



# Globaldiv

## GLOBALDIV NEWSLETTER

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### Editorial: PAG - The Plant and Animal Genome conference: a glimpse into the future of animal and plant genetics

The last XVIII Plant and Animal Genome Conference (PAG), held in San Diego in January 2010, brought together the leading scientists and researchers involved in plant & animal genetics and related areas.

With over 50 countries represented, the Plant & Animal Genome Conference provided an international forum for the exchange of information on hot topics in basic and applied molecular genetics and genomics and a great opportunity to discuss the state of the art and perspectives of genomics applied to organisms of agricultural importance.

The general impression is that research in both plant and animal science is experiencing a great impulse by the exploitation of new technologies and that future directions point to a wider use of next-generation sequencing, high density SNP panels and gene expression methods. Applications based on novel technologies far outweighed any other type of presentation at the Conference. Re-sequencing of an organism appeared much easier and cheaper compared to even a couple of years ago. However, still a number of technical challenges are to be faced and overcome, to fully exploit the power of high-throughput approaches. Computing power and data storage are limiting factors. Methods and software for data management, error detection and analysis are still to be optimized. However, considering the exceptional high rate of recent technological and computational advances, all speakers seemed quite confident in the ability of researchers to solve these issues in the coming future.

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Among the interesting presentation given in animal genetics, particularly fascinating resulted the invited lecture entitled "Dynamic Duplications and Genome Evolution" held by Prof. Eichler from Washington University.

Prof Eichler showed how in the last years segmental duplications have been recognized as important mediators of both gene and genome evolution in humans and mouse. Segmental duplications are substrates of genome innovation, genomic rearrangements, and hotspots of copy number variation (CNV) within species. Furthermore, the duplications often encode protein products playing a role in the adaptation to specific ecological niches. Among mammalian species, commonly duplicated genes include those associated with innate immunity, drug detoxification, olfaction, and sperm competition. Unfortunately, regions of large-scale duplication are still particularly problematic for genome assembly, SNP mapping and genotyping. Prof. Eichler also gave a summary of the first systematic and genome-wide analysis of segmental duplications in the modern domesticated cattle (*Bos taurus*). Surveying the publicly available bovine genome sequence assembly by two well-established computational approaches, whole genome shotgun sequence detection (WSSD) and Whole Genome Assembly Comparison (WGAC) prof Eichler and co-authors estimated that 3.1% (94.4 Mb) of the bovine genome consists of recently duplicated sequences (= 1 kb in length, = 90% sequence identity). Similar to other mammalian draft assemblies, almost half (47% of 94.4 Mb) of these sequences have not been assigned to cattle chromosomes.

He concluded highlighting the importance of understanding the nature and pattern of segmental duplications in mammals, to provide fundamental insight into functional redundancy, adaptive evolution, and the structural dynamics of chromosomal evolution.

A number of other interesting presentations were organized in workshops devoted specifically to crop and animal species. The topics spanned from cattle and sheep genomes to aquaculture, from poultry genomics to host-pathogen interaction, including animal epigenetic, swine genomics, advanced genotyping strategies, phylogenomics, proteomics etc.

In conjunction with the 5 day scientific program and the two poster sessions, extensive software sessions were organized, to inform on what's presently available and about to come in the near future. These comprised an entire workshop organized by the National Center for Biotechnology Information (NCBI; [www. www.ncbi.nlm.nih.gov/](http://www.ncbi.nlm.nih.gov/))

Further, several private company presentations gave an excellent overview on the most recent and potential applications of the latest Next-Generation technologies.

The proceedings of the XVIII The Plant & Animal Genome Conference are downloadable from the congress web-site ([www.intl-pag.org](http://www.intl-pag.org)).

The next PAG meeting will be held in San Diego January 15-19, 2011.

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# Article of the month - The Yakutian cattle: A cow of the permafrost

**Juha Kantanen**

Siberia's last remaining indigenous breed of domestic cattle, the *Sakha Ynaga* (in Yakutian language), or Yakutian Cattle, inhabit the lands surrounding the Lena River in Russia's remote Sakha Republic (Yakutia). A Finnish multidisciplinary team of researchers from MTT Agrifood Research Finland and the University of Helsinki's Aleksanteri Institute explored the genetic uniqueness of the Yakutian cattle and the effect of social and cultural factors on the survival of the breed through periods of major upheaval in Russia's history. The findings of this study have now been published in the book *Sakha Ynaga - Cattle of the Yakuts*.

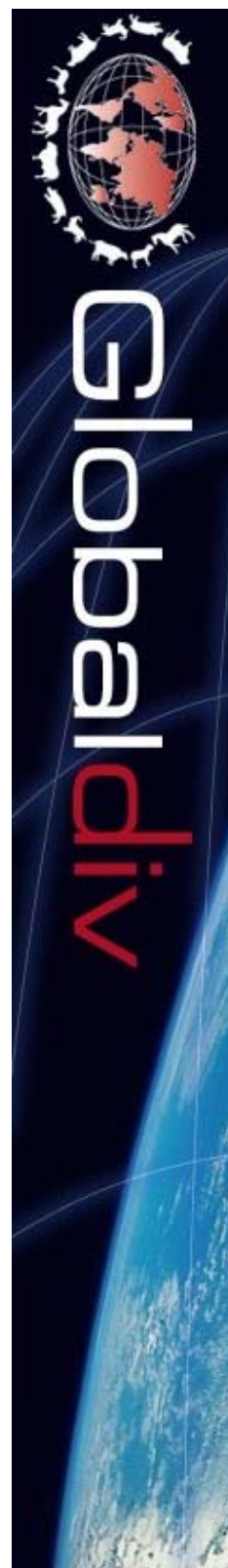
## The last Siberian native cattle breed

About 150 kilometres north of the Arctic Circle, exists a unique population of Yakutian Cattle in the harsh conditions of the world's coldest populated region. The relationship with the Yakutian Cattle has enabled the people of the region to inhabit this land of permafrost, where the temperature can drop to  $-50^{\circ}\text{C}$ , where winters are long and summers short and where grain production is not possible.

The Yakutian Cattle are currently an endangered cattle population of small census size. The Laboratory of Cattle Breeding of the Yakutian Research Institute of Agriculture in Yakutsk maintains records on the Yakutian Cattle. The current population is 1,200 head, of which more than 500 are dairy cows. The population size has remained stable during recent years. Up to 74% of the Yakutian Cattle are distributed in the three northern villages of Dzhargalakh, Kustur and Batagay-Alyta (also called Sakkyryr), collectively termed the Eveno-Bytantay district. During the last decade, the Yakutian Cattle were returned to the southern part of the Sakha Republic from where they had vanished and are therefore currently found also in the village of Uluu-Syhyy and on four farms closer to the capital of Sakha, Yakutsk City.

The Yakutian Cattle are purebred aboriginal cattle population that produces milk and meat. Animals have been used also as a source of draft power. Yakutian Cattle are characterised by their small size, deep but relatively narrow chest and short, firm legs. The live weight of cows ranges from 350 to 400 kilograms and that of bulls from 500 to 600 kilograms. The breeding bulls stand from 115 to 127 centimetres high, on average 121 centimetres, at the withers. The wither height of cows is typically 110 to 112 centimetres.

The current average annual milk yield of the Yakutian Cattle is approximately 1,000 kilograms. The milk has a high percentage of fat and protein, on average 5.03% and 4.69% respectively.





## A multidisciplinary study

During its four field research expeditions to Yakutia, the Finnish research team gathered important findings on the many genetic and sociocultural dimensions involved in animal genetic resource conservation. The material for the study came from DNA marker analyses, field observations, interviews with inhabitants from the northern Siberian villages and with local and governmental authorities, media research, statistical demographic data, and historical records. The research project was part of the Russia in Flux research programme of the Academy of Finland. The genetic analyses were also part financed by the Finnish Ministry of Agriculture and Forestry.

The researchers shed light on the importance of Yakutian Cattle to cattle owners, villagers, researchers and local authorities in the region, and to the future of the region's villages.

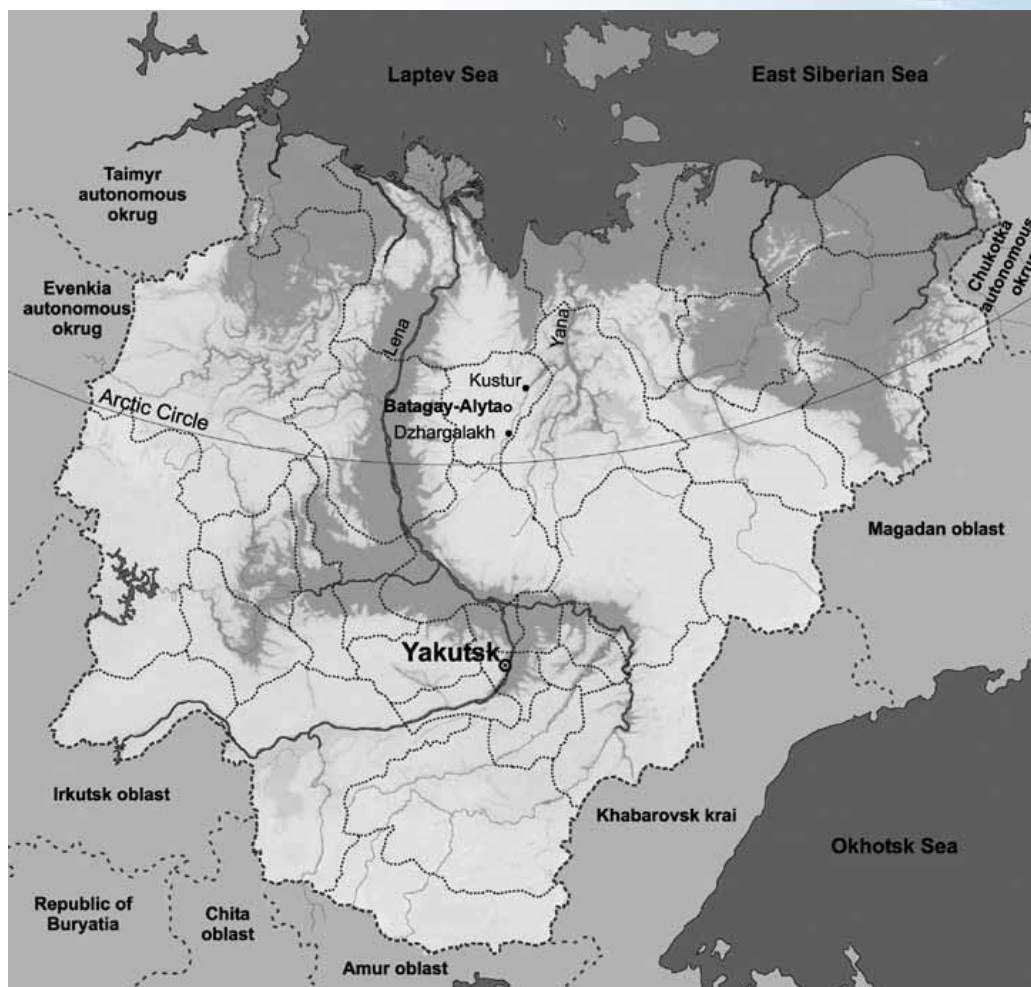


Figure 1. Geographical location of the Eveno-Bytantay district in the Sakha Republic.



## DNA marker analyses

The genetics of the Yakutian Cattle have been investigated by comparing DNA marker data of the Yakutian Cattle with the DNA data of several European and Asiatic cattle breeds. These studies have revealed insights into the history of the Yakutian Cattle and the current genetic diversity.

Analysis of mitochondrial DNA (mtDNA) sequences showed that the taurine T3, T2 and T4 mtDNA haplogroups are segregating in the Yakutian Cattle. The T4 has found so far in eastern Asia, but not in the Near Eastern cattle breeds. The mtDNA study indicated that the Yakutian Cattle share prehistorical maternal ancestries with the domesticated Near Eastern cattle. In addition, the Y-chromosomal data suggest that the Yakutian Cattle have affinity with some European and Near Eastern cattle breeds.

Analysis of autosomal DNA markers showed that the Yakutian Cattle are differentiated from other studied breeds and display a lower level of genetic diversity than several other Eurasian cattle breeds. This observation can be explained by long-term geographic and genetic isolation at the northern limit of the species range. On the other hand, foundation stocks of the Yakutian Cattle might have been small.

## Socio-diversity as a guardian of biodiversity

The Yakutian Cattle have many distinct values. Six different value categories were identified: ecological, economic, social, political, cultural, and ethical. The rural people of northern Siberia have traditionally relied on their cattle during times of social upheaval, such as the Russian revolution and the soviet collapse. During the soviet era, it was the actions and defiance of traditional cattle breeders and individual scientists which saved the Yakutian Cattle from otherwise certain loss through crossbreeding.

Views were shown to be unanimous regarding the need to preserve the breed, but the reasons for holding this common view varied. The local inhabitants and experts saw the cattle as vital to securing the self-sufficiency and vitality of their local village communities. Their main goal was to develop economically sustainable cattle production. The view among the experts and authorities in the republic's capital Yakutsk were, on the other hand, primarily interested in preserving the cattle's gene pool for the development of agriculture throughout the wider republic. The region's press media and, but also the Yakutsk authorities, emphasised the importance of the cattle as part of the cultural heritage of Yakutia. This shared desire to preserve the Yakutian Cattle has led to the Sakha Republic's own, and possibly the world's very first, domestic breed conservation law.

The biggest indigenous herd is currently held on the former Lenin Sovkhoz state farm in the village of Kustur, the present-day experimental farm of the Agricultural Research Institute of Yakutia, but it is also common for ordinary people such as teachers, bakers and reindeer herders to keep a few cows for their own domestic use, and the cattle are also bred by several private farmers and co-operatives. The study indicated how the conservation of genetic resources is supported by such diverse social structures.







Figure 2. The bull in the state farm is nervous because two new bulls arrived in the cowshed last night. The rotation of bulls between the three villages (Dzhargalakh, Kustur and Batagay-Alyta) was launched after a ten year break. Photograph by Anu Osva.

The book can be ordered - see bibliography section of this newsletter

## The breed (??) of the month - The Alpaca

**Mike Bruford (Cardiff University) and Jane Wheeler (CONOPA, Lima, Peru)**

First, an explanation! The question-mark in the title refers to the fact that (1) the alpaca is not a breed, but a domestic species (*Vicugna pacos*), and (2) the modern alpaca does not have any recognised breeds: it is a domestic animal for which the word 'breed' is singularly inappropriate! Indeed there are many reasons why the breed concept is non-operational in South American livestock, some of which are explained below.



The alpaca was originally domesticated around 7,000 years ago in the Peruvian Andes and its ancestral origins have been the subject of intense debate (Wheeler 1995), since there were two potential wild ancestors, the guanaco (*Lama guanicoe*) and vicuña (*Vicugna vicugna*) extant at this time, and these species are still present in the Andes today. In 2001 Kadwell and colleagues provided the first molecular genetic evidence using both nuclear and mitochondrial DNA that its ancestor was far more likely to have been the vicuña (Figure 1). This evidence was considered convincing enough to result in the scientific nomenclature for this species to be changed from *Lama pacos* (a name which reflected the original opinion that the guanaco was the alpaca's ancestor) to *Vicugna pacos* (Gentry *et al.*, 2004). Although still not universally accepted, ironically this finding was first predicted by Darwin in volume 1 of his "The variation of animals and plants under domestication" in 1868!

The main product that the alpaca has traditionally been raised to produce is fine, lanolin-free wool and archaeozoological evidence from camelid mummies points to the existence of exceptionally fine wool alpaca varieties in the Andes hundreds of years before the arrival of the Spanish conquistadors. Unfortunately the camelid raising tradition in both pre- and post-Hispanic Andean communities was exclusively oral, so we have no documentary evidence for the existence or otherwise of 'breeds' of alpaca before the Spanish arrival in 1530, although it is likely that different colour varieties were separately maintained for different cultural practices. Quipus (the so-called 'talking knots' used by the Incas) were probably used by the yana (the hereditary cast of alpaca and llama herders under the Inca) to keep herd records and determine breeding schedules, and the resultant animals may have reached the level of breeds in the present day definition of the term, but this tradition lost during the conquest. Within 100 years after the arrival of the Spanish, 80-90% of both the indigenous human and livestock populations had disappeared (Wheeler, 1995).

Since that time, due to the loss of knowledge and genetic resources associated with this major event and the application of inappropriate sheep-rearing practices learned from the colonialists, alpaca quality has declined dramatically from pre-Hispanic standards, especially in Andean countries, despite the fact that alpaca wool is an extremely important component of the local economy and of the wealth of the rural poor. More than 3 million alpaca are currently raised in the Peruvian Andes alone and the species is also found in Ecuador, Bolivia, Chile and Argentina. At the same time alpaca raising has become both fashionable and economically significant outside South America in recent decades, especially in the USA and Canada, Australia, Switzerland and the UK. The application of modern breeding methods in



Figure 1. The vicuña (*Vicugna vicugna*).  
Photo: Jane Wheeler.

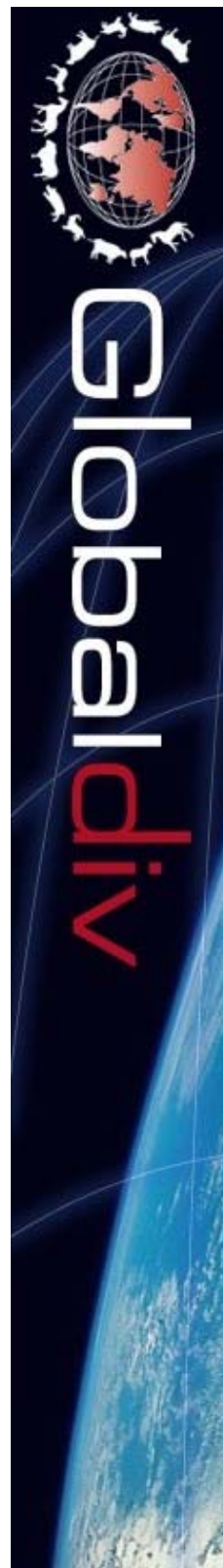






Figure 2. Brown suri alpaca

these countries means that wool quality is being optimised at a rate that outpaces the countries in which these species were once indigenous. High quality alpaca wool can sell for prices considerably higher than most fine sheep wool. Today, alpaca are mainly divided into two varieties - suri (or longwool alpaca, see figure 2) and huacaya (or curly wool alpaca, see figure 3) which may be relics of breed types selected by pre-Hispanic herders, with different colours being selected within these wool types (mainly white as seen in the figure below: more than 20 colours occur).

Unfortunately, Andean producers have failed to maintain wool quality due to poor husbandry practices and a lack of control. Chief among these problems has been the

ongoing practice of hybridising alpaca with the other domestic south American camelid, the llama (*Lama glama*, originally domesticated from the guanaco) to increase the weight of fleece for sale, because of a policy of paying producers by weight as opposed to fibre quality and diameter. Although the archaeological mummies indicate that llamas were bred for fine fibre production, they are particularly known for their role as pack animals and it has long been assumed that this was their only role in prehispanic times. Llamas were used extensively as pack animals by the Incas during the expansion of their empire prior to the arrival of the Spanish. In the post-conquest chaos, however, traditional breeding practices and knowledge were lost, and the few surviving alpacas and llamas were relegated to areas of extreme elevation where the Spanish, and their Old World sheep, could not survive. It is likely that, in this context, hybridization of the two domestic camelids began. Unfortunately, the llama X alpaca crosses produce fertile offspring of intermediate size with poor quality, coarse wool. In recent years the practice of hybridization has become common place since the industry fiber purchase policy has been, until very recently, payment by weight without consideration of fiber quality. Kadwell *et al.* (2001) have since found evidence for hybridization in more than 80% of alpacas tested across the Andes, and worryingly it is not possible to detect hybridization using quantitative characters alone. Although some of the wool producers in the Andes have their own elite herds which have been selected to produce fine (< 25 micron) fibre, the vast majority of alpaca husbandry in the region still lacks the application of best practice and so the fibre produced remains uncompetitive compared to cashmere or pashmina wool, which is up to 6 microns finer.



Figure 3. White huacaya alpaca  
(Photo: Jane Wheeler)



The solution, therefore, for Andean countries, lies in a concerted effort to document the current situation regarding alpaca genetic resources, including the understanding the current levels of cross species hybridization and aligning this approach to detailed phenotypic characterization. In this way the most genetically valuable populations can be identified, conserved and ultimately used for the improvement of other populations in the region. This will require a mammoth effort but with the alpaca genome having recently been sequenced, huge potential exists to undo the damage done by our European forebears and return the alpaca to the elite of fibre producing livestock in the not-too-distant future.

## References

Darwin CR. 1868. The variation of animals and plants under domestication. John Murray, London.

Gentry A, Clutton-Brock J, Groves CP. 2004. The naming of wild animal species and their domestic derivatives. *J. Arch. Sci.* 31, 645-651.

Kadwell M, Fernandez M, Stanley HF, Wheeler JC, Rosadio R and Bruford MW. 2001. Genetic analysis reveals the wild ancestors of the llama and alpaca. *Proc. R. Soc. Lond B.* 268, 2575-2584.

Wheeler J. 1995. Evolution and present situation of the South American camelidae. *Biol. J. Linn. Soc.* 54, 271-295.

## Events calendar

- Armidale Animal Breeding Summer Course 2010 - University of New England, Armidale, NSW Australia - Wednesday 27 January - Friday 5 February 2010. Course Audience: Postgraduate students and other professionals  
[www.cattlenetwork.net/2010.htm](http://www.cattlenetwork.net/2010.htm)
- Precision Dairy Management, Toronto (Canada), 2-5 March 2010, Progressive Dairy Operators 1st Triennial Conference "Technology for Today & the Future"  
[www.precisiondairy2010.com](http://www.precisiondairy2010.com)
- Global Conference on Agricultural Research for Development (GCARD) - Enhancing Development Impact from Research: Building on Demand, 28-31 March 2010, Montpellier, France  
[www.egfar.org/egfar/website/gcard](http://www.egfar.org/egfar/website/gcard)

## Bibliography

The book of the Article of the month can be ordered from Bookstore Tiedekirja at: [www.tiedekirja.fi](http://www.tiedekirja.fi)

Sakha Ynaga. Cattle of the Yakuts

Eds. Leo Granberg, Katriina Soini & Juha Kantanen

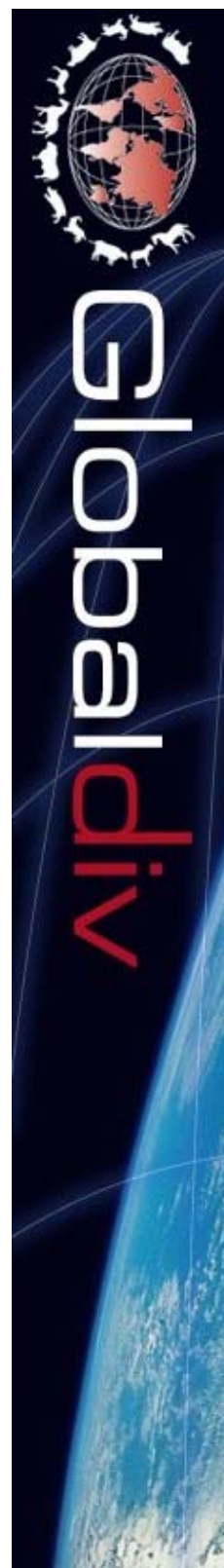
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