

Applications of bio-techniques in genetic improvement programs to synthesize new lines of small animals in the Arabian countries

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Abstract

A crossbreeding program between Ardi Saudi goats (A) with the Syrian goats (Damascus, D) was started in 2006 in two experiments (Jouf and Qassim) applying bio-techniques of estrous synchronization and artificial insemination to improve milk and meat production. In rabbits, few numbers of new lines were synthesized in our Arabian countries using different criteria and methods of selection and crossbreeding. In this concept, Saudi 2 and APRI rabbits (as maternal lines) and Alexandria and Saudi 3 (as paternal lines) and Moshtohor (as multipurpose line) were being formed to be convenient in hot climate. The most common selection criteria used in selection programs to develop new maternal lines were related with litter size at birth or at weaning and milk production, while in paternal lines, post-weaning daily gain or marketing weight are commonly selected individually. Spanish V-line rabbits genetically selected for more than 35 generations were introduced in various developing countries (as alive animals or as frozen embryos) and by using recent bio-techniques and applying selection and /or crossbreeding programs with local lines, this line was widely distributed in some hot countries of the world like Egypt and Saudi Arabia.

In rabbits, direct selection had little or moderate effects on litter and lactation traits, while it had considerable effects on post weaning growth and feed conversion. Direct heterotic effects were evidenced for litter size, litter weight, and milk yield. Crossbred does and dams gave favourable heterotic effects on litter traits, milk yields and components and milk conversion ratio. Direct heterosis for body weights raised in hot countries were mainly positive and ranging from 1.3 to 14.5 %, but the estimates for maternal heterosis were mainly low and ranging from 0.2 to 5.3 %. Crossbred dams gave moderate maternal heterotic effects ranging from 4.8 to 18.7%. Neither individual heterosis, nor maternal heterosis were evidenced for meat quality traits. Crossbred bucks were associated with an existence of heterotic effects in ejaculate volume (11.6%), sperm concentration (10.5 %), percentages of motile (9.8%) and living sperms, along with a reduction in percentages of abnormal (-10.8%) and dead sperms (-23.5%). Crossbred dams gave maternal heterotic effects on some semen parameters in their progeny of crossbred bucks. The recent molecular technologies were used only in developing countries to detect the associations between phenotypic traits and genetic markers and three markers were detected for litter and milk traits and body weights.

In goats, The favourable estimates of direct and maternal heterosis for some litter and lactation traits and most growth traits would be an encouraging factor for the goat producers in hot climate countries to use crossbred does and dams on commercial scale. Crossbred dams had considerable maternal heterotic improvements in their crossbred daughters in terms of larger litter size, heavier litter weight at birth and weaning, pre-weaning mortality and milk production and components (2.4 to 28.1 %). Crossbred dams could produce crossbred bucks characterized by higher volume of ejaculate, higher semen quality with more concentration and motile sperms, along with lesser percentages of abnormal sperms and dead sperms than their crossbred daughters. Direct recombination losses were of little importance for the majority of the traits and they were generally lower than the estimates of direct heterosis.

Keywords: Small Animals, Bio-techniques, Genetic improvement programs, Selection, Crossbreeding, Synthetic lines.

Introduction

Nowadays, synthetic lines are being developed in hot climate countries by crossbreeding and selection for defined objectives (El-Raffa, 2007; Khalil and Al-Saef 2008; Youssef *et al.*, 2008; Iraqi *et al.*, 2009). These lines, depending on their specialization, perform better than the standard of the original breeds and the current production tends to rely on them. In our Arabian

countries, little numbers of synthetic maternal and paternal lines of rabbits were synthesized using different criteria and methods of selection and crossbreeding (Al-Seaf *et al.*, 2008).

Long-term selection experiments carried out in rabbits for more than 10 generations were few (El-Raffa, 2000; Khalil *et al.*, 2005; Youssef *et al.*, 2008; Iraqi *et al.*, 2009). Nowadays, synthetic lines are being formed in Egypt and Saudi Arabia by crossbreeding and

selection for defined objectives (El-Raffa, 2007; Khalil and Al-Saef 2008; Youssef *et al.*, 2008; Iraqi *et al.*, 2009). Some attempts to develop new lines already done and V-line has proved to be advantageous to standard Californian and New Zealand White for litter size traits and daily gain (Iraqi *et al.*, 2006). Recently in Egypt, new synthetic lines of rabbits called Moshtohor and APRI as maternal lines and Alexandria as a paternal line were being formed to be convenient in hot climate. Till now, multi-purpose synthetic lines were not formed to be used on small and large scales. Three-way crossing will be beneficial in this concept. This scheme has the advantage of exploiting at each generation the entirety of the effect of heterosis (direct and maternal), but it requires a complex scheme, based on the maintenance and selection of the pure stocks and the multiplication and diffusion of the crossbred bucks and does. This program makes possible to provide farmers with improved animals, while ensuring their independence.

In order to improve the productivity of goats, there is a great deal to increase the productivity of native goat breeds in our Arabian area through crossbreeding programs. In the last two decades, new assisted reproductive technologies in goats had been applied successfully (Lazaris *et al.*, 2002; Wheeler *et al.*, 2003; Baldassarre and Karatzas, 2004). In this concept, artificial insemination and estrus synchronization could be used as new powerful and successively tools in planned breeding programmes to increase the rates of genetic improvement in goats (Thibier, 1996; Leboeuf *et al.*, 2000, 2003).

The main objectives of this article are concentrated in evaluating sustainable genetic improvement programs in the Arabian countries in terms of: (1) programs of selection and crossbreeding used to develop new synthetic lines; (2) estimates of selection responses obtained; (3) direct and maternal heterotic improvements obtained from crossbreeding; (4) Molecular analyses and attempts to identify the specific genetic markers.

Genetic improvement programs achieved in the Arabian countries

In practice, the following programs were used to improve the farm animals genetically in our Arabian countries (Khalil and Al-Saef, 2008; Khalil *et al.*, 2011):

Producing specialized strains that are selected to produce F1 females, which are crossed with a sire of another strain to produce terminal product. This method has the advantage of exploiting at each generation the entirety of the effect of heterosis (direct and maternal), but it requires a complex scheme, based on the maintenance and selection of the pure

stocks and the multiplication and diffusion of the crossbred females. It is the reason why these turnkey programs are rarely used in developing countries, except in some small or large scale projects in Egypt and Saudi Arabia. They need an important investment and create a technical and economical dependence which does not usually fit the social and economical environment.

Creating a synthetic line by crossing females of a local population or breed (well adapted to the environment) with imported males or semen from a selected strain to produce F1 population; it will be bred without selection during few generations, avoiding consanguinity, and constitute a nucleus submitted to selection. This program makes possible to provide farmers with improved animals, while ensuring their independence. It lets to the farmers to adapt their strategy of renewal of their herd and they can practise self-replacement without loss of the genetic level, buying males or the two sexes to the nucleus.

Selection within pure local breeds. This program is less used, for different reasons: local populations performances are usually very low, even if they are well adapted and imported breeds often do not adapt to poor environments and, in both cases, heterosis are not completely exploited.

In rabbits:

Summaries for lines developed in Egypt and Saudi Arabia through crossbreeding and selection are presented in Tables 1, 2 and 3.

In Saudi Arabia, a national project of rabbit production was established to detect the possibilities of producing meat rabbits under industrialized and hot conditions (Khalil *et al.*, 2002, 2005). For this reason, special emphases were paid to construct a genetic improvement programme to develop new lines of meat rabbits convenient for this hot country. Accordingly, V-line rabbits were imported in 2000 from Spain and were crossed with desert Saudi rabbits (Gabali, G). This program was based on an evidences stating that V-line rabbits and their crosses could produce efficiently under hot climatic conditions (Khalil *et al.* 2002; Al-Sobayil and Khalil 2002). From this program, two synthetic lines (Saudi-2 as a maternal line with the structure of $((\frac{3}{4}V\frac{1}{4}S)^2)^2$ and Saudi-3 as a paternal line with the structure of $((\frac{3}{4}S\frac{1}{4}V)^2)^2$) were developed from crossing Saudi Gabali with V-line rabbits, both selected for litter weight at weaning and individual weight at 84 d (Table 1). Details concerning the development of these new lines were presented by Khalil *et al.* (2002, 2005) and Al-Saef *et al.* (2008).

In Egypt, great efforts have been made since 1998 to select for one exotic maternal line under local conditions and to develop and select local lines based

partially on local breeds. An Egyptian-Spanish programme was established involving Alexandria University, Animal Production Research Institute (APRI, Cairo) and Benha University. V-line rabbits were imported in 1998 from Spain and various selection experiments were practiced. The first line was developed from crossing Baladi Red with V-line and this maternal line named APRI and it was selected for litter weight at weaning (Youssef *et al.*, 2008; Table 1). A synthetic paternal line named Alexandria was originated in Alexandria University from crossing V line with Baladi Black and selection was practiced for daily weight gain during 28-63 days of age (El-Raffa, 2007; Table 2). In March 2003, a selection program was started to produce a synthetic multi-purpose line named Moshtohor resulting from crossing Sinai Gabali with V-line and selection was practiced for litter weight at weaning and live weight at 56 days (Iraqi *et al.*, 2007, 2008; Table 3).

In goats:

In Saudi Arabia, a crossbreeding program between Ardi Saudi goats (A) as a native breed with Syrian goats (Damascus, D) was started in 2004 in two experiments (Jouf and Qassim) applying bio-techniques of estrous synchronization and artificial insemination (Khalil *et al.* 2012). Breeding does of Ardi goats were randomly divided into two groups, 120 doe in each experiment. Each group of Ardi does was subdivided into two subgroups to be inseminated artificially from semen of elite bucks of the same breed and of Damascus breed. Crossbred does of $\frac{1}{2}D\frac{1}{2}A$ were backcrossed with Damascus bucks to get the genetic group of $\frac{3}{4}D\frac{1}{4}A$ and such breeding plan permitted to produce four genetic groups of AA, DD, $\frac{1}{2}D\frac{1}{2}A$ and $\frac{3}{4}D\frac{1}{4}A$ in each experiment separately. The main objectives of this study were: (1) To characterize genetically the native Ardi breed of goats, (2) Improving the productivity of such breed for meat production through crossbreeding, and (3) Applying updated technologies of estrous synchronization and artificial insemination to shorten the generation interval in such genetic improvement program.

Table 1: Programs used to create synthetic maternal lines

Synthetic line and origin	Founder breeds	Selection criteria	Selection methodology	Number of generations	Selection response per generation
Saudi-2, Saudi Arabia (Khalil <i>et al.</i> , 2005)	V line and Saudi Gabali	LWW + W12	BLUP animal-repeatability model	11	LSB= 0.18 kit/litter; LSW= 0.16 kit/litter; LWW= 62g/litter; WW= 8.6g/kit
APRI, Egypt. (Youssef <i>et al.</i> , 2008; El-Raffa, 2007)	V line and Baladi Red	LWW	BLUP animal-repeatability model	7	

LSB = litter size at birth; LSW = litter size at weaning; LWW= litter weight at weaning; WW = weaning weight; W12: weight at 12 weeks.

Table 2: Programs used to create synthetic paternal lines

Synthetic line and origin	Founder breeds	Selection criteria	Selection methodology	Number of generations	Selection response per generation
Alexandria, Egypt (El-Raffa, 2007)	Line V and Baladi Black	ADG (28-63d)	Individual selection using BLUP	7	
Saudi-3, Saudi Arabia (Khalil <i>et al.</i> 2002, 2005)	Line V and Saudi Gabali	LWW + W12	Individual selection using BLUP	10	W12= 38g; ADG= 0.6g; LSB= 0.14 kit/litter; LSW= 0.12 kit/litter; LWW= 35g/litter

LSB = litter size at birth; LSW = litter size at weaning; LWW= litter weight at weaning; ADG= average daily gain.

Table 3: Programs used to create synthetic multi-purpose paternal line

Synthetic line and origin	Founder breeds	Selection criteria	Selection methodology
Moshtohor, Egypt (Iraqi <i>et al.</i> , 2008)	Sinai Gabali and line V	LWW+ 56-d weight	Two-stage selection using BLUP

LSB = litter size at birth; LWW= litter weight at weaning; ADG= average daily gain.

Selection responses

In rabbits:

In selection experiments carried out in developing countries, definite methodologies have been proposed to estimate selection responses. One of them is based on regressing the estimates of the breeding values on generations and this approach depends on the genetic parameters and the model used (Moura *et al.*, 2001). The other methodologies are not depend on the genetic parameters and the model itself but they are dependent on another approach through using the control population which could be an unselected population (Khalil *et al.*, 2002, 2005), or using the population selected divergently (Moura *et al.*, 1997). As presented in Table 1, genetic responses obtained from long-term selection experiments for litter size and other litter traits were found to be moderately considerable. Selection experiments for growth rate notifying successful responses in most experiments carried out in Brazil (Moura *et al.*, 1997). Khalil and Al-Saef (2008) stated that does selected for litter size at weaning presented significant responses in feed intake (3%) and milk yield (6%). A response of 62 g per litter was recorded when selecting for litter weight at weaning. Estimates of direct selection responses per generation were moderate and ranged from 8.7 to 12.6 g for weaning weight, and 18 to 68 g for marketing weight (Moura *et al.*, 1997; Khalil *et al.*, 2005). Selection for growth rate has little or somewhat moderate effects on carcass characteristics and meat quality when the rabbits were selected at the same stage of maturity. Selection for litter weight at weaning achieved considerable responses in growth rate with maintaining high litter components and feed conversion.

Sustainable direct and maternal heterotic improvements

In rabbits:

Different crossbreeding experiments carried out in Egypt (e.g. Khalil *et al.*, 1995; Khalil and Afifi, 2000; Abd El-Aziz *et al.*, 2002; Iraqi *et al.*, 2007; Youssef *et al.*, 2009) indicated that direct heterotic effects were evidenced for litter size, litter weight, and milk yield in most of the possible crossbred does obtained. Consequently, both producers and processors in this area could potentially benefit economically through using crossbred does. Also, estimates of maternal heterosis were favourable and indicating that crossbred dams had considerable maternal heterotic effects in terms of larger litter size, heavier litter weight at birth and weaning, favourable feed conversion ratio, and efficient milk to litter gain conversion ratio than their crossbred daughters (Khalil *et al.*, 2005), *i.e.* crossbred does and dams

gave favourable heterotic effects on litter traits, milk yields and components and milk conversion ratio.

For postweaning growth, estimates of direct heterosis for body weights raised in hot countries were mainly positive and ranging from 1.3 to 14.5 %, but the estimates for maternal heterosis were mainly low and ranging from 0.2 to 5.3 %, *i.e.* crossbred dams had little heterotic maternity over their purebred dams in these growth traits. Abdel-Ghany *et al.* (2000a,b) and Afifi *et al.* (1994) for crossing New Zealand White with Baladi Black or Baladi Red in Egypt found that heterosis percentages ranged from 2.7 to 9.5% for post-weaning body weights and gains.

For carcass traits, Afifi *et al.* (1994) found that direct heterosis percentages from crossing New Zealand White X Baladi Red in Egypt ranged from 1.0 to 4.7 % and this indicating that crossbreeding in rabbits was associated with a little improvement in the carcass performance. In Saudi Arabia, Al-Saef *et al.* (2008) showed non-favorable negative estimates of maternal heterosis of -65.5 g, -6.7 g, -5.3 g and -12.2 g for hot carcass, offal, fat and bone weights, respectively; *i.e.* crossbred dams gave significant negative maternal heterotic effects on carcass traits ranging from 4.8 to 18.7%. For meat quality traits, neither individual heterosis, nor maternal heterosis were significant.

For semen parameters, direct heterosis given by Khalil *et al.* (2007) indicated that crossbred bucks were associated with an existence of heterotic effects in some semen parameters. Such crossing was associated with an increase in ejaculate volume (11.6%; $P < 0.05$), sperm concentration (10.5 %; $P < 0.05$), percentages of motile (9.8%) and living sperms, and libido of bucks ($P < 0.05$) along with a reduction in percentages of abnormal (-10.8%) and dead sperms (-23.5%; $P < 0.05$). Reviewed estimates of maternal heterosis for semen characteristics were favourable and moderate (Khalil *et al.*, 2007); indicating that crossbred dams gave maternal heterotic effects on some semen parameters in their progeny of crossbred bucks. Consequently, crossbred dams could produce crossbred bucks characterized by higher volume of ejaculate with more concentration and motile sperms, along with lesser percentages of abnormal sperms and dead sperms than their crossbred daughters.

In goats:

Khalil *et al.* (2012) found that the heterotic increments were mostly significant and ranging from 3.0 to 11.4 % for body weights and daily body gains and 2.4 to 28.1 % for carcass traits relative to the parental purebreds, while the estimates for meat composition traits were mostly non-significant although crossbred have shown reductions in moisture, ether extract and ash in meat of the carcass. The maternal heterotic

increments in body weights and daily body gains were mostly significant and the estimates ranged from 1.0 to 27.0 %.

The estimates of direct heterosis expressed as percentages relative to the parental purebreds have shown a range of 4.9 to 26.5 %, 3.4 to 39.5 %, 3.1 to 6.9 %, and 3.0 to 11.4 % for semen parameters, litter traits, milk traits and body weights and gains, respectively. Direct heterosis in crossbred kids relative to the founder breeds were mostly significant and ranging from 2.4 to 48.2 % for edible carcass traits and 3.5 to 14.6% for non-edible carcass traits, while the estimates for meat composition traits were mostly non-significant although crossbred have shown reductions in moisture, ether extract and ash in meat of the carcass. Significant direct heterotic improvements were recorded in the dairy and meat experiments for ejaculate volume (0.075 ml vs 0.085 ml), sperms concentration (0.25×10^9 per ml vs 0.11×10^9 per ml), total motile sperms (0.275×10^9 per ml vs 0.125×10^9 per ml), and total sperms output (0.33×10^9 per ml vs 0.155×10^9 per ml), associated with significant reduction in percentage of dead sperms (5.5% vs 1.55 %). For litter and milk traits, crossbred litters were associated with significant heterotic improvements in litter size at birth, litter size at weaning, litter weight at birth, litter weight at weaning, pre-weaning mortality, daily milk yield, fat in milk, solids not fat, protein, and ash; being 0.08 kid, 0.09 kid, 0.245 kg, 1.560 kg, -7.65 %, 71 g, 0.12%, 0.30%, 0.14%, and 0.025 % respectively in the dairy experiment, while the corresponding estimates in the meat experiment were 0.07 kid, 0.045 kid, 0.195 kg, 1.03 kg, -2.5 %, 52 g, 0.15%, 0.21%, 0.14% and 0.015 %. The actual heterotic increments in body weights of the dairy experiment were 0.205, 0.362, 0.729, 0.481, 0.497, 0.435 and 0.712 kg at 0, 4, 8, 12, 16, 20 and 24 weeks of age, while the respective significant heterotic increments in meat experiment were 0.212, 0.551, 0.711, 1.125, 1.497 0.797 and 0.875 kg. For daily body gains, heterotic increments were 18, 55, 45, 60, 45 and 60 g in the dairy experiment and 15, 85, 40, 40, 40 and 50 g in the meat experiment during age intervals of 0-4, 4-8, 8-12, 12-16, 16-20 and 20-24 weeks, respectively.

Crossbred dams in the dairy and meat experiments showed significant heterotic improvements in their crossbred bucks for ejaculate volume (0.058 ml vs 0.055 ml; $P < 0.05$), sperms concentration (0.15×10^9 per ml vs 0.09×10^9 per ml; $P < 0.05$), total motile sperms (0.225×10^9 per ml vs 0.085×10^9 per ml; $P < 0.05$), and total sperms output (0.58×10^9 per ml vs 0.115×10^9 per ml; $P < 0.01$), associated with favourable significant increases in motile sperms (3.3 % vs 4.05 %; $P < 0.05$) and live sperms (3.7 % vs 2.25

%; $P < 0.05$) along with a reduction in percentage of dead sperms (4.3% vs 2.25%; $P < 0.05$) in the semen of the dairy experiment; the estimates of maternal heterosis for semen parameters ranged from 3.3 to 34.1 %. Crossbred dams showed significant heterotic improvements in litter and milk traits of their crossbred does, being 0.15 kid, 0.11 kid, 295 g, 2.340 kg, -4.9 %, 82 g, 0.35 %, 0.23 % and 0.03 % for litter size at birth, litter size at weaning, litter weight at birth, litter weight at weaning, mortality, daily milk yield, SNF, lactose, and ash, respectively; the estimates of maternal heterosis for litter and milk traits ranged from 2.8 to 25.5%. The actual maternal heterotic increments in body weights of the dairy experiment were 0.130, 0.202, 0.219, 0.288, 0.305, 0.300 and 0.554 kg at 0, 4, 8, 12, 16, 20 and 24 weeks of age, while the respective significant heterotic increments in the meat experiment were 0.165, 0.859, 2.135, 1.421, 1.375, 1.286 and 1.298 kg. For body gains, maternal heterotic daily increments were 7.5, 4.5, 6.5, 2.0, 3.5 and 3.0 g in the dairy experiment and 33.5, 31.5, 7.0, 15.0, 10.0, and 5.0 g in the meat experiment during age intervals of 0-4, 4-8, 8-12, 12-16, 16-20 and 20-24 weeks, respectively; the estimates of maternal heterosis for body weights and gains ranged from 1.0 to 27.0 %.

Molecular analyses

In rabbits:

Molecular analyses for economic traits to be used in genetic improvement program in rabbits are very limited. In this concept, RAPD technique is one of the most widely used techniques in applications of molecular biology for identifying the markers linked to traits of interest without the necessity for mapping the entire genome (Bardakci, 2001). RAPD marker of OPF09700 explained variation ranged from 10 to 14.7% for rabbit litter weight, gains, pre-weaning mortality and milk yield, while OPF12900 marker explained 14.7 and 16.8% of the variation for body weight at 4 and 8 weeks of age, respectively (Khalil *et al.*, 2008). In practice, Microsatellite DNA is currently the most useful marker of choice for a wide range of molecular genetic studies in rabbits. Before building the genetic linkage map for QTLs for important traits in local and synthesized breeds, we must make some preliminary tests for variability within the breed and knowing which markers can be used and will be informative. The markers must be polymorphic to be useful. Actually, there were 305 initial sequences (AJ874368–AJ874672), a set of 183 were cytogenetically mapped in rabbits by Chantry-Darmon *et al.* (2006) and they are referred as INRA microsatellites. The second set were seven microsatellite sequences (D1Utr4, D3Utr2, D5Utr3, D6Utr4, D7Utr4, D12Utr2 and D19Utr2) and this

assigned to chromosomes 1, 3, 5, 6, 7, 12 and 19, respectively (Korstanje *et al.* 2001, 2003). These markers are referred as Utrecht microsatellites. However, the first step of developing the genomic resources of rabbits was taken in August 2004 with the announcement by the National Human Genome Research Institute (USA) of a program for the partial sequencing of the rabbit genome, together with that of eight other mammals (<http://www.nih.gov/news/pr/aug2004/nhgri-04.htm>).

Till now, marker-assisted selection (MAS) is not generally used in current rabbits' selection programs in developing countries and the recent molecular technologies were used only in these countries to detect the associations between phenotypic traits and genetic markers. Khalil *et al.* (2008) used RAPD markers to search for the linkage between markers and quantitative traits and they used 526 rabbits in this analysis from a sire-granddaughters design in their selection program. From a total of 40 primers (10-mer) used in their study, five primers (OPA12, OPA19, OPA20, OPF09, and OPF12) were able to identify five polymorphic fragments at molecular weights of 1500, 1100, 1200, 700 and 900 bp, respectively, and only three markers of these markers (OPF12₉₀₀, OPA19₁₁₀₀, and OPF09₇₀₀) showed significant associations with phenotypic traits, which indicated the presence of linkage between the three markers for litter and lactation traits and body weight at 4 and 8 weeks of age. Recently, El-Zarei (2010) detected five markers to differentiate between individuals for carcass traits and to study the association between these markers and some carcass, tissues composition traits and meat quality traits.

Genomic selection

Applications and Methodology

Implementing genomic selection conceptually proceeds in the following steps:

1. Estimation of the effects of chromosome segments in a reference population.
2. Prediction of genomic EBVs (GEBVs) for animals not in the reference population, for example selection candidates.
3. Three distinct categories of animals (training, validation, and application) are involved in WGS. In practice whole genome selection has been applied successfully to the selection of AI young bulls in the dairy industry.

For analyzing SNPs data, Verbyla *et al.* (2010) reported that at each loci (total number of locus, p) there are three possible combinations of two alleles (e.g. A or B), the homozygote of one allele (AA), the heterozygote (AB) and the homozygote of the other allele (BB). These are then

quantitatively represented by 0, 1 and 2 respectively. Subsequently, phenotypic records at each time point were modelled as:

$$y = \mu 1_n + \sum X_j \beta_j + Z u + e$$

where y is the vector of phenotypes of the trait being analysed for all n individuals, μ is the mean, 1_n is a vector of ones of length n, X_j is a vector of indicator variables representing the genotypes of the jth marker for all individuals ($x_{ij}=0,1,2$), β_j is the size of the QTL effect associated with marker j, u is the vector of random polygenic effects of length n (Z is the associated design matrix) and is assumed to be normally distributed, $u \sim N(0, \delta^2 u A)$ where A is the pedigree derived additive genetic relationship matrix and e is the residual error also assumed to be normally distributed, $e \sim N(0, I \delta^2 e)$ where I is the nxn identity matrix. The prior distributions for the variances of the random polygenic effects and the residual were uninformative flat priors of the form $X^2(-2, 0)$. The GEBV at each time point were calculated as:

$$GEBV = \hat{u} + X\beta + e$$

Genomic selection (Advantages)

Whole genome selection (WGS) has the following advantages:

It is an approach to use DNA markers that are distributed throughout the entire genome. Genes affecting the most economic important traits are distributed throughout the genome and there are relatively few that have large effects with many more genes with progressively smaller effects.

Traditional marker-assisted selection (MAS) focuses only on those regions which are relatively certain to influence the trait of interest and leaves most of the genome and much of the genetic variation unaccounted for, while whole genome selection puts the greatest emphasis on those regions with the largest effects (that we can be most certain of) and still accounting appropriately for the more ambiguous genetic variation in the remainder of the genome.

It uses genotypes of thousands of single nucleotide polymorphism markers (SNP), like those from the 50,000 (50K) SNP chip, to predict breeding values (EBVs).

It is similar to the marker sets for DNA tests being offered now, but with much more density throughout the genome. Therefore, it allows SNPs with smaller effects on target traits to be used effectively. In theory, this will allow WGS to account for a greater proportion of genetic variation.

The same set of SNP could be used for all traits, because the SNP in the test span the entire genome.

Genomic selection is not a replacement for our current procedures and programs, but it will enhance our current programs by providing more reliable PTAs for young animals (especially sires). This will lead to more use of younger AI sires with moderately reliable PTAs and increase genetic progress for production traits as well as for health traits, reproductive traits and longevity.

Genomic selection will change breeding programs in rabbits and other small animals in the near future, already happens in dairy cattle since it has the same reliability for all traits in both sexes and it will shorten the generation intervals.

It improves the possibilities to select for functional traits (e.g. health, fertility) and improves also the selection against unfavorable recessive alleles.

Utilizing the genomic relationships and it provides new tools for risk management in breeding programs

Genomic selection (Disadvantages)

- 1) As compared to current DNA tests based on dozens to hundreds of SNP, whole genome selection would have greater cost per animal, because it uses the 50K chip.
- 2) Still need relatives for good EBV's and breeding programs.
- 3) Animals will be selected when sexually mature.

Updated future research work of genetic improvement programs

In order to produce a new synthetic multipurpose line in Egypt, we have to use three-way crossing among lines synthesized recently in Egypt (APRI, Moshtohor and Alexandria) and to use the genomic selection in such breeding program. To achieve this event, APRI bucks will be crossed with Moshtohor does to get the F₁ cross of ½APRI½M,

then does of this F₁ cross will be crossed with Alexandria bucks to get ½A¼APRI¼M and then the progeny of this cross will be inter-se mated (½A¼APRI¼M)² for three generations to produce the multi-purpose line (Figure 1). Across generations, animals will be selected using a BLUP genome methodology.

CONCLUSIONS

- 1) Specialized maternal or paternal lines were recently developed to be used in Egypt on commercial scale.
- 2) Synthesizing multi-purpose lines are necessary to be established in the national rabbit industry.
- 3) The favourable estimates of direct and maternal heterosis reviewed for lactation, growth and carcass traits and heat-stress physiological parameters would be an encouraging factor for the producers in our Arabian area to use crossbred does and dams on commercial scale (Khalil *et al.*, 2002; Al-Saef *et al.*, 2008).
- 4) Insignificant recombination effects for milk traits and growth traits gave an impression to conclude that crossbred does resulting from crossing V-line with native breeds of rabbits in hot climate countries could be effective to develop multipurpose synthetic lines having more available heterosis to be used in commercial production in hot countries.
- 5) Till now, marker-assisted selection (MAS) is not generally used in current rabbits' selection programs in developing countries and the recent molecular technologies were used only in these countries to identify the associations between phenotypic traits and genetic markers (Khalil *et al.*, 2008).
- 6) Genomic selection is much better than classical BLUP if there are no known relatives, and just better if there are (as reported by Legarra *et al.*, 2008).

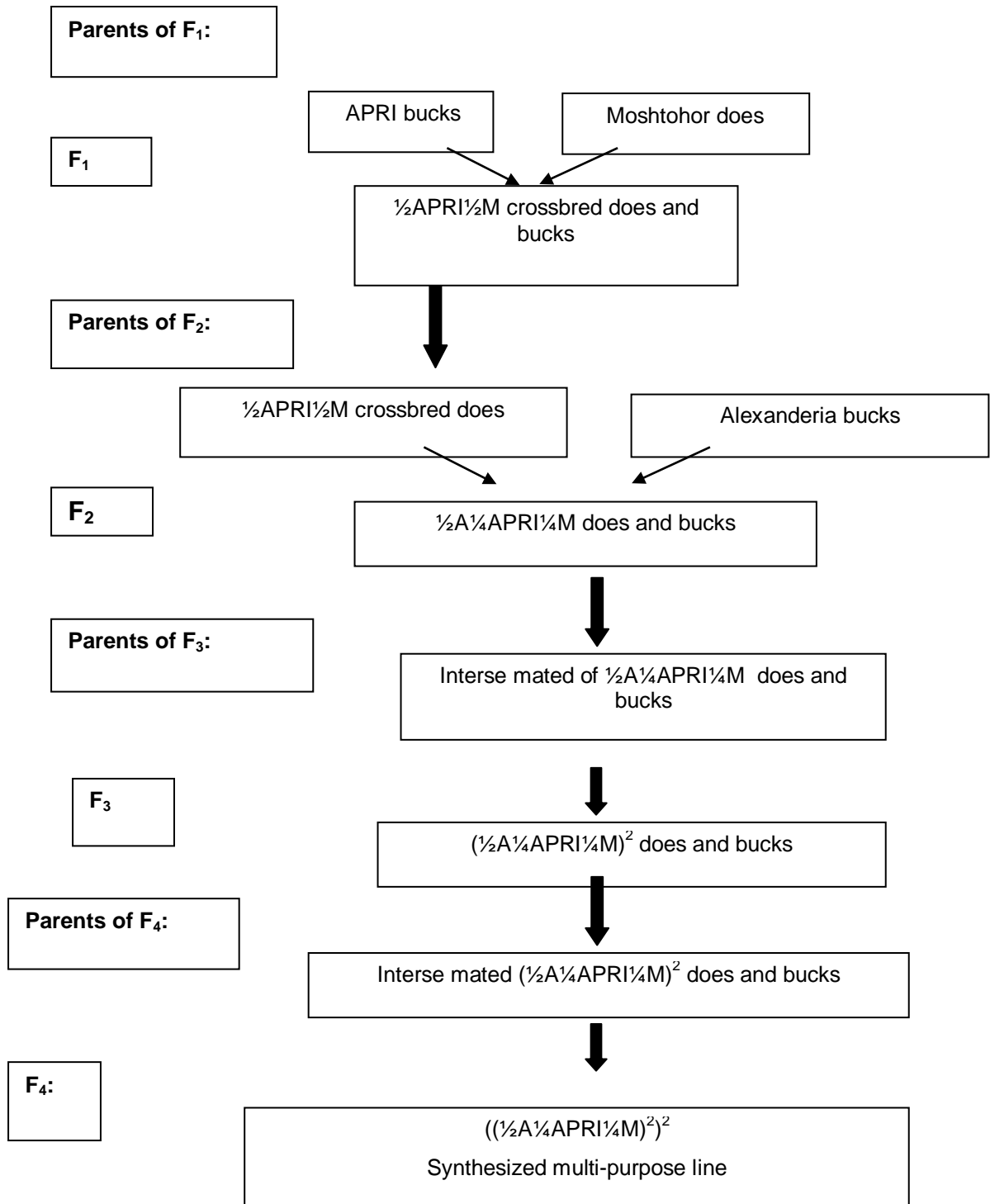


Figure 1: Diagram of three-way crossing to syntheses the multi-purpose line.

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