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GENETIC PARAMETERS FOR MEAT PRODUCTION IN RABBITS. 1 - NON CARCASS COMPONENTS.

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SUMMARY : Data of 122 males rabbits, randomly sampled from 19 sires of New Zealand White breed raised on two farms in Sharkia Governorate, Egypt, were analysed to provide estimates of heritabilities for non carcass components and to obtain estimates of genetic and phenotypic correlations among these components. All rabbits were slaughtered when reached a live body weight of approximately 2 kg. The weights of non carcass components and hot carcass were recorded and dressing percentages were also calculated. Least squares analysis of variance showed that weights of rabbit non carcass components were more influenced by the effect of farm adjusted to the effect of slaughter weight, whereas they were slightly influenced by the effect of sires within farm. Generally, the heritability estimates for gastrointestinal tract and its components except stomach (h^2 = 0.24) were high, ranged between 0.40 to 0.60 and were very high for trachea (h^2 = 0.78), testes (h^2 = 0.94) and kidney fat (h^2 = 0.94) whereas the weights of urinary bladder, head, ears, pituitary gland, kidneys and lungs were moderately heritable, ranged from 0.21 to 0.39. The remaining traits showed low heritability estimates ranged between 0.02 and 0.14. Estimates of genetic and phenotypic correlations were high only between the weights of liver, testes and kidney fat and the weights of the other traits. Results suggested the possibility of improvement liver, testes or kidney fat weights by direct selection.

RESUME : Paramètres génétiques de la production de viande chez le lapin. Composants hors carcasse.
Pour améliorer les estimations des hérétabilités des composants hors carcasse et obtenir entre ces composants des correlations phénotypiques et génétiques, les données concernant 122 lapins mâles issues de 19 lignées de mâles NZW, ont été analysées. Les lapins ont tous été abattus lorsqu'il atteignaient approximativement 2 kg. Les poids des composants hors carcasse et de la carcasse chaude ont été enregistrés et les rendements à l'abattage ont été calculés. L'analyse de variance par les moindres carrés montre que les poids des composants hors carcasse n'étaient pas influencés par l'effet ferme lié à l'effet poids à l'abattage, tandis qu'ils étaient légèrement influencés par l'effet mâles selon les fermes. En général, les estimations d'héritabilités pour les composants du tractus gastrointestinal, excepté l'estomac (h^2 = 0.24) étaient élevées, atteignant 0.40 à 0.60, et étaient très élevées pour la trachée (h^2 = 0.78), les testicules (h^2 = 0.94) et le gras rénale (h^2 = 0.94), tandis que les poids de la vessie, de la tête, des oreilles, de la glande pituitaire, des reins et des poumons étaient modérement héritables, allant de 0.21 à 0.39. Les autres composants ne montraient que de faibles estimations d'héritabilité, de 0.02 à 0.14. Les estimations des correlations génétiques et phénotypiques étaient élevés seulement entre les poids du foie, des testicules et du gras rénal par rapport aux autres composants. Ces résultats suggèrent une possibilité d'améliorer le poids du foie, des reins et des testicules par sélection directe.

INTRODUCTION

In meat producing animals, measurements of some easily assessed or obtained traits, such as preslaughter weights, carcass yield (i.e. dressing percentage) or non carcass components (i.e. offals) of slaughter animals, may provide a reliable method of indirect selection for carcass traits and slaughter yield. The extent to which these can be incorporated into a selection program is partly determined by the extent to which they are inherited. The gradually increasing consumption of meat in future years, especially in developing countries, could be met by the increase of production countries, could be met by the increase of production coming from short cycle animals such as rabbits, (LEBAS, 1983).

At present, the information concerning inheritance of non carcass and carcass traits in rabbits, in general, is limited as compared with other livestock. The main objective of the present study were to derive

estimates of heritabilities and genetic and phenotypic correlations for various non carcass components of New Zealand White rabbits under Egyptian conditions.

MATERIALS AND METHODS

Data of 122 random male rabbits born in 1993 by 19 sires of New Zealand White breed raised on two farms at Sharkia Governorate, Egypt. The number of 12 sires and 63 of their male offsprings were raised by the Faculty of Agriculture, Zagazig University (Farm 1) and 7 sires and 59 of their male offsprings raised in the farm of San El Hager Investment Company for Agriculture and Food Security (Farm 2). Rabbits were identified at weaning, at about 35 days of age. They were fed, *ad libitum*, for 60 days in average on commercial pelleted rations with 16.3 % crude protein, 12.44 % crude fibre and 2670 Kcal/kg diet till they attained the marketing body weight of approximately 2 kg. Live weights were recorded at weaning and at weekly intervals from weaning until slaughter. All rabbits were weighed after being held overnight without food. They were slaughtered and the weight of blood was recorded (the difference between slaughter weight and animal weight after the complete bleeding). After complete bleeding, the animals was dressed according to BLASCO *et al.*, and the weight of distal parts of fore and hind legs (i.e. feet), pelt and ears were recorded. Then, the body was eviscerated and weights of the following organs were recorded : the gastrointestinal tract (full an empty), the empty urinary bladder, the stomach (clean and dripped), the small intestine (clean and dripped), the gut fat, the pancreas, the spleen, the testes and the gall bladder. After dressing, the carcass was weighed (i.e. hot carcass weight) including the head without eats, the lungs, the oesophagus, the trachea, the liver, the heart, the heart fat, the kidneys and kidney fat. The above mentioned organs were removed later from the carcass and weighed and also the brain, eyes, the tongue and pituitary, the thymus and the suprarenal glands and the carcass were chilled at 2°C for 24 hours. The dressing percentage was calculated as the ratio between hot carcass and slaughter weight. Overall means and standard deviations for slaughter weight, hot carcass weight, dressing percentage and also for weights of non carcass components studied are given in Table 1.

The data were analysed by the least squares procedure (HARVEY, 1987). The following mathematical model was used to describe the observations :

$$Y_{ijk} = U + F_i + S{:}F_{ij} + b(X_{ijk} - X) + e_{ijk},$$

where :

Y_{ijk} is the observation on k^{th} rabbit, under i^{th} farm and j^{th} weight of rabbit ;

Table 1 : Overall means and standard deviation (S.D.) for slaughter weight (g), hot carcass (g) dressing percentage (%) and weights (g) of rabbit non carcass components.

Traits	Mean	S.D.
Slaughter weight	2105	235.86
Blood weight	52	10.77
Head weight	136	13.54
Liver weight	71	12.63
Kidneys weight	13	1.69
Kidney fat weight	14	5.28
Heart weight	7	0.65
Heart fat weight	4	1.25
Pelt weight	253	30.45
Ears weight	39	6.26
Fore feet weight	20	2.31
Hind feet weight	50	4.99
Gastrointestinal tract weight full	365	47.63
Gastrointestinal tract weight empty	155	18.73
Empty stomach weight	26	5.11
Empty small intestine weight	48	8.83
Empty large intestine weight	81	13.92
Gut fat weight	6	2.40
Lungs weight	10	1.78
Pancreas weight	9	3.29
Eyes weight	4	0.56
Brain weight	8	0.93
Urinary bladder empty weight	3	1.11
Oesophagus weight	2	0.63
Thymus gland weight	4	1.14
Testes weight	5	1.55
Tongue weight	5	0.47
Spleen weight	1	0.54
Trachea weight	1	0.45
Pituitary gland weight	0.01	0.01
Suprarenal glands weight	0.2	0.08
Gall bladder weight	0.81	0.42
Hot carcass weight	1291	454.79
Dressing percentage	59	2.18

U is the overall population mean ;

F_i is the fixed effect of i^{th} farm, i = 1, 2 ;

$S{:}F_{ij}$ is the random effect of the j^{th} sire within the i^{th} farm ;

b is the regression coefficient of Y_{ijk} on slaughter weight, X_{ijk} is the value of slaughter weight for k^{th} rabbit of i^{th} farm and j^{th} slaughter weight ;

X is the overall average of slaughter weight ;

e_{ijk} is the random error.

The data were pooled to study genetic and phenotypic parameters of non carcass components. The heritability was estimated by paternal half-sib correlation method as suggested by HAZEL and TERRIL

(1945). The phenotypic and genetic correlations were computed according to HAZEL *et al.* (1943).

RESULTS AND DISCUSSION

Least squares analysis of variance for farm, sires within farm and regression on slaughter weight effects for the traits studied are shown in Table 2. Farm effects were highly significant (P<0.001) on kidney fat, fore feet, hind feet, empty gastrointestinal tract, empty stomach, empty large intestine, empty urinary bladder, gall bladder, pancreas, thymus gland, brain, eyes and suprarenal gland weights and significant (P<0.05) on pelt, full gastrointestinal tract and gut fat

Table 2 : Adjusted means and standard errors (S.E.) and analysis of variance of rabbit non carcass traits (weights in g).

	Overall		Mean Squares			
	Mean [1]	S.E.	Farm [2]	Sire [3]	RSW [4]	Error [5]
Blood	52	1.01	319.84	121.34	374.65	101.42
Head	135	1.32	196.23	200.65	2675.81***	122.32
Liver	71	2.51	404.24	257.49*	1070.77***	133.08
Kidneys	13	0.16	0.89	3.16	33.90***	2.35
Kidney fat	14	0.71	172.11***	55.04	117.50	18.83
Heart	7	0.56	4.04	31.79	35.32	37.89
Heart fat	4	0.15	3.09	2.44*	9.62**	1.36
Pelt	253	3.52	6463.31*	1402.80*	7730.72***	706.13
Ears	39	0.70	234.47	56.67	32.23	34.03
Fore feet	20	0.21	75.06***	2.89	16.60	5.13
Hind feet	50	0.41	306.91***	20.67	417.47***	20.18
Gastrointestinal tract full	366	4.21	11485.42	1671.04	23021.14***	2159.86
Gastrointestinal tract empty	156	2.16	5530.80***	527.39*	2857.47***	266.12
Stomach	26	0.44	690.69***	23.57	115.31*	20.25
Small intestine	48	1.04	365.09	122.65*	266.11*	69.22
Large intestine	81	1.27	1235.79***	130.82	517.22	194.85
Gut fat	6	0.27	39.18	8.37*	16.24	4.40
Lungs	10	0.19	13.10	4.24	3.46	2.84
Pancreas	9	0.27	544.86***	8.54	35.29*	6.10
Eyes	4	0.05	4.48***	0.21	0.65	0.27
Brain	8	0.08	13.30***	0.79	2.03	0.75
Urinary bladder	3	0.12	13.54***	1.54	3.64	1.06
Oesophagus	2	0.08	0.73	0.65*	0.30	0.35
Thymus gland	4	0.11	17.01***	1.40	0.46	1.15
Testes	5	0.22	9.56***	5.40**	0.37	1.85
Tongue	5	0.06	0.32	0.36*	0.14	0.19
Spleen	1	0.06	0.85	0.43*	0.59	0.23
Trachea	0.99	0.06	0.15	0.43**	0.11	0.17
Gall bladder	0.81	0.03	5.67***	0.11	0.003	0.12
Pituitary gland	0.01	0.001	0.00001	0.00003	0.0001*	0.0002
Suprarenal gland	0.20	0.01	0.14***	0.004	0.002	0.007
Hot carcass	1292	41.99	120572.08	158230.96	3611525.54	214840.29
Dressing percentage	59	0.21	16.43	5.11	2.16	4.58

[1] Means are least squares estimates ; [2] df = 1 ; [3] df = 17 ; [4] df = 1 ; [5] df = 102
* P<0.05 ; ** P<0.01 ; *** P<0.001
RSW : regression on slaughter weight.

weights , while they were non significant (P>0.05) for blood, empty small intestine, spleen, liver, oesophagus, head, testes, ears, tongue, pituitary gland, kidneys, kidney fat, trachea, lungs, heart, heart fat, hot carcass weights and dressing percentage.

Sire effects were highly significant (P<0.001) only on weights of testes. Kidney fat, (P<0.01), on trachea weight only and significant (P<0.05) on pelt, empty gastrointestinal tract, empty small intestine, spleen, liver, oesophagus, tongue, gut fat and heart fat weights, while non significant (P>0.05) on all other traits.

Regression of each one of traits considered on slaughter weight was highly significant (P<0.001) for pelt, hind feet, full gastrointestinal tract, empty gastrointestinal tract, liver, head and kidneys weights, significant (P<0.01) for kidney fat, heart fat weights and (P<0.05) for empty stomach, empty small intestine, pancreas and pituitary gland weights, while non significant (P>0.05) for all other traits.

Among traits studied, only blood, ears, lungs, heart, hot carcass weights and dressing percentage were not affected by any one of factors considered in the statistical model, whereas pelt weight and empty gastrointestinal tract weight were the only traits affected by all the factors considered.

It seems from these results that rabbit non carcass components were more influenced by the effect of farm compared withe the effect of slaughter weight, whereas they were slightly influenced by the effect of sire.

Numerous factors can affect weight traits and carcass yield of rabbits. OUYAHOUN and CHERIET (1983) concluded that body composition (prerenal fatty tissue, carcass yield, relative weight of liver) was highly affected by the genetic and dietary factors. Also, LEBAS and OUHAYOUN (1987) studied the effect of dietary protein level, housing conditions and season on growth and slaughter traits of rabbit and reported that most growth and body composition traits were affected by the studied variables. However, MOURA *et al.* (1991) concluded that month of birth and parity were major environmental factors influencing individual weight performance of rabbits from weaning to slaughter. Generally, the organ weights obtained in the present study were not far from the values reported previously by other authors (RAO *et al.*, 1978 ; FENELL *et al*, 1990 ; ORAVCOVA and BEBER, 1991 a, b).

Heritability estimates

Heritability estimates for rabbit non carcass components weights with the exception of fore feet, full gastrointestinal tract, large intestine, gall bladder, eyes, suprarenal gland, heart weights and hot carcass weight are presented in Table 3. Negative sire components of variance for these traits forced their elimination from the remaining calculations.

Table 3 : Heritability estimates (h^2) with standard errors (S.E.) for rabbit non carcass traits*.

Traits	h^2	S.E.
Blood	0.12	0.26
Head	0.37	0.31
Liver	0.52	0.34
Kidneys	0.21	0.28
Kidney fat	0.94	0.31
Heart fat	0.45	0.32
Pelt	0.55	0.34
Ears	0.39	0.31
Hind feet	0.02	0.23
Gastrointestinal tract (empty)	0.54	0.34
Stomach	0.10	0.25
Small intestine	0.45	0.32
Gut fat	0.50	0.33
Lungs	0.29	0.29
Pancreas	0.24	0.28
Brain	0.03	0.24
Urinary bladder	0.26	0.29
Oesophagus	0.48	0.33
Thymys gland	0.14	0.26
Testes	0.94	0.39
Tongue	0.51	0.33
Spleen	0.48	0.33
Trachea	0.78	0.37
Pituitary gland	0.27	0.29
Dressing percentage	0.07	0.25

* K for sires/farm variance component = 6.25

The heritability estimates of weights of empty gastrointestinal tract, gastrointestinal tract components except stomach weight ($h^2 = 0.10 \pm 0.25$) and pancreas weight ($h^2 = 0.24 \pm 0.28$) and pelt weight were high, ranging from 0.40 to 0.60, but are generally higher for trachea weight ($h^2 = 0.78 \pm 0.37$) and testes weight ($h^2 = 0.94 \pm 0.39$), whereas the weights of urinary bladder, head, ears, pituitary gland, kidneys and lungs were moderately heritable, ranging from 0.21 to 0.39. The weights of fat depots were highly heritable ; 0.45 ± 0.32 and 0.50 ± 0.33 respectively for heart fat and gut fat, or very highly heritable (0.94 ± 0.39) for kidney fat. The heritable estimates for the remaining traits

were generally low, ranging from 0.02 to 0.14. It seems that testes weight and fat depots weights of the carcass were the most heritable traits.

Interrelationships among non carcass components weights

Phenotypic and genetic correlations among various non carcass components weights are given in Table 4. Estimates of genetic and phenotypic correlations showed high associations between some non carcass traits like pelt, testes, gastrointestinal tract, fat depots and the other traits ; for simplicity, only interrelationships between empty gastrointestinal tract weight with non carcass components weights, between dressing percentage with non carcass components weights and between kidneys fat weights with various non carcass components weights were considered in the discussion of results.

a) Correlation of empty gastrointestinal tract weight with various non carcass components weights

The phenotypic correlations indicate high positive relationships between empty weight of gastrointestinal tract and stomach, small intestine and large intestine weights and moderate positive relationships with blood weight. On the other hand, empty gastrointestinal tract weight is moderately negative related to dressing percent. The relationships withe the other non carcass components were low and positive (liver, ears, kidneys, spleen, lungs and heart fat weights) or negative (pelt, thymus gland, testes, eyes and kidney fat weights) and essentially zero fort the other components.

Most of the genetic correlations between empty weight of gastrointestinal tract and ten various non carcass components weights were high and negative and varied widely from 0.52 (for tongue weight) to 0.96 (thymus gland weight). Moderate negative relationship existed between empty gastrointestinal tract weight and spleen weight. Moderate but positive relationships existed with both blood, pelt and liver weights.

b) Correlations of pelt weight with various non carcass components weights

Estimates indicate that pelt weight has a low and, in most cases, positive phenotypic association with various non carcass components weights. However, head, tongue, and kidney fat weights have a moderate and positive phenotypic association with pelt weight.

Moderate genetic relationships were observed between pelt weight and both empty gastrointestinal tract weight (-0.37), pituitary gland weight (0.35), testes weight (0.41) and kidney fat weight (0.30). However, spleen, thymus gland, tongue and brain weights showed a high and positive genetic correlation with pelt weight, respectively 0.88, 0.51, 0.60 and 0.71. This indicates that selection for a heavy spleen, thymus gland, tongue and brain weights showed a high and positive genetic correlation with pelt weight, respectively 0.88, 0.51, 0.60 and 0.71.

c) Correlations of dressing percent with various non carcass components weights

The phenotypic correlations showed low (essentially zero) to moderate (essentially positive) relationships between dressing percent and various non carcass components weights. Moderate negative relationship existed with stomach weight.

Most of the genetic correlations between dressing percent and the various non carcass components weights were moderate to high but positive (kidneys, head, blood, testes, spleen, brain and tongue) or negative (ears and empty gastrointestinal tract).

d) Correlations of kidney fat weight with various non carcass components weights.

Estimates indicate that kidney fat has a moderate phenotypic associations with pelt weight (0.41), pancreas weight (0.47), gut fat weight (0.45) and dressing percent (0.33). However the other non carcass components showed a low (positive or negative) association with kidney fat (essentially zero).

Moderate and positive genetic correlations were found between kidney fat weight and pelt weight, head, tongue and lungs weights. Moderate negative relationship existed with kidneys weight. However, brain ($r = 0.92$), gut fat ($r = 0.58$), empty gastrointestinal tract ($r = 0.76$), liver ($r = 0.63$), thymus ($r = 0.72$) and pituitary gland ($r = 0.85$) showed a high genetic association with the weight of kidney fat. These results indicate that genes influencing kidney fat have a large negative influence on weight of both gastrointestinal tract, liver, thymus gland and pituitary gland, whereas it has a positive influence on weight of both brain and gut fat.

Examination of the rabbit literature indicates that genetic parameter estimates of rabbit non carcass traits were not found. The estimates obtained here were apparently the first published genetic estimates based on non carcass data. However, if the commercial rabbit industry is to develop and expand, all aspects of meat production will have to be evaluated not only the various aspects of production efficiency of live

Table 4 : Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among weights of rabbit non carcass traits

Traits	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
Blood (X_1)		>1	0.31	0.86	0.95	*	0.53	0.13	−0.88	>1	0.43	>1
Pelt (X_2)	0.17		−0.37	−0.07	−0.08	*	0.23	0.88	−0.15	>1	0.51	0.41
Gastrointestinal tract empty (X_3)	0.31	−0.11		>1	>1	*	>1	−0.37	0.03	−0.08	−0.96	−0.83
Stomach (X_4)	0.27	−0.03	0.52		0.47	*	>1	0.14	0.08	>1	>1	>1
Small intestine(X_5)	0.34	−0.11	0.53	0.36		*	−0.55	0.08	−0.36	0.27	>1	−0.98
Large intestine(X_6)	0.07	−0.08	0.72	0.11	−0.10		*	*	*	*	*	*
Pancreas (X_7)	0.10	0.21	−0.06	−0.16	0.04	−0.03		0.91	>1	0.13	0.02	0.87
Spleen (X_8)	0.29	−0.00	0.19	0.16	0.06	0.13	−0.10		−0.97	>1	0.37	−025
Liver (X_9)	0.07	−0.03	0.28	0.31	0.30	0.08	0.00	0.17		0.45	−0.15	0.03
Head (X_{10})	0.06	0.42	0.04	−0.18	−0.06	0.13	0.08	0.07	−0.11		>1	−0.05
Thymus gland (X_{11})	−0.06	0.08	−0.16	0.02	−0.09	−0.16	−0.05	−0.03	0.07	−0.14		0.40
Testes (X_{12})	−0.02	0.28	−0.12	−0.11	−0.09	−0.07	0.12	−0.10	−0.06	0.17	0.13	
Ears (X_{13})	0.30	0.21	0.29	0.19	0.29	0.12	−0.01	0.20	0.05	0.22	0.01	−0.06
Tongue (X_{14})	0.14	0.34	0.00	0.08	−0.02	−0.04	0.14	0.13	−0.18	0.24	0.00	0.15
Brain (X_{15})	0.08	0.03	−0.03	0.04	0.04	−0.05	0.13	0.01	0.02	0.16	−0.01	−0.01
Eyes (X_{16})	−0.08	0.08	−0.18	−0.06	0.04	−0.22	0.11	0.09	0.03	0.06	−0.01	0.10
Pituitary gland (X_{17})	0.10	0.00	0.09	0.05	0.09	0.05	0.04	0.06	0.03	0.06	−0.11	−0.08
Gut fat (X_{18})	0.15	0.28	−0.06	−0.07	0.02	0.05	0.33	0.04	0.16	0.12	−0.01	0.07
Kidneys (X_{19})	0.30	0.17	0.28	0.16	0.18	0.14	0.04	0.31	0.23	0.16	−0.10	−0.22
Kidney fat (X_{20})	0.07	0.41	−0.14	−0.20	−0.10	−0.06	0.47	−0.13	−0.04	0.13	0.23	0.23
Suprarenal g. (X_{21})	0.00	0.09	−0.05	−0.04	−0.04	0.04	0.11	0.03	0.07	−0.09	0.17	0.08
Lungs (X_{22})	0.24	0.05	0.12	0.08	0.05	0.10	−0.02	0.30	−0.02	0.17	−0.07	−0.14
Heart (X_{23})	−0.01	−0.01	0.05	−0.01	0.01	0.05	0.06	−0.04	0.06	0.06	−0.06	−0.03
Heart fat (X_{24})	0.23	0.10	0.12	0.16	0.06	0.08	0.12	0.12	0.11	0.22	0.25	0.20
Hot carcass (X_{25})	0.06	0.07	0.04	−0.02	0.02	0.04	0.08	−0.01	0.04	0.09	−0.06	0.02
Dressing percent (X_{26})	−0.10	0.10	−0.31	−0.33	−0.09	−0.24	0.24	−0.05	−0.23	0.31	−0.06	0.29

animals, but also carcass yield, non carcass components beside the preservation and marketing of rabbit meat. On the other hand, the results of heritability estimates of the present study showed high values for some non carcass traits like pelt, empty gastrointestinal tract, testes, tongue, gut fat, kidney fat, liver and trachea. In addition, most of the genetic and phenotypic correlations of these traits withe the other traits considered were high (especially the genetic correlations) only for liver, testes and kidney fat. Thus, genetic progress should be attainable for some non carcass components, especially those of economical importance, by direct selection on liver,; testes or kidney fat weights, whereas there is a little chance to improve the other traits. These traits could be used in further studies for evaluating growth, carcass composition or carcass quality.

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Table 4 (continued)

Traits	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}	X_{18}	X_{19}	X_{20}	X_{21}	X_{22}	X_{23}	X_{24}
X_1	>1	−0.13	−0.54	*	−0.03	0.22	>1	−0.09	*	>1	*	−0.07
X_2	>1	0.60	0.71	*	−0.35	0.05	0.27	0.30	*	>1	*	0.19
X_3	−0.23	−0.52	−0.54	*	0.24	−0.19	>1	−0.76	*	0.04	*	−0.61
X_4	>1	−.053	>1	*	>1	−0.19	>1	>1	*	0.93	*	0.62
X_5	0.15	−0.32	−0.26	*	−0.13	>1	>1	0.00	*	0.66	*	>1
X_6	*	*	*	*	*	−0.87	*	*	*	*	*	*
X_7	−0.16	0.35	>1	*	−0.09	*	>1	>1	*	0.99	*	0.32
X_8	>1	−0.27	>1	*	−0.17	0.63	0.54	−0.29	*	0.58	*	−0.39
X_9	0.33	0.67	>1	*	0.11	0.61	0.92	−0.63	*	0.30	*	−0.11
X_{10}	>1	0.60	−0.14	*	−0.19	0.20	>1	0.32	*	>1	*	−0.09
X_{11}	0.10	0.68	>1	*	>1	0.20	−0.99	−0.72	*	0.80	*	−0.23
X_{12}	−0.53	0.25	>1	*	−0.43	0.31	>1	0.26	*	−0.09	*	−0.20
X_{13}		0.68	>1	*	0.06	−0.11	>1	−0.20	*	>1	*	0.57
X_{14}	0.27		>1	*	0.16	0.54	−0.45	0.41	*	0.80	*	0.06
X_{15}	0.09	0.17		*	−0.09	0.12	0.37	0.92	*	0.72	*	>1
X_{16}	0.04	−0.06	0.31			*	*	*	*	*	*	*
X_{17}	0.15	0.12	0.24	0.14			*	−0.85	*	0.13	*	0.59
X_{18}	−0.08	0.07	0.01	0.07	0.06			0.58	*	>1	*	−0.86
X_{19}	0.29	0.10	−0.09	−0.14	−0.04	0.00		−0.33	*	0.16	*	0.13
X_{20}	0.07	0.10	0.09	0.07	−0.18	0.45	−0.02		*	0.37	*	−0.22
X_{21}	−0.11	0.09	0.17	0.10	−0.07	0.14	0.04	0.16		*	*	*
X_{22}	0.25	0.13	0.12	0.02	−0.02	0.09	0.32	−0.10	0.04		*	0.67
X_{23}	−0.02	−0.06	−0.23	−0.08	0.11	0.02	0.07	0.00	−0.27	−0.44		*
X_{24}	0.19	1.08	0.04	0.03	0.01	−0.04	0.10	0.04	0.03	−0.11	0.18	
X_{25}	0.01	−0.02	−0.19	−0.07	0.13	0.02	0.04	0.04	−0.29	−0.44	0.93	0.19
X_{26}	0.00	0.23	0.08	0.08	−0.10	0.10	−0.05	0.33	−0.12	−0.01	0.03	−0.04

All estimates >0.250 are significant at P<0.01 ; All estimates >0.191 <0.250 are significant at P<0.05 ; otherwise are insignificant ; * Genetic correlations were not calculated due to negative variance components.

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