recognised to some measurements. In dairy cattle, relationships of type with production (Veerkamp and Brotherstone, 1997; Kadarmideen and Wegmann, 2003) and/or with longevity (Larroque and Ducrocq, 2001; Vukasinovic *et al.*, 2002) have been widely investigated in order to use type traits as predictors of herd life. A major problem associated with the use of type traits in genetic programs is the high number of traits scored and their high degree of interrelationships. Indeed, traits referring to the same part of the body usually show a high genetic correlation (Sieber *et al.*, 1987). In dual purpose breeds, redundant information among type traits is often observed due to recording of many traits linked to muscularity, udder, etc. Factor analysis is recognised as a useful tool for removing the redundancy from correlated variables deriving a new set of uncorrelated variables called "factors" (Vukasinovic *et al.*, 1997). The aim of this study was to analyse the use of factor analysis to obtain factor scores to use for animal breeding values estimation (EBV) rather than the single type traits. The Rendena breed was used as case study.

MATERIAL AND METHODS – Twenty-three type traits scored linearly with a 1-5 scale by a single evaluator on 2800 primiparous Rendena cows were analysed with the SAS FACTOR procedure (SAS, 1990). Data resulted from a previous editing that excluded cows with incomplete measurements or records that did not meet the animal model fixed effects used to estimate multi trait variance components (Misztal *et al.*, 1993), i.e., herd-year of score (HY: 1,….,369; about 8 animals/HY), calving season (CS: 1,….,8), age at first calving (AFC: 22 to 46 mo. of age) and days in milk (DIM: 10 to 350 d from calving) both included as linear and quadratic covariates. Other than animals with record (daughters of 304 sires, i.e. about 9 daughters/sire) 4708 ancestors, accounting 2 unknown parents, were also included in variance components estimation. Phenotypic factor scores (FS) from standardized type traits were then calculated for each animal using the factor pattern coefficients kept from the eigenvalueone criterion (i.e., retaining only factor with eigenvalue ≥1) and after a VARIMAX rotation method of factors. FS were then used to estimate variance components for each hypothetical variable using the model and the pedigree as above. Single trait EBV's for the 23 type traits and for each factor was then calculated. Comparison between single type traits EVB's and factors EBV's was carried out using the CORR procedure to obtain correlation both among EBV's values and EBV's ranking (SAS, 1990).

RESULTS AND CONCLUSIONS – Table 1 shows the factor pattern coefficients for the seven factors retained with the eigenvalueone method. The seven factors explain about 63% of the total variation among the 23 type traits. Factors P1 and P2 have the highest magnitude, accounting for 21 and 12% of the total variation, respectively. Pattern coefficients for factors (multiply by 100 and rounded) are reported in Table 1 only if ≥|30|. These coefficients allow a quite good interpretation for at least six of the seven latent factors. Indeed, P1 shows large positive loadings from fleshiness traits and body condition, while P2 includes traits related mainly with animal size. On the other hand, mammary traits load factors P3 and P4, with the former linked mainly to mammary size and the latter with mammary suitability. These results are consistent with factor analysis performed by Sieber *et al.* (1987) in Holstein cows. Furthermore, P5 and P6 are loaded by feet and legs and by farmer judgement, while thinness remains undetermined and basically not linked to any factor.
As expected correlation analysis (Table 2, for only values ≥30) between type EBV's and factors' EBV shows a pattern very similar to the loading pattern on latent factors. Indeed, EBV's obtained for P1 are highly correlated with the EBV's for fleshiness traits (0.86<r<0.90) and also the rank correlation indicates small variation in EBV's ranking using P1-EBV's rather than EBV's from single fleshiness traits (0.81<r<0.87). In addition, EBV's for mammary size and suitability factors (i.e., P3 and P4) show high correlation with EBV's linked to size (rear udder height and width) or suitability of the udder (suspensory ligament and teat length). These results suggest a possible use of latent factors from type traits in genetic evaluation, since the genetic analy-

Table 1. Phenotypic factors and loading for type traits (coefficients ≥|30|) after Varimax rotation.

	Varimax Phenotypic Factors								
Traits	P1	P2	P3	P4	P5	P6	P7	Communality	Eigenvalues
Stature		85						0.77	4.851
Body length		86						0.75	2.822
Thorax depth		77						0.64	2.000
Thorax length	51	64						0.68	1.419
Front fleshiness	86							0.75	1.155
Back fleshiness	90							0.82	1.080
Buttocks side view	88							0.80	1.044
Thigh thickness	86							0.77	0.938
Body condition	78							0.61	0.895
Thinness			39					0.25	0.859
Rump angle							79	0.75	0.780
Rump width	31	65						0.53	0.757
Rear legs side view					78			0.68	0.628
Foot angle					-60			0.43	0.594
Fore udder attach			65					0.49	0.557
Rear udder height			78					0.67	0.477
Rear udder width			79					0.66	0.447
Udder depth			-40	41	-33		42	0.66	0.387
Suspensory ligament				67				0.51	0.379
Teat placement side view			39	37			-42	0.56	0.317
Teat length				-70				0.56	0.254
Disposition						71		0.52	0.201
Milkout						66		0.52	0.160
Variance explained (%)	0.21	0.12	0.09	0.06	0.05	0.05	0.05		

Table 2. Correlation coefficients (only values ≥30) between EBV's for type and phenotypic factors.

	EBV's correlation							Rank correlation						
Traits	P1	P2	P3	P4	P5	P6	P7	P1	P2	P3	P4	P5	P6	P7
Stature		87		-					84				-	
Body length		87		-					84					
Thorax depth		76				-			72				-	
Thorax length	42	57						40	52					
Front fleshiness	86							81						
Back fleshiness	90							87						
Buttocks side view	90					-		87	-				-	
Thigh thickness	86							82						
Body condition	76							71						
Thinness			41							37				
Rump angle						-	86				-		-	83
Rump width		60							57					
Rear legs side view					81						-	78		
Foot angle					-65							-62		
Fore udder attach	-		59	-				-		54	-			
Rear udder height			80			-				76			-	
Rear udder width			80							77				
Udder depth				46			51				40			43
Suspensory ligament				72				-			69			
Teat placement side view							-52							-47
Teat length				-75	-					-	-72			
Disposition			-			73	-			-			71	-
Milkout		-				75			-				73	

sis indicates the absence of great changes in the phenotypic relationship between latent factors and type traits. This approach, sometimes refused by other Authors because of the difficulties in interpretation of factors composition (Vukasinovic *et al.*, 1997), would avoid the use of final scores, particularly when they do not reflect a biological basis but are referred as deviation from an "ideal".

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