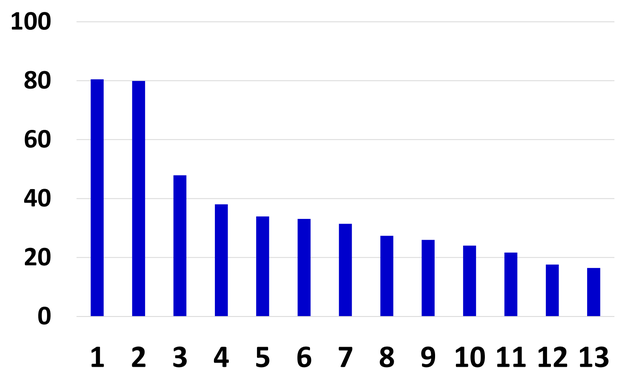
71st Annual Meeting of European Federation of Animal Science
2-4 December 2020, virtual meeting

Benefits of GS for meat sheep breeding programs according to the available pedigree and the level of AI

Purebred selection with different level of AI and pedigree information

A large number of breeds adapted to specific environment (e.g. grassland, harsh and mountainous areas) X production systems



Distribution of the AI level according to main breeds

6 breeds without AI (only Natural mating)

Huge variation of pedigree information (Sire) accross breeds

Benefit of genomic selection?

Is GS beneficial whatever the level of AI and the pedigree information available?

Assessed through full stochastic simulation
Selection of a maternal trait for 25 years

Comparison of 3 strategies :

- **CS**: Classical Selection
- **GS_M**: Genomic Selection based on a sire reference population
- **GS_MF**: genomic selection based on a sire + dam reference population

MAIN RESULTS

Natural mating based breeding programs

Strategy	Genotyped dams %	Dams with sire info. %	Annual genetic gain (ref: 100=0.081 $\sigma g/y$)
CS	0	0	100
		50	106
		100	142
GS_M	0	0	110
		50	142
		100	163
GS_MF	25	25	193
	50	50	194
	100	100	198

AI+Natural mating based breeding programs – incomplete pedigree

% AI	Strategy	Genotyped dams %	Dams with sire info. %	Annual genetic gain (ref: 100=0.170 $\sigma g/y$)
30	CS	0	25	100
			100	103
	GS_M	0	25	97
			100	112
	GS_MF	25	25	132
		100	100	140

AI+Natural mating based breeding programs – complete pedigree

% AI	Strategy	Genotyped dams %	Annual genetic gain (ref: 100=0.175 $\sigma g/y$)
30	CS	0	100
	GS_M		109
	GS_MF	25	130
		100	136
60	CS	0	108
	GS_M		108
	GS_MF	25	136
		100	138
80	CS	0	112
	GS_M		108
	GS_MF	25	129
		100	136

Genomic selection based on a sire reference population is not always beneficial

Genomic selection based on a sire + dam reference population is always beneficial whatever the level of AI and pedigree completeness

The economic interest must be assessed

Jérôme RAOUL[1,2], Jean-Michel Elsen[2] **contact: jerome.Raoul@inrae.fr**
1 *Institut de l'Elevage, Castanet-Tolosan, France*
2 *UMR GenPhySE, INRAE, Castanet-Tolosan, France*
(accepted for publication in Animal)

This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Grant Agreement n°772787