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SOME BLOOD BIOCHEMICAL AS INDICATOR TO IMPROVE PRODUCTIVE AND REPRODUCTIVE PERFORMANCE IN RABBIT POPULATION

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SUMMARY - Genetic and environmental factors that influence serum and urine progesterone (SP and UP) and blood protein patterns were evaluated for 686 Bauscat does from 117 dams and 34 sires. The sire and dam within sire effects were significant for most blood traits. Progesterone was detected by RIA in fresh urine after conversion from pregnadiol to pregesterone. The heritability (h^2) for SP and UP at different periods of gestation were moderate. Gestation period (GP) showed negative highly significant genetic correlations (r_G) with each of SP, UP, Alb, Alb/Glo ratio and negative correlations with NEP11 and Glo. Litter size and weight at birth (LSB and LWB) showed positive r_G with each of SP, UP15, TP and Alb and negative r_G with NEP11. The r_G were negative between bunny weight at birth (BWB) and all progesterone and protein patterns. Genetic improvements of fertility based on progesterone and blood protein patterns in doe rabbits would be 41% or more as efficient as indirect selection. It was concluded that the h^2 were sufficiently high to permit selection on individual levels for some of the biochemical traits in doe.

Key words: Progesterone, pregnandiol, protein, heritability, genetic correlations.

INTRODUCTION

Blood biochemical traits could be important as indicator traits in modern animal improvement. The value of an indicator trait depends on 1. applied breeding scheme, 2. correlation between a particular indicator trait and the relevant production trait and 3. heritability of the indicator trait and production trait (Lovendahl *et al.*,1989).

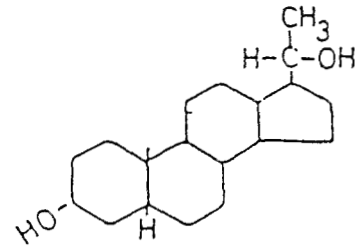
Metabolic differences among animals correlated with potential or ongoing production may be useful predictors of genetic merit for economic production traits (Peterson *et al.*, 1982). It seems that the association of doe rabbits performance with blood progesterone and protein patterns were not investigated so far. The purpose of the present study was to obtain estimates for the genetic parameters of efficacious and non-efficacious progesterone as indicator to improve productive and reproductive performance in rabbit population.

MATERIALS AND METHODS

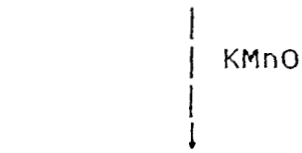
This work was carried out on Bauscat rabbits at San El-Hagar Agricultural Company Farm, San El-Hagar area, Sharkeya Province, Egypt. The animals were reared under similar environmental conditions. They were fed *ad libitum* on a commercial pelleted rabbit ration. The digestible energy was 2600 kcal per kg ration. Fresh water was provided all the time from automatic drinkers with nipples. The weaning age was 30 days. The performance traits included number of mating for conception (NMC); gestation period (GP); litter size (LSB), litter weight (LWB) and bunny weight at birth (BWB); stillbirths % (Sb%); preweaning mortality % (PWM %) and total mortality % (TM%).

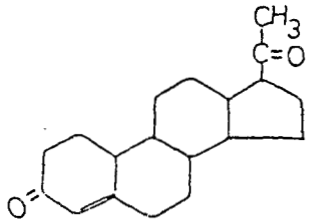
Blood samples (2 ml) were collected in glass tubes from marginal ear vein of each doe at 5, 11 and 15 days during the gestation period. One ml fresh urine was collected by catheterization at the same time. The blood samples were kept at 4°C for 12 hours in a refrigerator. Serum was separated by centrifugation for 20 minutes at 1000 xg and the serum was stored frozen (-20°C) until analysis. The progesterone levels (ng/ml) in serum and urine (SP & UP) were determined using the radioimm-unoassay kits from Diagnostic Products Corporation (Los Angeles). For estimating the efficacious progesterone, one milliliter of fresh urine was mixed with a drop of potassium permanganate ($KMn\ O_4$) 5 % for conversion of pregnanediol to progesterone by oxidation of the hydroxyl group (El-Darawany, 1992) as

shown below. Harrow and Mazur, (1968) reported that pregnanediol (Pregnane-3B, 20 diol) is the chief excretory product of progesterone and its presence in the urine indicates a progestational endometrium. Progesterone was detected by radioimmunoassay in urine after conversion. Efficacious progesterone level was that in urine and non-efficacious progesterone (NEP) level was obtained by subtracting the progesterone value in urine from its corresponding progesterone value in serum. Progesterone values followed by numbers 5, 11 and 15 days (SP5, SP11 and SP15) indicate days of blood collection during the gestation period. In serum samples at day 11 during gestation, estimations were carried out for total protein (TP) according to Weichselbaum (1946) and albumin (Alb) according to Doums *et al.* (1971).



Pregnane-3B,20 diol





Progesterone

Data on blood biochemical and performance traits of 686 does from 117 dams and 34 sires were statistically analyzed according to the following model: $Y_{ijklm} = \mu + S_i + D_{ij} + P_K + A_l + PA_{Kl} + e_{ijklm}$, where: Y_{ijklm} =blood biochemical or performance traits, μ = overall mean, S_i = a random effect associated with the *ith* sire assumed to be normally and independently distributed with expected mean zero and variance σ^2s, D_{ij} = a random effect associated with the *jth* dam nested within *ith* sire assumed to be normally and independently distributed with expected mean zero and variance σ^2d:s, P_k = effect due to k*th* parity of doe (k=1,... and 6), A_l = effect due to l*th* season of collection l=1,.. and 4 1=winter, 2=spring, 3=summer and 4=autumn), PA_{Kl} = Interaction of k*th* parity and l*th* season at collection, e_{ijklm} = a random residual component associated with the ijklm*th* observation assumed to be normally and independently distributed with expected mean zero and variance σ^2e.

Sire (σ^2s), dam within sire (σ^2d) and residual (σ^2e) components of variance were estimated by (Henderson's method 3) using SAS program (1989).The variance components (additive genetic variance V_A, common environ-ment {maternal effect} V_{EC} and residual environment V_{EW}) were partitioned from the sire V_A=4 σ^2s, dam within sire $V_{EC} = \sigma^2$d-σ^2s and residual $V_{EW} = \sigma^2$e-2σ^2s according to Falconer (1981). Heritability h^2 was estimated through the sire σ^2s, and dam within sire σ^2d and residual component of variances σ^2e, as $h^2 = 4\sigma^2s/(\sigma^2s+\sigma^2d+\sigma^2e)$. The repeatability coefficient (t) was calculated as, $t = (\sigma^2s+\sigma^2d)/(\sigma^2s+\sigma^2d+\sigma^2e)$. The genetic and phenotypic correlations were calculated by using paternal half-sib methods according to Harvey (1990).

RESULTS

The overall means ± S.E., coefficients of determination (R^2) and variations (C.V.%) and levels of significance from analysis of variance for productive traits,progesterone and protein patterns are given in Table 1. The sire and dam within sire effects were significant for performance and blood biochemical traits, except NMC, Sb, UP5, NEP5, NEP11 and Alb. Parity effect was significant for all performance traits and biochemical traits, except LSB, LWB, BWB, UP5, NEP5&15 and Glo. Seasons effects were significant for performance traits and not significant for all biochemical traits. Parity and season interactions were significant for GP, Sb and TM traits and not significant for all blood biochemical traits.

Table 1: Overall means ± S.E., coefficients of determination (R^2) and, variation (C.V.%) and source of variations for performance and biochemical traits.

Items	Overall mean ± S.D.	R^2 %	C.V. %	Source of variations				
				Sire	Dam:sire	Parity	Season	Parity* season interaction
Performance traits								
NMC(number)	1.73± 0.06	66.1	27.0	NS	NS	*	**	NS
GP (days)	31.33± 0.19	64.1	4.9	*	*	***	***	**
LSB(litter)	6.96± 0.35	81.3	31.0	**	*	NS	**	NS
LWB (gm)	425.22±18.96	81.0	26.9	*	*	NS	***	NS
BWB (gm)	62.78± 0.79	74.1	11.1	*	**	NS	**	NS
Sb (%)	1.11± 0.05	53.4	39.9	NS	NS	***	***	*
PWM (%)	0.76± 0.06	56.2	36.1	NS	*	**	*	NS
TM (%)	1.85± 0.10	55.0	38.6	NS	*	***	***	**
Progesterone patterns (ng/ml)								
SP5	5.97±0.13	76.4	12.4	***	***	***	NS	NS
SP11	13.06±0.30	70.5	14.7	***	**	***	NS	NS
SP15	5.73±0.16	80.5	13.7	***	**	***	NS	NS
UP5	5.56±0.10	59.0	18.4	NS	NS	NS	NS	NS
UP11	11.95±0.32	71.3	17.9	***	**	***	NS	NS
UP15	5.34±0.16	77.2	15.8	***	***	***	NS	NS
NEP5	0.41±0.05	60.0	34.0	NS	NS	NS	NS	NS
NEP11	1.11±0.07	67.6	37.8	NS	NS	***	NS	NS
NEP15	0.39±0.03	63.0	38.4	**	**	NS	NS	NS
Protein patterns (mg/dl)								
TP	6.27±0.04	68.1	5.5	*	*	***	NS	NS
Alb	4.23±0.03	69.3	7.7	NS	NS	***	NS	NS
Glo	2.04±0.04	65.0	14.4	***	**	NS	NS	NS
Alb/Glo ratio	2.13±0.05	66.5	19.9	*	**	***	NS	NS

Key to abbreviation for traits are given in Materials and methods
R^2 = Model sum of squares / total sum of squares.
***P<0.001, **P<0.01, *P<0.05, and NS = not significant.

Table 2 summarizes heritability (h^2), genetic (r_G) and phenotypic correla-tions (r_P) among some of reproductive and productive traits. Table 3 summarizes the genetic (r_G) and phenotypic correlations (r_P) among biochemical traits. The genetic (r_G) and phenotypic (r_P) correlations between blood biochemical traits and performance traits are shown in Table 4. Table 5 summarizes the heritability (h^2) and repeatability (t) of biochem-ical traits.

DISCUSSION

The overall means of biochemical traits (SP, UP, NEP, TP, Alb, Glo and Alb/Glo ratio) in this study agree with Corti *et al.* (1988) and El-Darawany (1992). Overall means of performance traits for Bauscat breed agree with Farghaly (1996a) for GP and Farghaly (1996b) for LSB.

The results from the analyses of variance show the importance of sire and dam within sire and parity effects on progesterone and protein patterns. The sire and dam within sire effects were significant (P<0.001&0.05) for many biochemical traits. These results indicated the possibility of genetic improvement for fertility traits by selection of sire.

Table 2: Heritability (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) among reproductive and productive traits.

	Characteristics numbers							
Characteristics	1	2	3	4	5	6	7	8
1. NMC	0.03 (0.06)	0.68	-0.37	-0.42	0.44	0	0.15	-0.03
2. GP	0.07	0.28 (0.19)	-0.71	-0.83	0.21	0	0.06	0.88
3. LSB	-0.14	-0.53	0.41 (0.15)	0.99	-0.64	0	-0.31	-0.15
4. LWB	-0.12	-0.55	0.97	0.42 (0.24)	-0.49	0	-0.38	-0.30
5. BWB	0.13	0.25	-0.63	-0.44	0.22 (0.17)	0	0.46	0.01
6. Sb	-0.04	0.25	-0.03	-0.08	-0.08	0	0	0
7. PWM	-0.004	0.20	0.02	0.02	0.008	0.07	0.07 (0.10)	0.47
8. TM	-0.02	0.31	-0.01	-0.05	-0.05	0.78	0.65	0.05 (0.08)

Standard errors (S.D.) are within parentheses on 2nd line of each row.
Phenotypic correlations (r_P) from 0.14 to 0.17: P<0.05, from 0.18 to 0.24: P<0.01 and > 0.24: P<0.001

Table 3: Estimates of genetic (above) and phenotypic (below diagonal) correlations for biochemical traits

Items	1	2	3	4	5	6	7	8	9	10	11	12	13
Progesterone													
1. SP5		0.94	0.98	0.95	0.93	0.96	0.53	-0.34	0.18	0.65	0.60	0.36	-0.32
2. SP11	0.87		0.94	0.90	0.99	0.97	0.77	-0.36	0.12	0.70	0.77	0.33	-0.21
3. SP15	0.88	0.84		0.96	0.97	0.99	0.36	-0.64	0.44	0.46	0.65	0.15	-0.10
4. UP5	0.80	0.75	0.72		0.89	0.88	0.76	-0.33	0.62	0.84	0.44	0.63	-0.64
5. UP11	0.87	0.93	0.84	0.73		0.99	0.75	-0.50	0.23	0.51	0.84	0.10	0.01
6. UP15	0.87	0.84	0.96	0.72	0.85		0.59	-0.55	0.30	0.53	0.72	0.19	-0.13
7. NEP5	0.02	-0.05	0.01	-0.57	-0.03	-0.004		-0.64	-0.88	0.63	0.50	-0.09	0.27
8. NEP11	-0.26	-0.12	-0.25	-0.19	-0.46	-0.27	-0.03		-0.73	0.89	-0.77	0.56	-0.24
9. NEP15	-0.11	-0.14	-0.03	-0.12	-0.17	-0.30	0.05	0.11		-0.25	-0.16	-0.18	0.13
Protein													
10. TP	0.54	0.59	0.55	0.44	0.55	0.57	-0.003	-0.08	-0.16		0.24	0.88	-0.79
11. Alb	0.60	0.62	0.56	0.49	0.66	0.61	-0.006	-0.29	-0.30	0.63		-0.24	0.42
12. Glo	-0.04	-0.01	0.02	-0.03	-0.09	-0.03	0.006	0.23	0.15	0.47	-0.39		-0.99
13. Alb/Glo ratio	0.23	0.21	0.18	0.20	0.30	0.24	-0.01	-0.30	-0.22	-0.14	0.66	-0.91	

Phenotypic correlations (r_P) from 0.14 to 0.17: P<0.05, from 0.18 to 0.24: P<0.01 and > 0.24: P<0.001

Table 5: Heritability and repeatability ± stander errors for biochemical traits.

Items	Heritability	Repeatability
Progesterone patterns		
SP5	0.31±0.09	0.53±0.21
SP11	0.19±0.07	0.45±0.19
SP15	0.39±0.13	0.74±0.26
UP5	0.13±0.06	0.44±0.16
UP11	0.28±0.11	0.41±0.14
UP15	0.44±0.16	0.60±0.23
NEP5	0.05±0.04	0.94±0.32
NEP11	0.08±0.06	0.49±0.10
NEP15	0.22±0.10	0.53±0.27
Protein patterns		
TP	0.05±0.06	0.22±0.10
Alb	0.06±0.04	0.56±0.21
Glo	0.19±0.07	0.31±0.13
Alb/Glo ratio	0.19±0.09	0.27±0.11

The low and negative r_P between the NMC and other traits may be due to the ovulation in doe rabbit having brought about by mating that causes physical stimulation of perineal, pudendal or vaginal areas of the doe. These results agreed with the findings reported by Ramirez and Beyer (1988). Litter mortality (Sb, PWM and TM) showed significant positive correlations with GP. Sb were highest in small LSB after a long GP. These results agreed with the findings reported by El-Darawany (1994) and Farghaly (1996a). The r_G between NMC and BWB were moderate and positive. The low h^2 of NMC, Sb, PWM and TM indicated a comparatively large influence of environ-mental effects, beside that improvement of these traits could be realized by improvement of management (Farghaly, 1996a).

The presence of pregnadiol in urine (UP) indicates a progestional endometrium (Harrow and Mazure, 1968). Therefore, the decline in UP (efficacious progesterone) concentration is accelerated in small LSB (El-Darawany, 1992). The r_P between LSB and each of SP and UP were positive and highly significant which confirms the above results. High r_G among SP, UP and NEP indicate the synergistic control of the same additive genes, influencing the biochemical traits studied.

The significant r_P between GP and both progesterone and protein patterns may be due to relationships between increasing LSB and increasing each of SP, UP, TP, Alb and Alb/Glo ratio. These results were in agreement with those reported by El-Darawany (1992). The high r_P between Sb and each of SP and UP may be due to relationships between progesterone level and embryonic mortality. These results were in agreement with those by Hafez (1987). The deficiency in TP and/or Alb may lead to insufficiency of the SP or efficacious progesterone and it could be considered as the main physiological aspect which affects adversely LSB and increase Sb. The significant r_P between protein and progesterone patterns obtained in the present study confirms the above results. These results agree with those reported by Arthur Guyton (1981) and Ayalon (1984) who clarified the relationships between the binding of progesterone to protein and endometrial cytosol in the female human and the cow, respectively. High r_G between SP5&15 and UP5&15 and each of LSB and LWB indicate that does having high levels of progest-erone in serum and urine tend to give higher LSB and LWB. Therefore selection according to the considered progesterone patterns would also improve the LSB and LWB.

The high repeatability (t) values for biochemical traits indicated that variation in external environmental conditions was low, thus decreasing temporary differences. Consequently, a single record may be sufficient to estimate the real potential and repeated measurements of biochemical traits are superfluous (Pirchner, 1983).

In conclusion, efficaci-ous progesterone was detected in fresh urine with a drop of $KMno_4$ (5%) for conversion of pregnandiol to progesterone. The genetic variation of biochemical traits appears to include non-additive components, but additive genetic components play an important part in the phenotypic variation of many traits studied. The high values of $h^2 > 0.19$ for SP (as indicator), as well as, positively high genetic correlations between these biochemical traits and each of performance

characteristics (LSB and LWB) and antagonistic relationships with litter mortality traits (Sb, PWM and TM) suggest that selection based on blood biochemical traits (as predictors production) would also improve the performance and decrease mortality traits in rabbit populations.

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Table 4. Genetic and phenotypic correlations (r_G and r_P) between biochemical traits and performance traits.

Items	Performance traits															
	NMC		GP		LSB		LWB		BWB		Sb		PWM		TM	
	r_P	r_G	r_P	r_G	r_P	r_G	r_P	r_G	r_P	r_G	r_P	r_G	r_P	r_G	r_P	r_G
Progesterone																
SP5	-0.10	-0.92	-0.48	-0.70	0.88	0.90	0.88	0.87	-0.52	-0.59	-0.06	0	-0.02	-0.10	-0.05	-0.09
SP11	-0.12	-0.12	-0.54	-0.66	0.90	0.91	0.91	0.98	-0.54	-0.71	-0.06	0	-0.02	-0.08	-0.05	-0.12
SP15	-0.11	-0.03	-0.49	-0.77	0.84	0.95	0.85	0.92	-0.48	-0.62	-0.12	0	-0.07	-0.06	-0.12	-0.14
UP5	-0.03	-0.12	-0.43	-0.50	0.73	0.89	0.73	0.77	-0.46	-0.85	-0.10	0	-0.01	-0.09	-0.08	-0.15
UP11	-0.08	-0.09	-0.60	-0.76	0.87	0.83	0.89	0.03	-0.50	-0.57	-0.17	0	-0.07	-0.09	-0.17	0.16
UP15	-0.09	-0.07	-0.51	-0.78	0.84	0.97	0.85	0.96	-0.47	-0.57	-0.18	0	-0.10	-0.05	-0.18	-0.11
NEP5	-0.09	-0.11	0.06	-0.08	-0.01	0.05	-0.004	0.08	0.05	-0.36	0.09	0	-0.01	-0.08	-0.07	-0.10
NEP11	-0.07	0.06	0.33	0.91	-0.18	-0.54	-0.21	-0.71	0.06	-0.55	0.32	0	0.16	0.64	0.35	0.41
NEP15	-0.04	-0.17	0.15	-0.28	-0.14	0.25	-0.15	0.13	0.03	-0.59	0.24	0	0.10	-0.17	0.24	0.37
Protein																
TP	-0.15	-0.39	-0.29	0.22	0.61	0.58	0.58	0.43	-0.45	-0.02	-0.05	0	0.004	-0.53	-0.04	-0.39
Alb	-0.11	-0.08	-0.42	-0.82	0.66	0.88	0.67	0.95	-0.38	-0.05	-0.28	0	-0.05	-0.48	-0.25	-0.13
Glo	-0.05	0.97	0.13	0.61	-0.03	0.16	-0.06	-0.03	-0.09	-0.99	0.26	0	0.06	-0.30	0.23	0.33
Alb/Glo ratio	-0.02	-0.06	-0.26	-0.62	0.26	-0.02	0.29	0.16	-0.06	0.91	-0.27	0	-0.09	0.41	-0.26	0.48

Phenotypic correlations (r_P) from 0.14 to 0.17: $P<0.05$, from 0.18 to 0.24: $P<0.01$ and > 0.24: $P<0.001$.