Genotype by environment interaction and response to selection for milk production traits in Lacaune sheep

S. Vouraki^{1,2}, S. Priskas¹, A. Argyriadou¹, P.D. Carvalho¹, J.-M. Astruc³, G. Lagriffoul³, R. Rupp⁴, G. Banos⁵, G. Arsenos¹

¹School of Veterinary Medicine, Faculty of Health Sciences, Aristotle University of Thessaloniki, Greece

²School of Agriculture, University of Ioannina, Arta, Greece

³Institute de l'Elevage, Castanet-Tolosan, France

⁴INRAE, INPT-ENVT, INPT-ENSAT, GenPhySE, Castanet-Tolosan, France

⁵Scotland's Rural College (SRUC), Edinburgh, UK





Background

- Improving dairy sheep milk production ->
 - Desirable breeding goal
 - Farm profitability
- Genetic evaluation combining data from animals reared in different countries >
 - Selection intensity increase → increased genetic gain
- Lacaune sheep in Greece and France

Important to identify

- Genotype by environment (G×E) interaction
- Response to selection (genetic gain) based on joint genetic evaluations





Objectives

- (i) To investigate genotype by environment interaction (G×E) for milk yield and composition in purebred Lacaune sheep reared in Greece and France

 (ii) To compare notential genetic gain from selection
 - (ii) To compare potential **genetic gain** from selection **across and within countries**





Animals and Farms

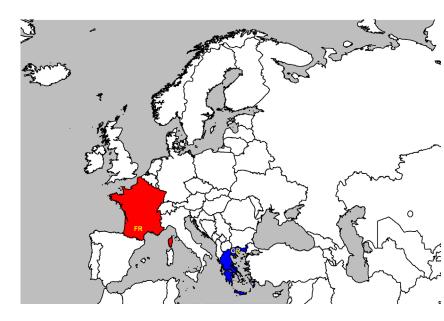
Greece

- 4 intensive farms
- 1,658 Lacaune ewes
- 1st-2nd lactation period
- Born after AI from imported Lacaune rams (n=14)

France

- 186 semi-extensive farms
- 4,859 Lacaune ewes
- 1st-7th lactation period
- Related to ewes in Greece

(6 common sires & 11 grandsires)









Phenotypes

- Individual monthly records
 - Milk yield
 - ✓ 5-6 measurements
 - Milk composition
 - √ ~3 samples in mid lactation
 - ✓ Fat & Protein content
- Milking period records
 - Milk yield → Fleishmann method
 - Milk composition → average of individual monthly records weighted for milk yield









Datasets

Characteristic	Greece	France		
Study period	2021-2022	2019-2022		
Number of ewes	1,658	4,859		
Number of sires	14	64		
Number of records	1,658	7,166		
Type of records	Single	Multiple		
Number of first parity records	858	4,047		
Number of third and above parity records	0	555		
Milking period length (days, SD)	168.7 (17.72)	168.8 (38.94)		
Age at lambing (months, SD)	20.4 (6.00)	20.5 (10.65)		
Days from lambing to first sampling (SD)	34.2 (6.66)	51.5 (11.82)		





Data analysis – Genetic parameter estimation

- Mixed linear models REML method
 - Fixed effects → farm, year, parity, milking period length, days from lambing, combination of test days
 - Random effects \rightarrow additive genetic (pedigree with 26,547 animals) & permanent environmental (French data \rightarrow repeated records)
- Variance components and genetic parameters
 - Univariate analyses
 - Approximate genetic correlations using common sire & grandsire EBVs



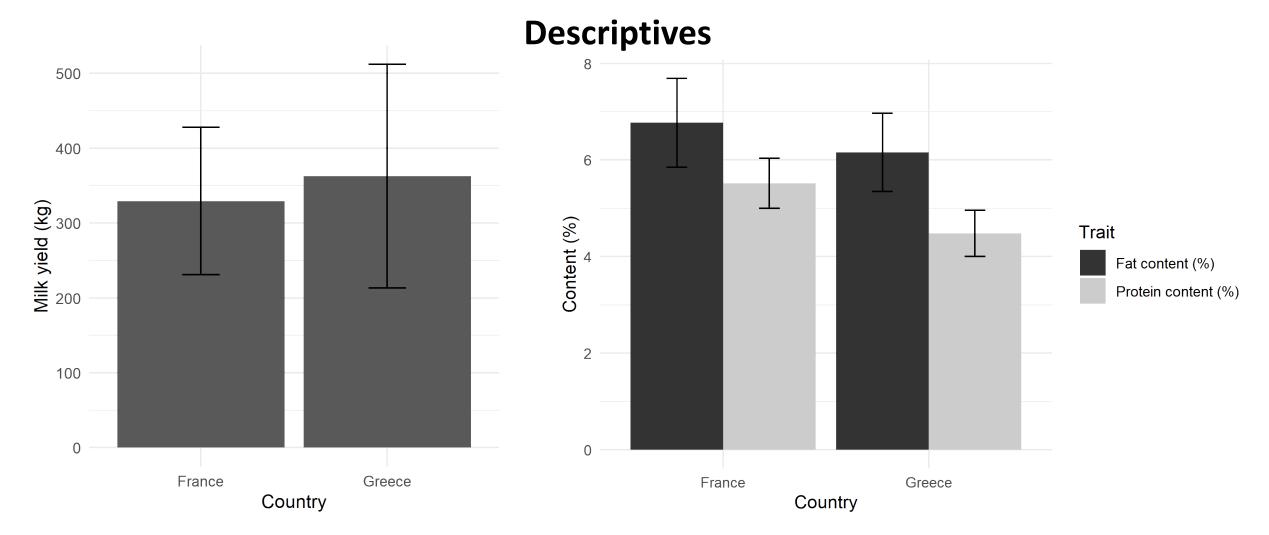


Data analysis – Response to selection

- $\Delta G = i \times r \times \sigma_A$
 - Selection candidates in Greece (n=30) & France (n=600)
 - Selection intensities (i) → Top 10 and 15 sires within & across country
 - Accuracy of selection (r) → Square root of sire EBV reliability
 - Additive genetic standard deviation (σ_A) \rightarrow Square root of additive genetic variance for each trait and country



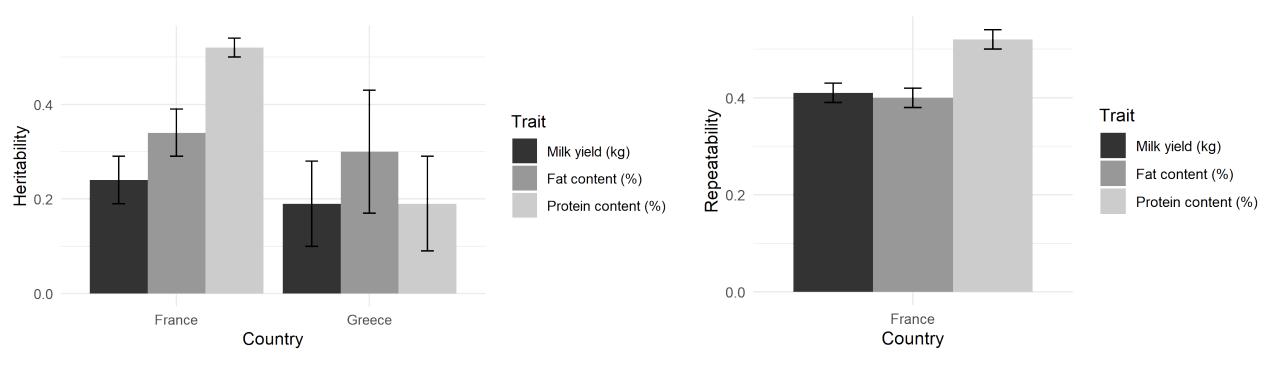








Heritability & Repeatability







Genetic correlations - G×E

	Milk yield (kg) – GR	Fat content (%) – GR	Protein content (%) – GR
Milk yield (kg) – FR	0.86 (0.13)*		
Fat content (%) – FR		0.57 (0.21)*	
Protein content (%) – FR			0.88 (0.13)*

^{*}Indicates statistically significant estimates (P<0.05)





Response to selection – Milk yield

Selection scenario	Top sires	N sires	PS%	i	r	σ_{A}	ΔG	ΔG%
Within Greece	10	30	33.3	1.07	0.84	42.05	37.62	45.78
Within Greece	15	30	50.0	0.78	0.84	42.05	27.56	35.57
Within France	10	600	1.7	2.46	0.81	26.60	53.18	99.89
Within France	15	600	2.5	2.32	0.81	26.60	50.22	100
Across Greece	10	630	1.6	2.48	0.79	42.05	82.80	100
Across Greece	15	630	2.4	2.34	0.79	42.05	77.47	100
Across France	10	630	1.6	2.48	0.81	26.60	53.24	100
Across France	15	630	2.4	2.34	0.81	26.60	50.18	100

PS=proportion selected, i=selection intensity, r=accuracy of selection, σ_A =genetic standard deviation of trait, ΔG =response to selection, ΔG %=percentage of genetic gain from genetic evaluation within compared to across countries





Response to selection – Fat content

Selection scenario	Top sires	N sires	PS%	i	r	σ_{A}	ΔG	ΔG%
Within Greece	10	30	33.3	1.07	0.88	0.41	0.38	50.16
Within Greece	15	30	50.0	0.78	0.88	0.41	0.28	39.98
Within France	10	600	1.7	2.46	0.84	0.46	0.95	100
Within France	15	600	2.5	2.32	0.84	0.46	0.90	100
Across Greece	10	630	1.6	2.48	0.75	0.41	0.76	100
Across Greece	15	630	2.4	2.34	0.75	0.41	0.72	100
Across France	10	630	1.6	2.48	0.79	0.46	0.91	100
Across France	15	630	2.4	2.34	0.79	0.46	0.86	100

PS=proportion selected, i=selection intensity, r=accuracy of selection, σ_A =genetic standard deviation of trait, ΔG =response to selection, ΔG %=percentage of genetic gain from genetic evaluation within compared to across countries





Response to selection – Protein content

Selection scenario	Top sires	N sires	PS%	i	r	σ_{A}	ΔG	ΔG%
Within Greece	10	30	33.3	1.07	0.74	0.05	0.04	40.96
Within Greece	15	30	50.0	0.78	0.74	0.05	0.03	31.83
Within France	10	600	1.7	2.46	0.84	0.30	0.63	99.83
Within France	15	600	2.5	2.32	0.84	0.30	0.59	100
Across Greece	10	630	1.6	2.48	0.77	0.05	0.09	100
Across Greece	15	630	2.4	2.34	0.77	0.05	80.0	100
Across France	10	630	1.6	2.48	0.84	0.30	0.63	100
Across France	15	630	2.4	2.34	0.84	0.30	0.59	100

PS=proportion selected, i=selection intensity, r=accuracy of selection, σ_A =genetic standard deviation of trait, ΔG =response to selection, ΔG %=percentage of genetic gain from genetic evaluation within compared to across countries





Conclusions

GXE interaction

- − Milk yield and protein content → Strong genetic correlations between the two counties → no presence of G×E interaction
- Fat content → Moderate genetic correlations between the two countries → some degree of sire re-ranking
- Joint genetic evaluation of Lacaune sheep in Greece and France \rightarrow Feasible
- Response to selection (genetic gain)
 - Sire selection across countries based on joint genetic evaluation → genetic gain increase
 for studied traits in both countries
 - Greece will benefit more (increase by 68.17%) compared to France (increase by 0.16%)





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