Session 25. First author e-mail:blahozc@aragon.es

FERTILITY OF SELECT RASA ARAGONESA RAMS CARRYING OR NOT THE *FecX*^{R} ALLELE OF BMP15 GENE WHEN USED IN ARTIFICIAL INSEMINATION

B. Lahoz[1], M.E. Blasco[2], E. Sevilla[3], J. Folch[1], A. Roche[2], F.J. Quintin[3], A. Martínez-Royo[1], A.I. Galeote[2], J.H. Calvo[1], E. Fantova[2], J.J. Jurado[4], J.L. Alabart[1].

[1]CITA de Aragón. Av. de Montañana 930. 50080-Zaragoza, Spain. [2]Carnes Oviaragón S.C.L. Calle G, Mercazaragoza. Cº Cogullada s/n. 50014-Zaragoza, Spain. [3]ATPSYRA-Gobierno de Aragón. Av. de Movera 580. 50194-Zaragoza, Spain. [4]INIA. Ctra. de La Coruña Km 7.5. 28040-Madrid, Spain

- A new mutation in BMP15 gene (*FecX*^{R} allele) responsible for increased ovulation rate and prolificacy in heterozygous (*FecX*^{R} / *FecX*$^{+}$) and sterility in homozygous (*FecX*^{R} / *FecX*^{R}) ewes has been recently found in the Rasa aragonesa sheep breed (Martínez-Royo et al., 2008. *Anim Genet* 39(3):294-297).
- This new mutation is similar to those previously described in Inverdale (*FecX*^{I}), Hanna (*FecX*^{H}), Belclare (*FecX*^{B}), Galway (*FecX*^{G}) and Lacaune (*FecX*^{L}).
- Before 2008, carrier (*FecX*^{R}) and non-carrier (*FecX*$^{+}$) select sires were used in cervical artificial insemination (AI) within a selection programme for prolificacy carried out in the farms of the cooperative UPRA-Carnes Oviaragón SCL.

OBJECTIVE

To compare fertility between carrier and non-carrier select sires used in AI.

MATERIALS AND METHODS

- Retrospective study of the inseminations carried out from 2003 to 2007 with 5 unrelated *FecX*^{R} carrier and 42 non-carrier selected sires.
- Synchronization: FGA sponges (12-14 days) + 480 IU eCG.
- Insemination: Cervical insemination with refrigerated semen (15ºC; 400·10^{6} spermatozoa/ewe) carried out 54.5 ± 1 h after sponge withdrawal by 9 inseminators.
- Artificial insemination lot (AI lot) definition: A group of 10-24 ewes inseminated the same day, with the same sire and in the same farm.
- Only were considered: AI lots with at least one lambing ewe, sires used in at least 3 AI lots, inseminators with at least 5 AI lots, and farms where both types of sires were used (Table 1).

Table 1. Number of farms, AI lots, inseminated ewes involved and mean AI lot fertility.

	Carrier sires (*FecX*^{R})	Non-carrier sire (*FecX*$^{+}$)
Number of sires	5	42
Number of AI lots	440	963
Number of inseminated ewes	5665	11851
Number of ewes/lot (mean ± SEM; range)	12.3 ± 0.1 (10-24)	12.9 ± 0.1 (10-24)
Number of farms	116	116
Fertility % (mean ± SEM; range)	58.2 ± 0.9 (8.3-100)	59.3±0.6 (8.3-100)

- Statistical analysis: Fertility of each AI lot was analyzed by the following mixed-model ANOVA, using SAS:

$$F_{ijklmnop} = \mu + G_i + A_j + Y_k + SMP_l + Y \cdot SMP_{kl} + I_m + S(G)_{ni} + F_o + \varepsilon_{ijklmnop}$$

F : AI lot fertility (100·lambing ewes / inseminated ewes)
μ : Grand mean
G_i : Sire genotype; 2 levels: Carriers (*FecXR*), non-carriers (*FecX+*); fixed effect
A_j : Age of sire; 2 levels: < 9, ≥ 9 years; fixed effect
Y_k : Year; 5 levels: 2003-2007; fixed effect
SMP_l : Six-month period; 2 levels: January to June, July to December; fixed effect
$Y \cdot SMP_{kl}$: Interaction; fixed effect
I_m : Inseminator; 9 levels; fixed effect
$S(G)_{ni}$: Sire nested within genotype; 47 levels (5 carrier and 42 non-carrier); random effect
F_o : Farm; 116 levels; random effect
$\varepsilon_{ijklmnop}$: Residual error

RESULTS

- No significant differences in fertility between both genotypes were found.
- Differences between age-of-sire groups (P<0.05), years (p<0.05), inseminators (P<0.0001), sires within genotype (P<0.01) and farms (P<0.0001) were found, as depicted in tables 2 and 3.

Table 2. ANOVA table.

Source of variation	DF	Type III SS	Mean Square	F Value	Pr > F
Genotype	1	0.015688	0.01568800	0.34	0.5630
Error (*)	32.7	1.500659	0.04594600	-----	--------
Age of sire	1	0.136832	0.13683248	5.33	0.0212
Year	4	0.336343	0.08408571	3.27	0.0111
Six-month period	1	0.004115	0.00411499	0.16	0.6891
Year x Six-month period	4	0.125815	0.03145384	1.22	0.2986
Inseminator	8	1.720422	0.21505271	8.37	0.0001
Sire(Genotype)	45	1.851918	0.04115373	1.60	0.0076
Farm	115	8.419670	0.07321452	2.85	0.0001
Error	1223	31.42129	0.02569198	-----	--------

(*) Error for genotype: 1.31·MS(Sire(Genotype)) - 0.31·MS(Error)

Table 3. Least squares means (LSMEANS) ± standard errors for genotype groups and all significant fixed effects in the model.

Genotype		Inseminator *	
Carrier	53.2 ± 2.1 ^{a}	1	42.6 ± 2.5 ^{a}
Non-carrier	54.3 ± 2.0 ^{a}	2	45.3 ± 5.7 ^{abc}
		3	45.7 ± 6.2 ^{abc}
Age of sire		4	54.0 ± 3.0 ^{bc}
< 9 y	56.8 ± 1.5 ^{c}	5	55.1 ± 2.1 ^{b}
≥ 9 y	50.7 ± 2.9 ^{d}	6	55.6 ± 1.9 ^{b}
		7	59.1 ± 8.0 ^{abc}
Year *		8	62.8 ± 4.9 ^{bc}
2003	50.1 ± 2.4 ^{a}	9	63.3 ± 2.1 ^{c}
2004	53.8 ± 2.4 ^{ab}		
2005	55.8 ± 2.3 ^{b}		
2006	55.7 ± 2.1 ^{ab}		
2007	53.1 ± 2.3 ^{ab}		

Means with different superscripts differ (at least, P<0.05)

* Bonferroni correction applied for multiple comparisons between means. a,b: P<0.01; c,d: P<0.05

CONCLUSION

These results show that fertility of *FecX*^{R} carrier sires (53.2±2.1%) was not significantly different from that of non-carrier sires (54.3±2.0%; lsmeans±standard error) when used in cervical insemination.