Sustainable **Shee**p **P**roduction

SusShep is a 3 year European project (2017-2020), with 8 European partners across Norway, France, Ireland & UK.

Key objectives of SusSheP:

- Provide new genetic tools for farmers to increase the longevity of ewes.
- Quantify labour input and carbon hoofprint in contrasting sheep systems.
- Develop more socially acceptable methods of AI by investigating ewe breed effects in the cervix.
- Maximise knowledge transfer and uptake of new innovations by farmers.

This newsletter will focus on our results to-date relating to sheep artificial insemination

Differences between ewe breeds in the cervix and its secretions are the principal factors why cervical artificial insemination (AI) with frozen-thawed semen works in Norway but not elsewhere. The molecular mechanisms underlying the sperm selection through the cervix remains to be elucidated.

• The **objective** of this study was to use RNAseq to profile the transcriptome of the ovine cervix in four European ewe breeds with known differences in pregnancy rates following cervical AI with frozen-thawed semen.

Materials and Methods

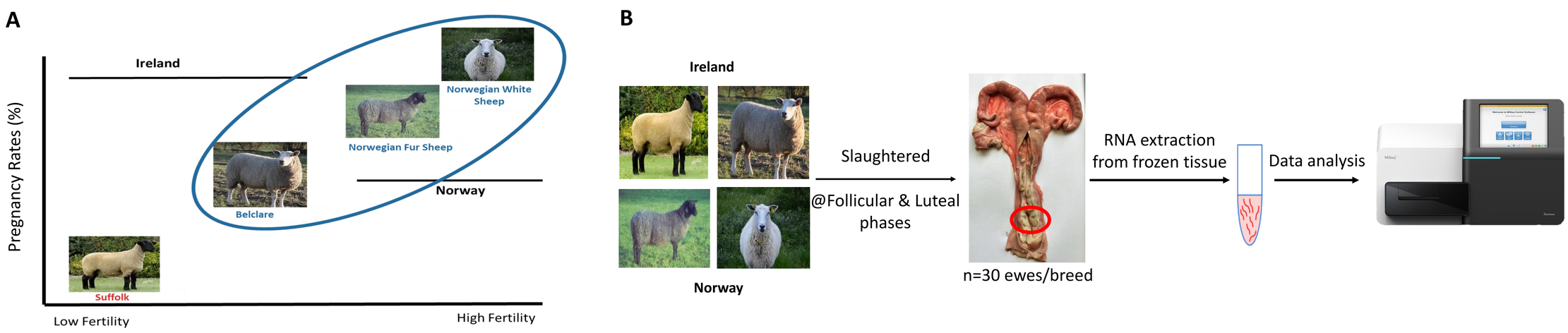

Figure 1. Experimental model. A) This study was carried out using two Irish ewe breeds (Belclare and Suffolk; high and low fertility, respectively) and two Norwegian ewe breeds (Norwegian White Sheep (NWS) and Fur; both with high fertility). **B)** Outline of cervical tissue collection. Cervical tissue samples were collected from four ewe breeds (n=30 ewes/breed) at both the follicular and luteal phase of the oestrus cycle.

Preliminary Results

1. Differential gene expression analysis

- Compared to the Suffolk:

At the **follicular phase** a total of 7232, 7716 and 510 genes were significantly differentially expressed in NWS, Fur and Belclare ewes, respectively.

At the **luteal phase**, 1661, 4984 and 2087 genes were differentially expressed in NWS, Fur and Belclare, respectively.

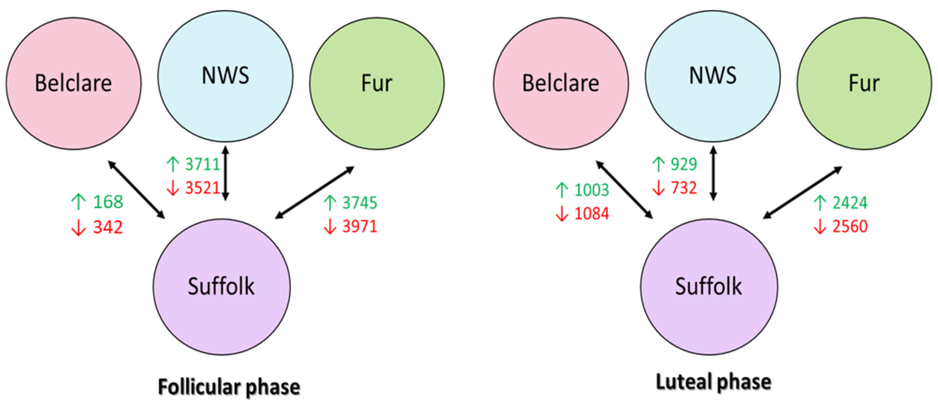

Figure 2. Genes that were up and down differentially regulated (FDR<0.01) in Belclare, NWS and Fur ewes compared to Suffolk ewes (reference level) at the follicular and luteal phases.

2. Conserved transcriptome

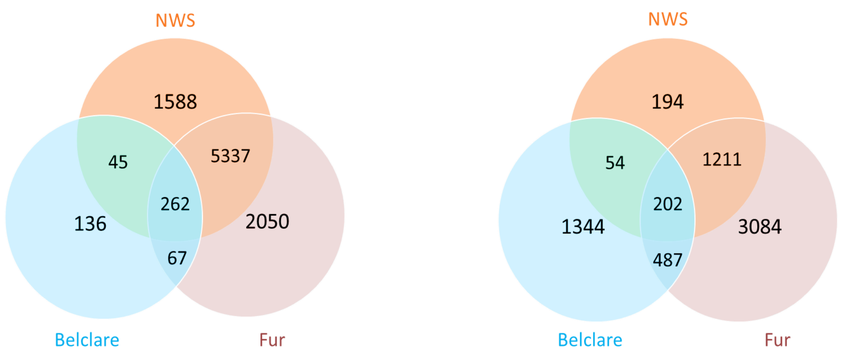

Figure 3. Venn diagrams with genes in common for the 3 comparisons at the follicular and luteal phases.

3. Phase specific differences in gene expression

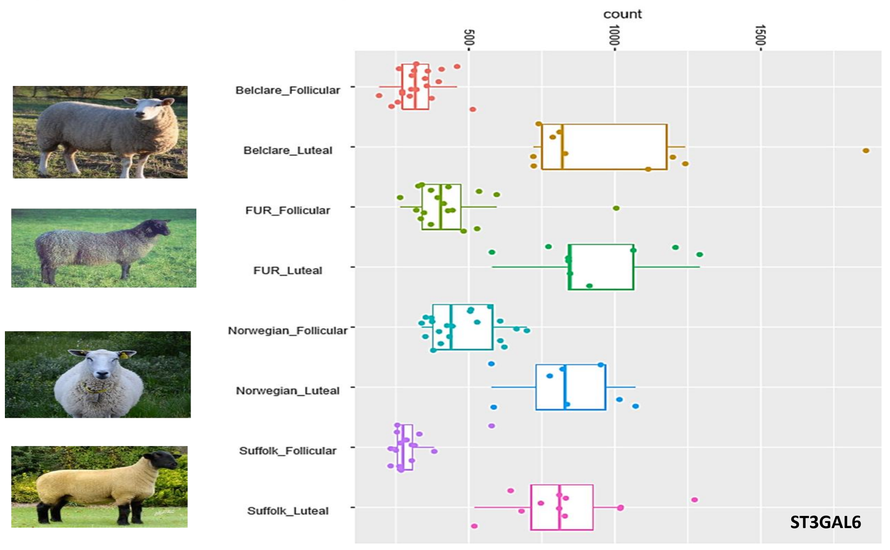

Figure 4. Glycosyl-transferase expression (sorted by normalised read counts) in each ewe breed at the follicular and luteal phases.

4. Breed-specific differences in gene expression

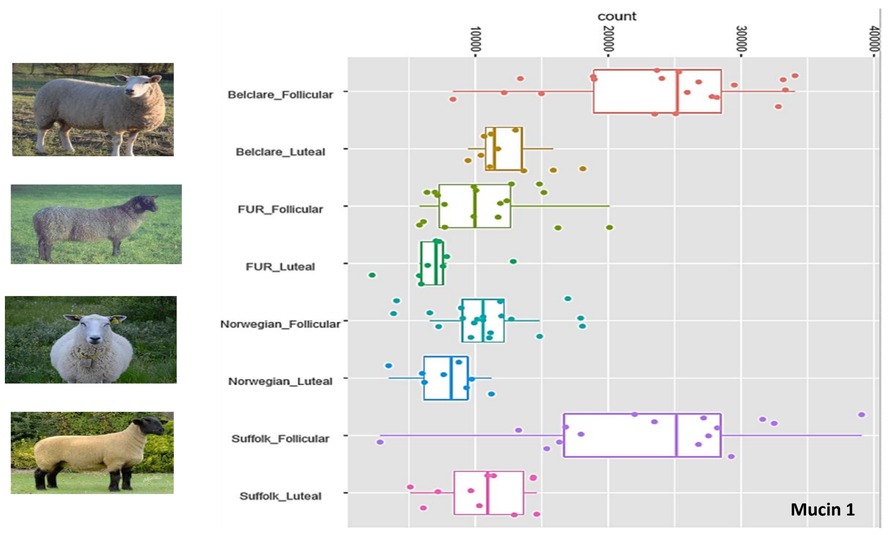

Figure 5. Mucin 1 expression (sorted by normalised read counts) in each ewe breed at the follicular and luteal phases. Mucin 1 is involved in mucus production and protection from infection.

Conclusion

- Significant **differences in gene expression** between **high** and **low fertility ewe breeds.**
- Pathways involved in **mucin biosynthesis**, **metabolite transport** and the **inflammatory response**.

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