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Genetic analysis for semen traits in a crossing program of Saudi Aradi with Damascus goats

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ABSTRACT

A crossbreeding program between Aradi Saudi breed (A) of goats with Syrian Damascus breed (D) was practiced for six years in two experiments (dairy experiment in Jouf and meat experiment in Qassim) applying bio-techniques of estrous synchronization and artificial insemination. The breeding plan permitted to produce four genetic groups of AA, DD, ½D½A and ¾D¼A in each experiment separately. A total number of 1800 ejaculates collected from 298 bucks were evaluated for volume of ejaculate (EV), pH, sperm concentration (SC), total motile sperm (TMS), total sperm output (TSO), percentages of motile (MS), live (LS), abnormal (AS) and dead sperms (DS). Animal models were used to estimate the heritabilities and permanent environmental effects, while a generalized least square procedure was used to estimate individual additive genetic effects, individual heterosis, maternal heterosis and individual recombination effects. Heritabilities for most semen characteristics were low or somewhat moderate and ranging from 0.08 to 0.23, while the permanent environmental effects were slightly higher than the respective heritabilities since the estimates ranged from 0.10 to 0.29. Estimates of individual additive effects for SC, TMS and TSO were in favour of Damascus bucks relative to Aradi bucks by 0.2, 0.43 and 0.44×10^9 per ml in the dairy experiment and by 0.08, 0.13 and 0.11×10^9 per ml in the meat experiment, respectively. Significant individual heterotic improvements (with a range of 4.9–26.5%) were recorded in the dairy and meat experiments for EV (0.075 ml *vs.* 0.085 ml), SC (0.25×10^9 per ml *vs.* 0.11×10^9 per ml), TMS (0.275×10^9 per ml *vs.* 0.125×10^9 per ml), and TSO (0.33×10^9 per ml *vs.* 0.155×10^9 per ml), associated with significant reduction in percentage of DS (5.5% *vs.* 1.55%). Crossbred dams showed significant maternal heterotic improvements in semen of their crossbred bucks in both dairy and meat experiments for EV (0.058 ml *vs.* 0.055 ml; $P < 0.05$), SC (0.15×10^9 per ml *vs.* 0.09×10^9 per ml; $P < 0.05$), TMS (0.225×10^9 per ml *vs.* 0.085×10^9 per ml; $P < 0.05$), and TSO (0.58×10^9 per ml *vs.* 0.115×10^9 per ml; $P < 0.01$), associated with favourable significant increases in MS (3.3% *vs.* 4.05%; $P < 0.05$) and LS (3.7% *vs.* 2.25%; $P < 0.05$) along with a reduction in percentage of DS (4.3% *vs.* 2.25%; $P < 0.05$); the estimates ranging from 3.3 to 34.1%. The estimates of individual recombination losses for most semen parameters were favourable and non-significant.

1. Introduction

There are some biotechnologies that have been applied successfully in goats (such as artificial insemination, estrous synchronization and multiple ovulation rates) and these techniques could be used as new powerful and

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successful tools in planning breeding programmes to increase the rates of genetic improvement in goats and to multiply rapidly the populations of elite breeds (Evans, 1991; Baldassarre and Karatzas, 2004; Gama and Bressana, 2011). The application of AI in goats with either fresh or frozen semen has not been extensively investigated and it is still in their infancy stage in the Arabian countries. AI may be also regarded as one technique that has made the greatest contribution to genetic improvement programs, mainly due to well-established methods for identifying males with the highest genetic merit. To maximize the benefits from applying AI in genetic improvement programme, it is necessary to use only the semen of males producing the largest number of high quality doses (Evans, 1991; Baldassarre and Karatzas, 2004; Gama and Bressana, 2011). The number of inseminating doses produced from each ejaculate depends on the volume, sperm concentration, and motile sperm after freezing/thawing. Also, techniques of semen preservation (fresh, refrigerated and frozen) and insemination (vaginal, cervical and intrauterine) are considered as very important techniques in genetic improvement programme in goats (Leboeuf et al., 2000; Baldassarre and Karatzas, 2004).

As well known, it is necessary to have the knowledge of genetic parameters to be used in evaluating the bucks in a genetic improvement program (Barillet, 2007; Shrestha and Fahmy, 2007a,b; Furstoss et al., 2009). In order to improve also the genetic make up of goats, studying some semen characteristics is of most importance, as this will enhance proper selection of proven bucks. Since 2006, a goat project of crossing Aradi Saudi breed (A) with Damascus breed (D) was established in Saudi Arabia to develop new lines of dairy and meat goats suitable for hot climate (Khalil et al., 2010). This program was performed applying some biotechnological techniques to accelerate the rate of genetic gain. The main objective of the present study was to estimate the additive, heterotic and recombination effects for some semen parameters in such crossbreeding program involving a Saudi Aradi (A) and Damascus (D) goats. However, bucks of two-breeds cross could demonstrate considerable potentiality in improving the productivity of goats in developing countries (Valencia et al., 2005; Barillet, 2007; Fahmy and Shrestha, 2000; Shrestha and Fahmy, 2007a,b). Also, reviewed studies concerning genetic and crossbreeding analyses for semen quality traits in goats raised in hot climate countries are scarce.

2. Materials and methods

2.1. Breeding plan

A crossbreeding program between Aradi Saudi goats (A) with Syrian Damascus goats (D) was started in 2006 in Saudi Arabia. Two experiments were practiced, one of them to develop dairy line (named dairy experiment) in Jouf research station and the second experiment to develop meat line (named meat experiment) in Qassim University. In the dairy line, selection was practiced for milk production traits, while in the meat line selection was practiced for body weight and carcass traits. The two lines are being selected by a BLUP methodology under animal model, following the two criteria of selection. The hottest month of the year is August with an average high and low temperature of 41 °C and 25 °C, respectively, whereas January is the coldest month of the year, with an average high and low temperature of 15 °C and 4 °C, respectively. The annual rainfall ranges from 0 to 3 mm. Does of Aradi goats were randomly divided into two groups and each group of Aradi does was subdivided into two subgroups to be inseminated artificially from semen of elite bucks of the same breed and of Damascus breed (Table 1). In both experiments, does of Damascus breed were randomly artificially inseminated from bucks of the same breed to produce purebred kids. Also, crossbred does of ½D½A were backcrossed with Damascus bucks to get the genetic group of ¾D¼A. Accordingly, the breeding plan permitted to produce four genetic groups of AA, DD, ½D½A and ¾D¼A in each experiment separately and a total number of 1400 kids fathered by 115 sires and mothered by 517 dams were obtained as shown in Table 1.

2.2. Housing and feeding

Animals were housed in semi-shaded/open front barn and fed on a commercial concentrate and alfalfa hay. The amount of concentrate and hay were calculated according to the nutritional requirements for goats (kids, does and bucks) depending on the animal ages and production status (National Research Council; NRC, 1981). Water, straw, salt and minerals supplemented in blocks were freely available to all animals. Animals were fed *ad libitum* individually.

2.3. Semen collection and evaluation of semen traits

A total number of 1800 ejaculates collected by artificial vagina from 298 bucks of different genetic groups were evaluated for semen traits. Semen was collected 2–3 times monthly all the year round. Immediately after collection, the semen tubes were placed in a water bath at 37 °C and samples were evaluated for some semen characteristics which including pH, volume (ml), sperm cells concentration ($\times 10^9$/ml), total motile sperm ($\times 10^9$/ml), total sperm output ($\times 10^9$/ml), spermatozoa motility (%), abnormal spermatozoa (%), living spermatozoa (%) and dead spermatozoa (%). All these procedures were performed within 10 min of collection using the standard techniques described by Pirohit et al. (1992) and Al-Ghalban et al. (2004). pH is determined using a litmus paper strip roll between the range of 5.5–8.0 and precise pH matches at every 0.2 intervals. Ejaculate volume was determined using a transparent graduated glass collection tube. Sperm cells concentration determined using a spectrophotometer, previously calibrated with a haemocytometer. Individual motility determined by placing a drop of semen diluted with 0.9% sodium citrate on glass slide and a coverslip was then placed over it and observation performed for the percentage of progressively motile sperm using a bright field microscope at high magnification (400×). Sperm viability (live/dead) and morphological abnormalities were determined using semen smears stained with eosin–nigrosin and examined under oil immersion objective at 1000× magnification. A total of 100 spermatozoa were examined per slide for each ejaculate and the percentage of non-viable and abnormal sperm cells were calculated.

Table 1
Number of does and bucks used in mating and number of kids born.

Experiment	Does			Bucks		Total kids
	A	D	½D½A	A	D	
Dairy experiment (Jouf)	161	30	157	19	56	977
Meat experiment (Qassim)	81	23	65	15	25	423
Total	242	53	222	34	81	1400

A: Ardi and D: Damascus.

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2.4. Models of statistical and genetic analyses

Data of each experiment were analysed separately. The animal model used in analysing the semen parameters was (in matrix notation):

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_a u_a} + \mathbf{Z_p u_p} + \mathbf{e}$$

where **y** is the vector of observed semen parameter for bucks; **b** is the vector of fixed effects of genetic group of buck, age of buck, and year-season of semen collection; $\mathbf{u_a}$ is the vector of random additive effect of the buck; $\mathbf{u_p}$ is the vector of random effects of the permanent non-additive effect of the buck; **X**, $\mathbf{Z_a}$ and $\mathbf{Z_p}$ are the incidence matrices relating records to the fixed effects, additive genetic effects, and permanent environment, respectively; and **e** is the vector of random error. The inverse of the numerator relationship matrix ($\mathbf{A^{-1}}$) was considered and $\mathrm{Var}(\mathbf{a}) = \mathbf{A}\sigma_a^2$, $\mathrm{Var}(\mathbf{p}) = \mathbf{I}\sigma_p^2$ and $\mathrm{Var}(\mathbf{e}) = \mathbf{I}\sigma_e^2$ were estimated where σ_A^2, σ_p^2 and σ_e^2 are variances due to the effects of individual additive effect, permanent environment, and random error, respectively. Inbreeding coefficients for progeny, sires and dams were calculated using program of Boldman et al. (1995). Heritabilities for different traits were computed from variance components estimated by **DFREML** of the animal model using the following equation: $h_A^2 = \sigma_A^2/(\sigma_A^2 + \sigma_p^2 + \sigma_e^2)$.

The procedure of generalized least squares (GLS) using CBE program of Wolf (1996) were used to estimate crossbreeding effects. Model of Dickerson (1973) were used in the program as summarized by Dickerson (1993) and Wolf et al. (1995). The linear model used was:

$$\mathbf{y} = \mathbf{X}\boldsymbol{b} + \mathbf{e},\ \mathbf{Var}(\mathbf{y}) = \mathbf{V}$$

where **y** is the vector of genetic groups means, **X** is the incidence matrix of the coefficients for crossbreeding effects, **b** is the vector of crossbreeding genetic parameters, **e** is the vector of residual effects, and **V** is the full covariance matrix of **y**. The coefficients relating genetic crossbreeding parameters to the means of the genetic groups are shown in Table 2 (Wolf et al., 1995). Because the reciprocal cross of Ax D was not carried out, the maternal additive effects showed a high co-linearity with the individual additive effects because the corresponding errors are highly correlated. For this reason, maternal additive effects were excluded from the model and the estimates of individual additive effects were interpreted as a balance between individual and maternal additive effects. Crossbreeding parameters of individual additive effects and individual and maternal heterosis were estimated using the CBE program of Wolf (1996). The parameters estimated are representing differences between lines in terms of individual additive genetic effects ($G^I = G_A^I - G_D^I$), individual heterosis (H^I), maternal heterosis (H^M) and individual recombination effects (R^I). Thus, we have four parameters to be estimated (a vector called **b**-vector): $\mathbf{b} = [(G_A^I - G_D^I) \quad H^I \quad H^M \quad R^I]$.

The estimates of **b** were calculated by the method of generalized least squares (GLS) using the following equation: $\hat{\mathbf{b}} = (\mathbf{X}/\mathbf{V}^{-1}\mathbf{X})^{-1}\mathbf{X}/\mathbf{V}^{-1}\mathbf{y}$.

3. Results and discussion

3.1. Means and variations

Means and standard deviations (SD) of semen traits for bucks used in the dairy and meat experiments are presented in Table 3. Estimates of semen parameters obtained in the present study were of normal limits and similar to those obtained by Chauhan and Anand (1990), Azawi et al. (1993), Ritar (1993), Singh and Purbey (1996), and Watson (2000). In most cases, bucks of the dairy experiment resulted in better semen characteristics compared to bucks of the meat experiment (Table 3). In both experiments, estimates of the semen parameters were encouraging in terms of ejaculate volume, sperms concentration, percentages of motile sperms, total motile sperms, and total sperm output.

3.2. Heritability and permanent environmental effects

Heritabilities estimated for most semen characteristics were low or somewhat moderate; ranging from 0.08 to 0.23 in the dairy experiment and from 0.10 to 0.19 in the meat experiment (Table 4). Accordingly, improvement in some semen characteristics of bucks could be achieved through selection of bucks based on their semen performance. Recently, Furstoss et al. (2009) found that heritabilities for concentration, number of spermatozoa, semen volume, motility score after freezing and percentage of motile spermatozoa after freezing per ejaculate were 0.32, 0.15, 0.25, 0.12 and 0.05 for the Saanen breed and 0.34, 0.25, 0.29, 0.17 and 0.03 for the Alpine breed, respectively.

Permanent environmental effects for semen traits were slightly higher than the respective heritabilities since the estimates ranged from 0.11 to 0.23 in the dairy experiment and from 0.10 to 0.29 in the meat experiment (Table 4).

3.3. Genetic groups' comparisons

Damascus bucks were not significantly different from Aradi bucks in most semen parameters of the dairy and meat experiments (Table 5). Volume of ejaculate and sperms concentration obtained for different genetic groups in the present study were lower than those recorded for Murciano-granadina breed (Roca et al., 1991, 1992). As cited in the literature, volume and number of sperms per ejaculate declined significantly in successive ejaculates (Prado et al., 2003). In both dairy and meat experiments, semen of ½D½A and ¾D¼A bucks showed positive and favourable effects on percentages of motile sperms, live sperms, and dead sperms, total motile sperms and total sperm output (Table 5), which could affect positively the conception rate. Volumes of semen ejaculates for the bucks of ½D½A and ¾D¼A were high although the semen was collected from some bucks of young age.

Although the semen samples were collected from bucks at an early age (8–10 months), volume of semen ejaculate, sperm concentration and motile sperms for all genetic groups were high. Differences among genetic groups in

Table 2
Genetic groups of bucks with their sires and dams and coefficients of the matrix relating genetic group means of bucks with crossbreeding parameters.

Genetic group				Mean	Coefficients of the matrix				
Kid	Sire	Dam	Grand-dam		D_A	D_D	H^I	H^M	R^I
AA	A	A		1	1	0	0	0	0
DD	D	D		1	0	1	0	0	0
½D½A	D	A		1	.5	.5	1	0	0
¾D¼A	D	½D½A	A	1	0.25	0.75	.5	1	0.25

D_A and D_D = individual additive genetic effects for the Aradi breed and the Damascus breed, respectively; H^I = individual heterosis; H^M = maternal heterosis; R^I = individual recombination genetic loss.

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Table 3
Means, standard deviations (SD) for semen traits of bucks used in the dairy and meat experiments.

Semen trait	No. of records	Mean	SD
Dairy experiment:	(Number of bucks = 204)		
Ejaculate volume, ml	1438	1.35	0.48
pH of semen	1364	7.14	0.18
Sperms concentration, $\times 10^9$ per ml	1323	3.57	1.40
Total motile sperms, $\times 10^9$ per ml	1182	3.45	2.12
Total sperm output, $\times 10^9$ per ml	1320	4.71	2.42
Sperms motility, %	1256	69.93	18.40
Live sperms, %	647	8.32	8.27
Abnormal sperms, %	1246	25.32	18.66
Dead sperms, %	1182	4.45	2.12
Meat experiment:	(Number of bucks = 94)		
Ejaculate volume, ml	362	1.22	0.70
pH of semen	362	7.05	0.43
Sperms concentration, $\times 10^9$ per ml	362	2.36	1.06
Total motile sperms, $\times 10^9$ per ml	357	2.39	1.91
Total sperm output, $\times 10^9$ per ml	360	3.91	2.12
Sperms motility, %	362	75.08	19.82
Live sperms, %	362	12.37	7.79
Abnormal sperms, %	362	20.58	17.74
Dead sperms, %	362	3.35	1.91

sperms abnormalities and dead sperms were significant (Table 5). Wide variations in the figures of semen parameters between genetic groups used might be due to: (1) volume of semen ejaculate varies from 0.6 to 3.1 ml depending on secretion of accessory sex glands, (2) sperms concentration ranged from 1.69×10^9 to 4.70×10^9/ml, and (3) pH ranged from 6.6 to 7.3 and this is a good index to estimate semen quality. In general, semen parameters for different genetic groups were close to what found in other studies (Nizza et al., 2003; Prado et al., 2003). The favourable estimates of dead sperms and abnormal sperms in all genetic groups of the present study are within the ranges of some reviewed studies in goats (Azawi et al., 1993; Arroita et al., 2000; Karagiannidis et al., 2000).

Crossbred bucks of ½D½A and ¾D¼A were associated with favourable estimates for most semen characteristics compared to purebred bucks (Table 5). For pooled data of crossbreds *vs.* purebreds, improvement rates in semen parameters of crossbred bucks were better than the average of purebreds in terms of ejaculate volume, sperms concentration, total sperm output, motile sperms, abnormal sperms, and dead sperms. Improvements obtained in semen parameters for crosses were expected and could be useful especially if one likes to use the semen of crossbred bucks on a large scale in artificial insemination programs. These improvements achieved in crossbred bucks of the present study could be explained on the basis that crossbreeding affects positively growth rate of the whole body (Khalil et al., 2010) and this leads to an early maturation of

Table 4
Proportions of the phenotypic variance due to genetic additive effects (h^2) and to permanent non-additive environmental effects (p^2) and random error (e^2) for semen traits in the dairy and meat experiments.

Semen trait	$h^2 \pm$ SE	$p^2 \pm$ SE	$e^2 \pm$ SE
Dairy experiment:	(Number of records = 1438, number of bucks = 204)		
Ejaculate volume	0.10 ± 0.11	0.17 ± 0.10	0.73 ± 0.04
pH of semen	0.08 ± 0.08	0.23 ± 0.08	0.69 ± 0.04
Sperms concentration	0.20 ± 0.11	0.15 ± 0.09	0.65 ± 0.04
Total motile sperms	0.09 ± 0.09	0.23 ± 0.09	0.68 ± 0.04
Total sperm output	0.17 ± 0.09	0.12 ± 0.08	0.71 ± 0.04
Sperms motility	0.09 ± 0.13	0.16 ± 0.12	0.75 ± 0.04
Live sperms	0.09 ± 0.20	0.14 ± 0.16	0.74 ± 0.09
Abnormal sperms	0.23 ± 0.27	0.23 ± 0.26	0.54 ± 0.04
Dead sperms	0.15 ± 0.14	0.11 ± 0.12	0.74 ± 0.05
Meat experiment:	(Number of records = 362, number o f bucks = 94)		
Ejaculate volume	0.13 ± 0.24	0.21 ± 0.24	0.66 ± 0.07
pH of semen	0.18 ± 0.20	0.10 ± 0.18	0.72 ± 0.07
Sperms concentration	0.18 ± 0.17	0.18 ± 0.16	0.64 ± 0.06
Total motile sperms	0.14 ± 0.15	0.20 ± 0.13	0.66 ± 0.06
Total sperm output	0.19 ± 0.16	0.20 ± 0.13	0.61 ± 0.07
Sperms motility	0.11 ± 0.10	0.15 ± 0.12	0.74 ± 0.06
Live sperms	0.10 ± 0.12	0.14 ± 0.16	0.76 ± 0.09
Abnormal sperms	0.11 ± 0.15	0.27 ± 0.12	0.62 ± 0.06
Dead sperms	0.12 ± 0.12	0.29 ± 0.10	0.59 ± 0.06

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Table 5
Least-square means and tests of significance for semen traits in different genetic groups of the dairy and meat experiments.

Semen trait	Aradi (A)	Damascus (D)	½D½A	¾D¼A
Dairy experiment:	(Number of records = 1438, number of bucks = 204)			
Ejaculate volume, ml	1.55 ± 0.02a	1.46 ± 0.04b	1.58 ± 0.05a	1.56 ± 0.04a
pH of semen	7.1 ± 0.01a	7.1 ± 0.01a	7.2 ± 0.02a	7.1 ± 0.02a
Sperms concentration, $\times 10^9$ per ml	3.6 ± 0.08ab	3.5 ± 0.11a	3.8 ± 0.16b	3.7 ± 0.12ab
Sperms motility, %	79.1 ± 1.9a	79.5 ± 2.3a	84.8 ± 3.0b	81.6 ± 2.5a
Live sperms, %	80.9 ± 2.01b	86.9 ± 2.17a	88.4 ± 2.88a	87.6 ± 2.56a
Abnormal sperms, %	7.3 ± 1.4a	8.1 ± 1.6a	8.2 ± 1.9a	11.1 ± 1.6b
Dead sperms, %	20.9 ± 1.9a	20.5 ± 2.2a	15.2 ± 3.0b	16.4 ± 2.5b
Total motile sperms, $\times 10^9$ per ml	4.23 ± 0.22a	3.80 ± 0.26b	4.29 ± 0.34a	4.24 ± 0.27a
Total sperm output, $\times 10^9$ per ml	5.53 ± 0.16a	5.09 ± 0.21b	5.64 ± 0.31a	5.89 ± 0.24c
Meat experiment:	(Number of records = 362, number o f bucks = 94)			
Ejaculate volume, ml	1.16 ± 0.52b	1.23 ± 0.06a	1.28 ± 0.08a	1.25 ± 0.09a
pH of semen	7.13 ± 0.03a	7.07 ± 0.04a	7.01 ± 0.04a	7.13 ± 0.05a
Sperms concentration, $\times 10^9$ per ml	2.53 ± 0.08a	2.61 ± 0.11a	2.68 ± 0.13a	2.66 ± 0.15a
Sperms motility, %	74.1 ± 1.7a	74.2 ± 2.1a	75.7 ± 2.6a	78.2 ± 3.1b
Live sperms, %	78.1 ± 3.2a	78.2 ± 2.8a	79.7 ± 3.2a	78.4 ± 3.4a
Abnormal sperms, %	13.2 ± 0.7a	12.1 ± 0.8a	12.9 ± 1.0a	15.2 ± 1.2b
Dead sperms, %	21.9 ± 1.3a	21.8 ± 1.7a	20.3 ± 2.1a	21.6 ± 2.4a
Total motile sperms, $\times 10^9$ per ml	2.55 ± 0.15a	2.58 ± 0.19a	2.69 ± 0.23b	2.65 ± 0.28b
Total sperm output, $\times 10^9$ per ml	3.12 ± 0.16a	3.13 ± 0.20a	3.85 ± 0.25b	3.24 ± 0.30c

Values having different letters (a, b) within each row are significantly different ($P < 0.05$).

the hypothalamus and the pituitary, which directly affects the growth of testes and finally the performance of the bucks.

3.4. Crossbreeding effects

3.4.1. Individual additive genetic effects

Estimates of individual additive effects for semen traits (expressed as differences of and Aradi breed minus Damascus) are presented in Table 6. The estimates for sperms concentration, total motile sperms and total sperm output were in favour of Damascus bucks by 0.2, 0.43 and 0.44×10^9 per ml in the dairy experiment and by 0.08, 0.13 and 0.11×10^9 per ml in the meat experiment, respectively (Table 6). The positive estimates of individual additive effects (expressed as percentages relative to the founder breeds in both experiments) for percentages of sperms motility and liveability and the negative estimate for the percentage of dead sperms were favourable and in favour of Damascus bucks. In the meat experiment, individual additive effects were also in favour of Damascus bucks by 5.8% for ejaculate volume, 3.1% for sperms concentration, and 8.6% for abnormal sperms relative to Aradi bucks. Garcia-Tomás et al. (2006a,b) stated that differences in individual genetic effects between two sire lines (C and R) in rabbits were significant and relevant for some semen production traits (*e.g.* concentration and total number of spermatozoa per ejaculate) and some semen quality traits (*e.g.* percentages of sperms viability, percentage of spermatozoa with normal apical ridge, percentage of sperm morphological abnormalities of neck-mid-piece and percentage of sperm with proximal cytoplasmatic droplet) and those differences were of high magnitude (about 50% of the actual mean) and in favour of line C for sperms concentration and total number of spermatozoa per ejaculate.

3.4.2. Individual heterosis

In both experiments, crossbred bucks obtained from crossing Aradi does with Damascus bucks were associated with considerable heterotic effects on most semen parameters (Table 7). Excluding pH, the estimates of individual

Table 6
Estimates of differences between Damascus and Aradi breeds in individual additive effects and their standard errors ($D^I \pm SE$) for semen traits in the dairy and meat experiments.

Semen trait	Dairy experiment $D^I = (D^I_D - D^I_A)$			Meat experiment $D^I = (D^I_D - D^I_A)$		
	Estimate	SE	D^I %[a]	Estimate	SE	D^I %[a]
Ejaculate volume, ml	−0.09*	0.038	−5.9	0.07*	0.022	5.8
pH of semen	0	0	0	−0.06	0.298	−0.8
Sperms concentration, $\times 10^9$/ml	0.2	0.52	5.4	0.08	4.23	3.1
Total motile sperms, $\times 10^9$/ml	0.43**	0.25	10.7	0.13	0.06	3.1
Total sperm output, $\times 10^9$/ml	0.44**	0.28	8.2	0.11	0.52	2.3
Sperms motility, %	0.4	1.16	0.5	0.1	1.65	0.1
Live sperms, %	6.0*	1.76	7.1	0.1	1.68	0.1
Abnormal sperms, %	0.8**	0.24	10.3	−1.1**	0.72	−8.6
Dead sperms, %	−0.4	0.18	−1.9	−0.1	0.32	−0.4

[a] $D^I\% = [D^I \text{ in units}/(\text{average of purebreds})] \times 100$.
* $P < 0.05$.
** $P < 0.01$.

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Table 7
Estimates of individual heterosis and their standard errors ($H^I \pm SE$) for semen traits in the dairy and meat experiments.

Semen trait	Dairy experiment			Meat experiment		
	Units	SE	H^I %[a]	Units	SE	H^I %[a]
Ejaculate volume, ml	0.075*	0.052	4.9	0.085**	0.03	7.1
pH of semen	0.1	0	1.4	−0.09	0.21	−1.2
Sperms concentration, $\times 10^9$/ml	0.25**	0.21	7.0	0.11*	0.06	4.2
Total motile sperms, $\times 10^9$/ml	0.275*	0.12	6.8	0.125*	0.07	4.8
Total sperm output, $\times 10^9$/ml	0.33*	0.09	6.2	0.155*	0.10	4.9
Sperms motility, %	5.5*	0.86	6.9	1.55	0.6	2.0
Live sperms, %	4.5*	1.32	5.3	1.55	1.42	1.9
Abnormal sperms, %	0.5*	0.06	6.4	0.25	0.52	1.9
Dead sperms, %	−5.5**	0.54	−26.5	−1.55**	0.45	−7.0

[a] $H^I\% = [H^I \text{ in units}/(\text{average of purebreds})] \times 100$.
* $P < 0.05$.
** $P < 0.01$.

heterosis for semen parameters expressed as percentages relative to the parental purebreds have shown a range of 4.9 to −26.5 in the dairy experiment and from 1.9 to 7.1% in the meat experiment.

As shown in Table 7, significant increases in the dairy experiment were recorded for ejaculate volume (0.075 ml), sperms concentration (0.25×10^9 per ml), total motile sperms (0.275×10^9 per ml), and total sperm output (0.33×10^9 per ml), associated with significant increases in sperms motility (5.5%) and live sperms (4.5%) along with a lesser percentage of dead sperms (5.5%). In the meat experiment, positive and significant estimates were recorded for ejaculate volume (0.085 ml), sperms concentration (0.11×10^9 per ml), total motile sperms (0.125×10^9 per ml), and total sperm output (0.155×10^9 per ml), associated with a significant reduction in dead sperms (1.55%). One of the explanations for positive heterotic effects in percent of sperm motility could be that sexual maturation in crossbred bucks was faster than in purebred bucks. García-Tomás et al. (2006a,b) found high variabilities in the estimates of individual heterosis for several semen characteristics, being practically negligible for sperm normalcy (about 2%) but very high for the percentage of spermatozoa with presence of cytoplasmatic droplet (57%).

3.4.3. Maternal heterosis (H^M)

In both experiments, the estimates of maternal heterosis for semen characteristics were significant and favourable for eight traits out of nine (Table 8). Crossbred dams in both experiments showed significant improvements in most semen parameters of their crossbred bucks progeny. In the dairy experiment, considerable increments were recorded in ejaculate volume (0.058 ml; $P < 0.05$), sperms concentration (0.15×10^9 per ml; $P < 0.05$), total motile sperms (0.225×10^9 per ml; $P < 0.05$), and total sperm output (0.58×10^9 per ml; $P < 0.01$), associated with favourable significant increases in motile perms (3.3%; $P < 0.05$) and live sperms (3.7%; $P < 0.05$) along with a lesser percentage of dead sperms (4.3%; $P < 0.01$). Similar trend was recorded in the meat experiment where crossbred bucks produced from crossbred dams recorded positive and significant estimates for ejaculate volume (0.055 ml; $P < 0.05$), sperms concentration (0.09×10^9 per ml; $P < 0.05$), total motile sperms (0.085×10^9 per ml; $P < 0.05$), and total sperm output (0.115×10^9 per ml; $P < 0.05$), associated with favourable significant increments in motile perms (4.05%; $P < 0.05$) and live sperms (2.25%; $P < 0.05$) along with a reduction in percentage of dead sperms (2.25%; $P < 0.05$).

The estimates of maternal heterosis expressed as percentages relative to the founder breeds for semen parameters were significantly moderate or high and ranging from 3.8 to 34.1% in the dairy experiment and 3.3–20.1% in the meat experiment. These favourable estimates of maternal heterosis show the interest of using crossbred dams to

Table 8
Estimates of maternal heterosis and their standard errors ($H^M \pm SE$) for semen parameters in the dairy and meat experiments.

Semen trait	Dairy experiment			Meat experiment		
	Units	SE	H^M %[a]	Units	SE	H^M %[a]
Ejaculate volume, ml	0.058*	0.018	3.8	0.055*	0.024	4.6
pH of semen	0.02	0.096	0.2	0.03	0.076	0.4
Sperms concentration, $\times 10^9$/ml	0.15*	0.039	4.2	0.09*	0.024	3.5
Total motile sperms, $\times 10^9$/ml	0.225*	0.086	5.6	0.085*	0.016	3.3
Total sperm output, $\times 10^9$/ml	0.58**	0.092	10.9	0.115*	0.059	3.6
Sperms motility, %	3.3*	0.164	3.9	4.05*	0.245	5.4
Live sperms, %	3.7*	0.336	4.4	2.25*	0.656	3.3
Abnormal sperms, %	2.4**	0.514	34.1	2.55**	0.456	20.1
Dead sperms, %	−4.3**	0.848	−20.7	−2.25*	0.245	−3.1

[a] $H^M\% = [H^M \text{ in units}/(\text{average of purebreds})] \times 100$.
* $P < 0.05$.
** $P < 0.01$.

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Table 9
Estimates of individual recombination loss (R^{l}) and their standard errors (±SE) for semen traits in the dairy and meat experiments.

Semen trait	Dairy experiment Loss ± SE	Meat experiment Loss ± SE
Ejaculate volume, ml	0.24 ± 0.15*	0.42 ± 0.18*
pH of semen	0.0	−0.04 ± 0.15
Sperms concentration, $\times 10^9$/ml	0.24 ± 0.08*	0.28 ± 0.06*
Total motile sperms, $\times 10^9$/ml	0.45 ± 0.32	0.87 ± 0.64
Total sperm output, $\times 10^9$/ml	1.62 ± 0.46*	0.94 ± 0.48*
Sperms motility, %	0.82 ± 0.65	0.45 ± 0.34
Live sperms, %	2.5 ± 1.52	0.48 ± 0.36
Abnormal sperms, %	0.66 ± 0.38	−0.64 ± 0.14
Dead sperms, %	−1.46 ± 0.86	0.92 ± 0.62

* $P < 0.05$.

produce crossbred bucks, *i.e.* crossbred dams could produce crossbred bucks characterized by high volume of ejaculate, high semen quality with more concentration and motile sperms, along with low percentages of abnormal and dead sperms.

3.4.4. Individual recombination effects

Estimates of individual heterosis for the majority of the studied traits (Table 7) were generally larger than the estimates of individual recombination effects (Table 9). Estimates of individual recombination losses for six traits out of nine of the semen parameters were non-significant. These favourable estimates indicate that epistatic recombination losses for these traits in crossbred bucks were of limited importance. In both experiments, individual losses in heterosis were recorded in three traits out of nine for ejaculate volume (0.24 and 0.42 ml), sperms concentration (0.24 and 0.28×10^9 per ml) and total sperm output (1.62 and 0.94×10^9 per ml). The significant estimates of recombination effects in some traits indicate that dominance effects on semen performance were dissipated by recombination losses. In goats, values in literature for recombination loss often are not significant or are significant but small (Mugambi et al., 2007). In general, the two-locus model of heterosis reflects dominance effect and half additive-by-additive interaction effects whereas the recombination effect included only half of the additive-by-additive interaction effects (Dickerson, 1993).

4. Conclusions

Individual additive effects for most semen traits studied were in favour of Damascus breed relative to the Aradi breed. Crossing Damascus (D) with Aradi (A) goats in hot climatic countries could produce crossbred bucks (½D½A and ¾D¼A) with reasonable semen parameters. The favourable estimates of individual and maternal heterosis obtained for most semen traits would be an encouraging factor for the goat producers in hot climate countries to use crossbred bucks on commercial scale.

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