

DEVELOPMENT OF GENOMIC TOOLS FOR SMALL RUMINANTS

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Sequencing the sheep and goat

- Early 2007, development of next-generation sequencing (NGS) allowed de novo sequencing of sheep (2014) and goat genomes (2013).
- Genome sequencing allowed in turn for creation of high-density chips.
- Illumina OvineSNP50 BeadChip - 54K SNP microarray (International Sheep Genomics Consortium) – 2010
- Illumina GoatSNP50 BeadChip - 52K SNP microarray – 2014

Genomic Selection

- Useful for dairy traits - selection of sires is hampered by a progeny testing period.
- Can also be useful for meat production breeds:
 - Traits that are measured later in the life of the reproductive females: reproductive ability, breeding seasonality, and longevity
 - Traits that require invasive or destructive evaluation measures of carcass composition and meat quality, which are typically recorded on the relatives of selection candidates and require animals to be sacrificed

Barriers in technology uptake

- Higher cost of genotyping – especially relative to the value of the animal
- Many valuable traits can be measured in both sexes before reproductive maturity (growth, ultrasound carcass measures, and some disease resistance measurements) - the potential to accelerate genetic progress is less compelling.

Genomic selection – feasible?

- The feasibility of genomic selection in small ruminants has been evaluated recently:
 - In meat sheep in Australia (2010-12) and New Zealand (2014)
 - In dairy sheep in France (2013-14)
 - In dairy goats in France (2013-14) and UK (2015)
- The challenge: the reference population
 - NZ: 13,420 Romney; 1,900 W. Pyrenees dairy sheep
 - UK: 2,400 goat
 - France: 2,700 goat; 4,800 Lacaune dairy sheep
 - Australia: 8,000 multibreed meat sheep

Results from GBLUP

- Despite small reference populations, genomic best linear unbiased prediction (GBLUP) resulted in greater accuracies of EBV than pedigree-based BLUP
 - 0.05 to 0.10 for carcass and meat quality traits in Australian sheep
 - 0.05 to 0.27 (mean = 0.13) per breed for meat, fleece, and litter size traits in New Zealand
 - 0.10 to 0.20 across milk production traits in Lacaune dairy sheep
 - French and UK dairy goat pop: 0.06 for milk yield and 0.14 for fat and protein content

The gain in accuracy - correlated with reference pop. size and genomic heritability

Accuracy and expected genetic gain can increase in the future

Major Genes

- GDF8 for muscling
- BCO2 for yellow fat
- Bmp15, Gdf9 and FecL genes for hyperprolificacy in sheep
- Prp for scrapie resistance in sheep and goats
- Tmem154 for resistance to MAEDI-VISNA
- Socs2 for mastitis susceptibility in sheep
- Casein genes for protein content in goat milk
- A 11.7-kb deletion for polledness in goats

Used in breeding programs: PrP (worldwide), FecL and α -s1 casein gene (French goats)

Pre-select candidates for progeny testing

Genomic tools for new traits

- Traits **with** routine genetic evaluations obtained from phenotypic and pedigree information.
 - Enhanced **accuracy** of genetic evaluations
- Traits **without** routine evaluations.
 - Will allow selection for **novel** but economically important traits.
 - Disease resistance (also ethical benefits in reducing the animals that need to be exposed to disease)
 - Feed efficiency – expensive to measure
 - Methane emissions – expensive to measure
 - Environmental Adaptation

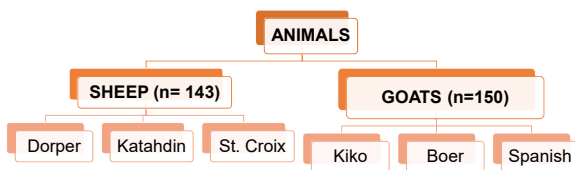
Resistance to internal parasites

- Leading cause of morbidity and mortality in the south central and south eastern U.S.
- No practical solution to internal parasites in small ruminants.
- Resistance to commercial anthelmintics limits the ability to control internal parasites in small ruminants
- Genomics: selection of small ruminants for internal parasite resistance is possible, genomics can help.

Current UF research

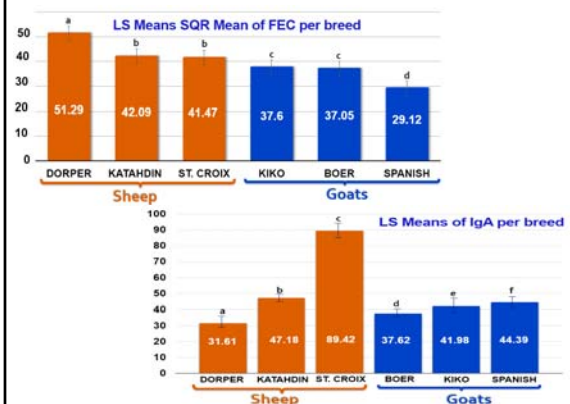
- PhD student Zaira Estrada
- Candidate genes for resistance to internal parasites
- Targeted sequencing of 100+ genes in ~300 resistant and susceptible sheep and goats
- SARE grant “Genetic Markers for Resistance to Gastrointestinal Nematode Infections for a Sustainable Florida Native Sheep Production”

Candidate gene approach - population



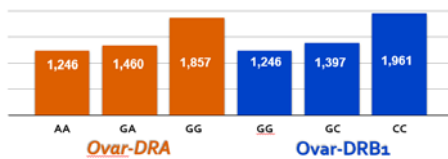
- Challenged with *Haemonchus contortus*
 - Parasitological parameters (FEC)
 - Hematological parameters (packed cell volume)
 - Immunological parameters (IgA, IgG and IgM)

Resistance/susceptibility levels



Candidate genes

- *Ovar-DRA* and *Ovar-DRB1* – genes part of the major histocompatibility complex.
- *Ovar-DRA*, in sheep and goats: A allele associated with 682 less FEC/g
- *Ovar-DRA*, in sheep: G allele associated with 1,503 less FEC/g



SARE grant

- “Genetic Markers for Resistance to Gastrointestinal Nematode Infections for a Sustainable Florida Native Sheep Production”
- 100 Florida Native sheep, extreme levels of resistance
- Identify and validate DNA markers in 100 selected genes
- Evaluate gene expression for the significant DNA markers associated with resistance to validate the results.