Abstract number 4722

Molecular-based estimates of effective population size in the rare Xalda sheep

F. Goyache*, I. Álvarez *, I. Fernández*, L. J. Royo*, L. Pérez-Pardal*, J. P. Gutiérrez†

***SERIDA-Somió, 33203 Gijón (Asturias), Spain.**
†Facultad de Veterinaria, UCM, 28040 Madrid, Spain

Empirical evidence of the usefulness of different molecular-based methods to estimate effective population size (Ne) for conservation purposes in endangered livestock populations is reported. The rare Xalda sheep pedigree (1851 individuals) was available and the polymorphism of 21 microsatellites in 285 Xalda individuals was analyzed using two different approaches:

a) individuals were assigned to a base population (BP) or 4 different cohorts (from C1 to C4) according to pedigree information;
b) individuals were assigned to groups G1 and G2 mimicking two random samplings separated by more than 1 generation interval.

Molecular Ne was computed using:
i) linkage disequilibrium ($Ne_{(D)}$);
ii) a temporal method based on F-statistics ($Ne_{(T)}$);
iii) an unbiased temporal method ($Ne_{(JR)}$);
iv) a Bayesian temporal method ($Ne_{(B)}$).

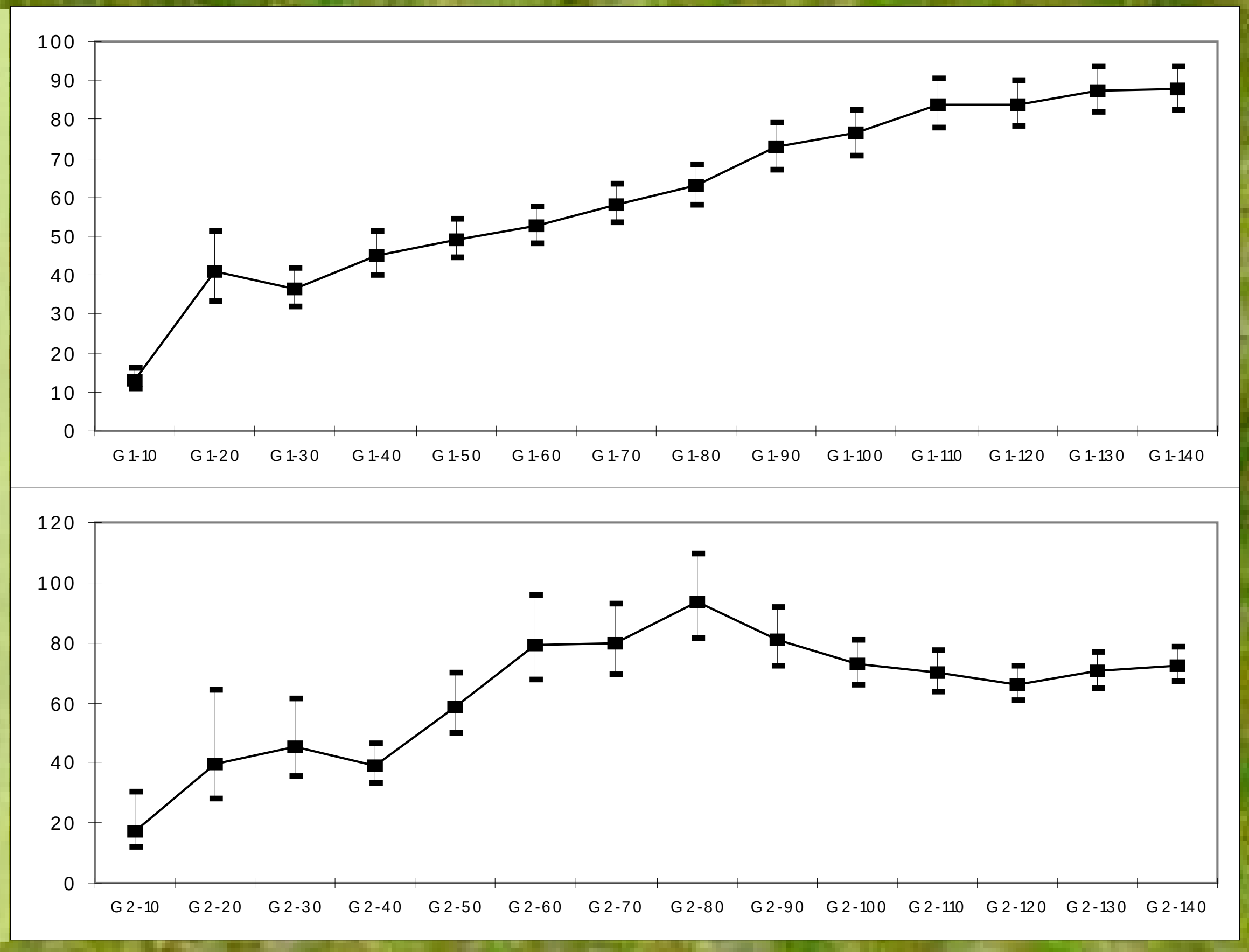
The estimates of $Ne_{(D)}$ decreased with pedigree depth from 68.4 for BP to 34.5 for C4 and from 87.9 for G1 to 70.4 for G2. The estimates of $Ne_{(T)}$, $Ne_{(JR)}$, and $Ne_{(B)}$ obtained using the first approach only presented consistent confidence intervals when temporal samplings involved BP, whilst those obtained for the sampling G1-G2 were similar for $Ne_{(T)}$ and $Ne_{(B)}$ (37.2 and 31.7) and lower for $Ne_{(JR)}$ (18), all of them showing narrow confidence intervals. Even though $Ne_{(D)}$ gathered the population changes due to pedigree accumulation, it was strongly affected by sampling size. Accordingly, repeated sampling would be beneficial. The temporal methods were strongly affected by a weak drift signal, particularly when samplings are not spaced sufficient generations apart.

The use of molecular-based estimates of Ne is not straightforward and their employment in livestock conservation programs should be carried out with caution. Sampling strategies (including sampling sizes, sampling periods and age structure of the sampled individuals) must be carefully planned to ensure that robust estimates of Ne are obtained.

Estimates of Ne in the Xalda sheep breed obtained using two temporal methods ($Ne_{(T)}$, Waples 1989; $Ne_{(B)}$, Berthier et al. 2002) with all possible combinations two by two of the five cohorts sampled. Confidence interval on 95% is in brackets. Sampling sizes for each sample regime is also provided.

Sampling		Estimates of *Ne* obtained using temporal methods		
Regime	Size	$Ne_{(T)}$	$Ne_{(JR)}$	$Ne_{(B)}$
From Base Population to Cohort 1	78-49	26.4 (18.0; 40.1)	21 (14; 37)	25.3 (16.7; 37.8)
From Base Population to Cohort 2	78-51	27.5 (20.3; 37.1)	14 (11;20)	17.8 (11.8; 27.1)
From Base Population to Cohort 3	78-71	51.9 (38.5; 69.8)	26 (20;38)	20.9 (15.4; 30.3)
From Base Population to Cohort 4	78-36	59.4 (42.8; 83.2)	30 (22; 47)	12.6 (8.8; 17.2)
From Cohort 1 to Cohort 2	49-51	17.8 (12.0; 27.0)	9 (7; 14)	9319.6 (0.0; 10000.0)
From Cohort 1 to Cohort 3	49-71	69.6 (43.9; 120.3)	31 (22;51)	54.9 (29.8; 180.8)
From Cohort 1 to Cohort 4	49-36	64.7 (41.5; 107.3)	39 (28; 64)	19.3 (14.2; 32.2)
From Cohort 2 to Cohort 3	51-71	81.8 (40.6; 295.4)	56 (-5755; 28)	8676.1 (137.7; 10000.0)
From Cohort 2 to Cohort 4	51-36	101.1 (51.3; 315.4)	66 (34; 1357)	6348.8 (0.0; 10000.0)
From Cohort 3 to Cohort 4	71-36	449.7 (70.9; ∞)	- 997 (- 82;98)	9232.7 (0.0; 10000.0)
From Group 1 to Group 2	143-142	37.2 (27.4; 50.7)	18 (13; 27)	31.7 (28.6; 34.4)

A test for sampling bias in the estimates of effective population size from linkage disequilibrium ($N_{e(D)}$) obtained in the groups 1 (Plot A) and 2 (Plot B) defined in the text. Subsamples including sequentially 10 additionally, randomly chosen, individuals of each group were used to asses $N_{e(D)}$ and 95% confidence intervals



Number of individuals involved and estimates of effective size for each defined cohort in the Xalda sheep breed obtained by linkage disequilibrium method ($Ne_{(D)}$; Hill, 1981) and pedigree information. For the linkage disequilibrium estimates the correlation among alleles (r) and confidence intervals on 95% (in brackets) are also described. Number of individuals included in the pedigree and genealogical, average equivalent complete generations (t), and mean individual increase in inbreeding ()in percentage), realised effective populations size () and their standard errors (in brackets) are also given

	Linkage disequilibrium (Hill, 1981)			Pedigree information			
	N	Estimate of *r*	$Ne_{(D)}$	N	T	$\overline{\Delta F}$	$\overline{N}_e$
Base population	78	0.01764	68.4 (63.5-73.8)	325	0.0	-	-
Cohort 1	49	0.02742	57.9 (50.9-66.6)	607	1.0	0.8 (± 0.2)	66.5 (± 13.4)
Cohort 2	51	0.02790	41.0 (37.3-45.2)	521	2.0	1.2 (± 0.2)	41.8 (± 5.4)
Cohort 3	71	0.02071	49.2 (45.4-53.6)	336	3.1	2.1 (± 0.2)	23.7 (± 1.7)
Cohort 4	36	0.03767	34.5 (31.0-38.7)	62	3.7	4.0 (± 0.4)	12.3 (± 1.3)
Group 1	143	0.01090	88.3 (82.9-94.3)	677	0.9	0.7 (± 0.1)	76.6 (± 13.0)
Group 2	142	0.01189	70.4 (66.7-74.4)	1174	2.7	1.4 (± 0.1)	36.8 (± 2.7)

SERIDA