

# Feed efficiency in small ruminants; genetic basis and novel traits for a complex trait *WP1 at a glance J.J. Arranz*

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- 1. Understand the **underlying components** of the complex trait "efficiency of feed resource use" in sheep and goats.
- 2. Generate **novel phenotypes to predict feed efficiency** using automated measures and biomarkers available on a large scale.
- 3. Estimate genetic parameters and detect genomic regions underlying the efficiency of feed resource traits in sheep and goats.
- 4. Quantify the extent, if any, of **genotype-by-environment (GxE) interactions** for efficiency of feed resource between different: (a) diets (i.e., local forages, concentrate, pastures) and (b) breeding systems (i.e., intensive vs extensive and/or agro-ecological).
- Measure at larger scale promising resource use efficiency phenotypes (from Task 1.1) for assessing the impact of their use in small ruminant breeding programmes.





**Task 1.1**: Identification & characterization of novel phenotypes related to resource use efficiency

Task 1.2: Analysis of the genetic determinism of feed efficiency

**Task 1.3**: Genetic correlations between phenotypes and production traits

**Task 1.4**: GxE interaction for the resource use efficiency-related phenotypes





Partner ID	Full name	Contact person	Animals
INRA	Institut National de la Recherche Agronomique		
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SRUC	Scotland's Rural College		
TEXELS	Texel Sheep Society		
Y-DG	Yorkshite Dairy Goats		
NSG	Norwegian Association of Sheep ad Goat Breeders		
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**INRAE-France** 

Romane (101)

Lacaune (55)

Alpine (49)

**AUTH-Greece** 

**INIA-Uruguay** 

**UNILEON-Spain** Assaf (40)



Norwegian White sheep (1600)



#### Task 1.1: Identification & characterization of novel phenotypes related to resource use efficiency



		Eva	luated	in:	
Group of traits	Proxy for feed efficiency	dairy sheep	dairy goat	meat sheep	Importance and potential use as large scale measurable proxy
	Body weights	x	x	x	Involved in RFI calculation (through metabolic weight and average daily gain) and can be considered as part of the proxies of feed intake and feed efficiency
	Muscle Depth and Backfat Thickness (ultrasound)	x		x	Can be used in the RFI calculation but its importance is low
Zootechnical	Milk yield	x	x		Involved in feed efficiency criteria (ratio and RFI) and can be considered as part of the proxies of feed efficiency
(routinely	Milk fat and protein contents	х	х		Involved in feed efficiency criteria (through energy corrected milk )
traits)	Body Condition Score	x	x	x	Trajectory of BCS are correlated with feed efficiency ratios in dairy sheep
	Wool traits (Greasy Fleece Weight, Clean Fleece Weight, average Fibre Diameter, Coefficient of Variation of Fibre Diameter, and Staple Length)			×	Can be used in the RFI calculation but its importance is low
Zootechnical (not routinely	greenhouse gas (CH <sub>4</sub> and CO <sub>2</sub> ) emissions and O <sub>2</sub> consumption			×	Can be used along with body weights and growth as proxies for feed intake, but gas emissions recording is currently not doable on a large scale. New technnologies are required to record gas emissions on a large scale.
recorded traits)	Morphological traits (chest width, chest depth, shoulder height )	x	x	×	Chest width might be considered as a proxy for body weight
	Average Daily Feed intake	x	x	x	Mandatory trait to estimate all feed efficiency criteria, but not recordable on a large-scale. We are looking for proxies for this trait.
Milk traits (not	metabolomics (NMR)	x			Milk fatty acids are proxies for feed efficiency traits (FCR and RFI).
routinely	milk fatty acids composition (gas				energy intake. Milk metabolome and MIR spectra still need to be
recorded)	chromatography)	X			analysed.
	milk protein, lactose	x			
	fine composition (MIR spectra)	x			
Blood traits	plasma metabolomics (NMR)	x		x	Citrate, malate and amino acids can be considered as proxies for feed efficiency, but NMR is not doable routinely. New technnologies are required to record these metabolites on a large scale.
(not routinely	targeted metabolites (β-HB)	х	Х		These targeted metabolites still need to be analysed as potential
recorded traits)	NEFA, total proteins, and hormones	x			proxies for feed efficiency.
	plasmatic <sup>15</sup> N natural abundancies			×	15N natural abundancies is a good proxy for FCR under a forage-based diet, but this trait is currently too expensive to be recordable on a large-scale
faecal traits	NIRS			x	No good prediction of feed intake nor feed efficiency when individual are tested under a unique diet.
	pH, Ammonia,	х			
Duminal Insite	microbiota (16s and/ or 18S sequencing)	x		x	These traits are recorded in order to understand the biology
Ruminal traits	metabolomics (NMR)	х		X	fand afficiency because the compling is not deable routinely
	volatile fatty acids (gas chromatography)	x		x	rese streams because one sampling is not usable routinely.
Milk molecular traits (not	RNAseq in milk cells	x			These traits are recorded in order to understand the biology
routinely recorded)	Whole-genome bisulfite sequencing of milk cells	x			underlying teed efficiency. They can not be considered as proxies for feed efficiency because the sampling is not doable routinely.





## Performance of Proxies: **Zootechnical traits**

Group of traits <sup>1</sup>	Trait <sup>2</sup>	Species <sup>3</sup>	Experimental Commercial	Reference FE trait	Protocol	Prediction performances <sup>4</sup>	# animals on which the prediction performance was assessed	Ease of recording
Zootechnical	RFI	DG	Commercial		cf. D1.1	NA	6124	2
Zootechnical	Body weights	MS	Experimental	RFI	growing lambs, 100%concentrate ad libitum	R <sup>2</sup> =0.07 ±0.05	277	1
Zootechnical	Body weights	MS	Experimental	FCR	growing lambs, 100%concentrate ad libitum	R <sup>2</sup> =0.20 ±0.09	277	1
Zootechnical	Body weights	MS	Experimental	Feed intake	growing lambs, 100%concentrate ad libitum	R <sup>2</sup> =0.71 ±0.05	277	1
Zootechnical	Body weights	MS	Experimental	RFI	8 months old lambs, 2/3 forage +1/3concentrate ad libitum	R <sup>2</sup> =0.32 ±0.10	166	1
Zootechnical	Body weights	MS	Experimental	Feed intake	8 months old lambs, 2/3 forage +1/3concentrate ad libitum	R <sup>2</sup> =0.59 ±0.09	166	1



## Performance of Proxies: Rumen Microbiota

Group of traits <sup>1</sup>	Trait <sup>2</sup>	Species <sup>3</sup>	Experimental Commercial	Reference FE trait	Protocol	Prediction performances <sup>4</sup>	# animals on which the prediction performance was assessed	Ease of recording
Zootechnical	Residual Energy Intake (approximated)	DS	Commercial	REI	cf. D1.2	Not available, no reference trait	4680 Lacaune, 536 Manech Tête Rousse, 361 Manech Tête Noire, 538 Basco-	2
Ruminal microbiota	6S or 18S sequencing	MS	Experimental	RFI	growing lambs, 100%concentrate ad libitum	16S :R <sup>2</sup> =0.02 ±0.02 ; 18S : R <sup>2</sup> =0.02 ±0.02	277	3
Ruminal microbiota	6S or 18S sequencing	MS	Experimental	FCR	growing lambs, 100%concentrate ad libitum	16S :R <sup>2</sup> =0.17 ±0.08 ; 18S : R <sup>2</sup> =0.05 ±0.04	277	3
Ruminal microbiota	6S or 18S sequencing	MS	Experimental	Feed intake	growing lambs, 100%concentrate ad libitum	16S : R <sup>2</sup> =0.08 ±0.06; 18S : R <sup>2</sup> =0.04 ±0.04	277	3
Ruminal microbiota	6S or 18S sequencing	MS	Evnerimental	DEI	8 months old lambs, 2/3 forage +1/3concentrate ad	16S : R <sup>2</sup> =0.09 ±0.07;	165	a
Ruminal microbiota	6S or 18S sequencing	MS	Experimental	Feed intake	8 months old lambs, 2/3 forage +1/3concentrate ad	165 : R <sup>2</sup> =0.08 ±0.06; 185 : R <sup>2</sup> =0 12 + 0.09;	166	3



# Performance of Proxies: Faecal NIRS

Group of traits <sup>1</sup>	Trait <sup>2</sup>	Species <sup>3</sup>	Experimental Commercial	Reference FE trait	Protocol	Prediction performances <sup>4</sup>	# animals on which the prediction performance was assessed	Ease of recording
	( i			(	growing lambs,			
NIRS	faecal NIRS				100%concentrate ad			
		MS	experimental	RFI	libitum	R <sup>2</sup> =0.02	91	1
					growing lambs,			
NIRS	faecal NIRS				100%concentrate ad			
		MS	experimental	FCR	libitum	R <sup>2</sup> =0.04	91	1
					growing lambs,			
NIRS	faecal NIRS				100%concentrate ad			
		MS	experimental	Feed intake	libitum	R <sup>2</sup> =0.12	262	1
					8 months old lambs,			
NUDC	faces I NUDC				2/3 forage			
NIKS	Taecal NIKS				+1/3concentrate ad			
		MS	experimental	FCR	libitum	R <sup>2</sup> =0.15	47	1
					8 months old lambs,			
NIDS	factal NIDS				2/3 forage			
INIKO	Idecal INIKS				+1/3concentrate ad			
			experimental	Feed intake	libitum	R <sup>2</sup> =0.19	164	1



#### Performance of Proxies: Molecular information

Group of traits <sup>1</sup>	Trait <sup>2</sup>	Species <sup>3</sup>	Experimental Commercial	Reference FE trait	Protocol	Prediction performances <sup>4</sup>	# animals on which the prediction performance was assessed	Ease of recording
Epigenetic marks in milk somatic cells	DNADML (Differencial Metilated Loci)	DS	experimental	RFI, FCR	Lactating animals, cf. D1.1	R <sup>2</sup> = 0.344 (RFI) R <sup>2</sup> = 0.332 (FCR)	28	3
Milk composition	Milk fatty acid profile	DS	experimental	RFI, FCR	Lactating animals, cf. D1.1	R <sup>2</sup> = 0.720 (RFI) R <sup>2</sup> = 0.745 (FCR)	39	2
Milk composition	Untargeted metabolome	DS	experimental	RFI, FCR	Lactating animals, cf. D1.1	R <sup>2</sup> = 0.170 (RFI) R <sup>2</sup> = 0.580 (FCR)	39	2
Milk somatic cells whole transcriptome (DEG)	RNA-seq	MS	experimental	RFI, FCR	Lactating animals, cf. D1.1	R <sup>2</sup> = 0.234 (RFI) R <sup>2</sup> = 0.3532 (FCR)	24	3



#### Task 1.2: Analysis of the genetic determinism of feed efficiency

#### Genetic parameters of Feed efficiency trais: $h^2$

Population	NEICMR	REI	RFI	CH4	MY	FP	PP	LC	BW	DMI	BCS	CD	CW	HW
Lacaune	0.10	0.11			0.16	0.36	0.43							
Chios					0.11	0.13		0.01						
Frizarta					0.05	0.15		0.14						
YDG					0.25-0.35				0.3-0.1	0.3-0.6				
Alpine		0.18			0.19									
Saanen		0.20			0.20									
NWS				0.34										
Merino			0.34	0.37										
Romane														
Texel									0.16					
Suffolk									0.22					
Charollais									0.14					
BMC											0.062	0.177	0.129	0.176
MV											0.296	0.245	0.180	0.321
RO											0.161	0.273	.060	0.32





#### Task 1.2: Analysis of the genetic determinism of feed efficiency

# **Biological Basis of Feed Efficiency: Transcriptomic Data**





Task 1.3: Genetic correlations between phenotypes and production traits

- **Phenotypic** correlations have been estimated with high precision in all commercial small ruminant populations analyzed.
- The estimated genetic correlations between FE proxies and productive traits have been presented in
  DL 1.2
- A negative correlation between milk fat content and production in <u>Greek breeds</u> has been observed.
- In <u>Lacaune</u> the FE proxies show a positive correlation with MY and a negative with milk fat and protein contents
- In <u>Yorkshire dairy goats</u>, the correlations show that selection for increased MY results in decreased feed intake.
- In the case of <u>Merino</u>, no correlation between RFI and grease fleece weight has been detected





Task 1.4: GxE interaction for the resource use efficiency-related phenotypes

**Three Case studies:** 

- 1. Lacaune dairy sheep
  - Greece vs France (AUTH & INRAE)
- 2. Romane meat sheep (INRAE
  - extensive vs intensive
  - concentrate vs hay
- 3. Alpine and Saanen dairy goats (INRAE)
  - extensive vs intensive
  - season vs out of season breeding

DL1.4 & ML1.4 : M56







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