

The International Sheep Genomics Consortium (ISGC) is seeking new research collaborations to investigate monogenic traits and disease genes which are segregating in sheep. If you have access to ovine animal resources with associated phenotypic records, and you like to have these animals genotyped at 50,000 SNP at no cost, then please read on.

Background

In partnership with Illumina, the sheep consortium launched the SNP50 BeadChip in early 2009. The SNP50 BeadChip has been used extensively for genome wide association studies (GWAS) and the implementation of genomic selection. It is very well suited for the fine-mapping of monogenic traits, and a number have already been successfully characterised. Examples include microphthalmia in Texel, dwarfism/achondroplasia in both Cheviot and Texel, junctional epidermolysis in German Black Headed sheep, the presence or absence of horns (poll) and yellow muscling found in Perendale.

The Opportunity

The consortium currently has SNP50 BeadChips available to genotype up to 150 animals. Our primary interest is use of these BeadChips to investigate (i) autosomal recessive diseases which are likely to be caused by a single gene or mutation and/or (ii) any phenotypic trait which has sufficient evidence to indicate it is likely to be monogenic.

A precondition of collaboration is that the research findings are published, as the consortium operates purely in the public domain. **If you have access to animal materials, and would like to join the consortium to investigate the genetic basis of phenotypic variation, please write to the ISGC secretary Dr James Kijas (James.Kijas@csiro.au) for more information.**

Also, see below additional details from a poster prepared for presentation at the Plant and Animal Genome conference 2011.

Brian Dalrymple¹ for the International Sheep Genomics Consortium²

¹CSIRO Livestock Industries, Brisbane, Queensland 4067, Australia. ²www.sheepmap.org

**Do you have access to sheep which segregate a monogenic phenotype?
Would you like to have these animals genotyped at 50,000 SNP at no cost?
If you answered yes, keep reading as **the ISGC is seeking
new collaborations to map recessive disorders afflicting sheep.****

Role of the ISGC

The ISGC has developed a range of resources for the *ovine* research community (see Table 1 and [1]).

One of these resources is the *ovine* SNP50 BeadChip which enables genotyping of 50,000 SNP distributed across the genome.



The chip is very well suited for the fine-mapping of monogenic traits. Table 2 lists a number of studies where genes have been mapped to small genomic regions.

Figure 1 shows an example where the BeadChip was used to fine map the mutation causing a limb malformation phenotype in Cheviots [2].

Importantly, few animals are needed to successfully map traits which display autosomal recessive inheritance.

New Projects

The consortium is seeking new research collaborations to investigate disorders/traits which have not yet been examined using genome wide association.

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- * autosomal recessive diseases which are likely to be caused by a single gene or mutation
- * any phenotypic trait which has sufficient evidence to indicate it is likely to be monogenic

A precondition of collaboration is that the research findings are published, as the consortium operates purely in the public domain. If you have access to animal materials, and would like to join the consortium to investigate the genetic basis of phenotypic variation, please write to Dr Brian Dalrymple or Dr James Kijas (James.Kijas@csiro.au) for more information.

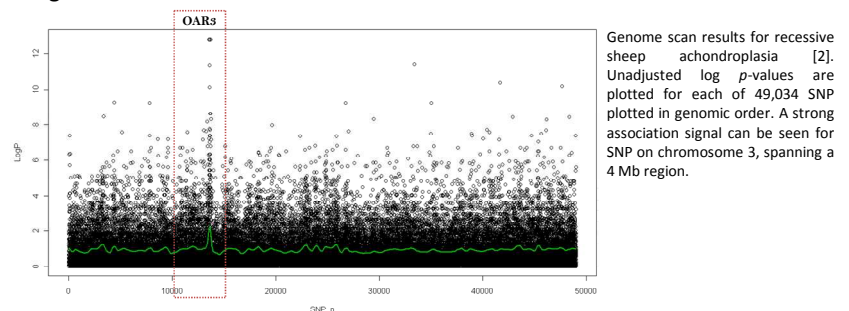
Table 1

Genomic Resource	Description and Reference
Draft Reference Genome	Launched here at PAG 2011: Cattle and Sheep Workshop
Linkage Map	Microsatellite based linkage map produced through genotyping of the International Mapping Flock. See Maddox <i>et al.</i> , 2001
Virtual Sheep Genome	Comparative analysis of BAC end sequences to generate a virtual assembly http://www.livestockgenomics.csiro.au/vsheep/
CHORI-243 BAC library	A 12 fold coverage BAC library constructed from a single male Texel. Sequencing contributed to the draft reference genome assembly.
Illumina GA sequence and 76,000 SNP	Deep re-sequencing of pooled genomic DNA from 60 animals identified approximately 76,000 SNP.
Roche 454 sequence and 595,000 SNP	Three-fold coverage of 454 sequence derived from six animals. Alignment identified approximately 595,000 SNP. https://isgdata.agresearch.co.nz/
Ovine SNP50 BeadChip	Illumina Infinium based platform for genotyping 50,000 SNP
INRA 1200-rad RH Panel	RH panel used for the assignment of sequence tagged sites. See Laurent <i>et al.</i> , 2007.
USDA 5000-rad RH Panel	RH panel used for the assignment of sequence tagged sites.

Table 2

Trait	Description	Map Location	Contacts and Reference
Achondroplasia	Limb malformation in UK Cheviots	OAR3: Mb 153 – 157	James Kijas/Steve Bishop [2]
Chondroplasia	Dwarfism/Limb malformation in Texel	OAR4: 1 Mb region	Dorrian Garrick [3]
Microphthalmia	Ocular abnormality in Texel	OAR22: <i>PITX3</i> mutation	Cord Drogemuller [4]
Poll	Absence of Horns	OAR10: <i>RFXP2</i> gene	John McEwan [5] and Jon Slate [6]
Junctional Epidermolysis	Skin disease of German Black Headed sheep	OAR12	Ottmar Distl [7]
Yellow Fat	Yellowing of adipose tissue in Perendale	OAR15	John McEwan

Figure 1



[1] ISGC *et al.* (2010) *Animal Genetics* 41(5): 449 - 453
 [2] ISAG Abs P5026 (2010); james.kijas@csiro.au; stephen.bishop@roslin.ed.ac.uk
 [3] PAG Abs P579 (2010); dorian@iastate.edu
 [4] PLoS ONE (2010) e8689; cord.drogemuller@itz.unibe.ch

[5] ISAG Abs P3095 (2010); john.mcewan@agresearch.co.nz.
 [6] j.slate@sheffield.ac.uk
 [7] ottmar.distl@tiho-hannover.de
 [8] www.sheepmap.org

Acknowledgments. The International Sheep Genomics Consortium is a group of scientists with a shared interest in the genetics and genomics of sheep. The consortium holds periodic phone conferences, and anyone interested to participate can contact the secretary (James.Kijas@csiro.au). Funds to purchase the SNP50 BeadChips described in this project were obtained from an International Science Linkage Grant (CG090143). The authors wish to thank Prof Frank Nicholas for making this possible. The full list of organizations, along with the key researchers active in ISGC projects, can be found at <http://www.sheepmap.org>