Globaldiv

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Editorial: The NEXTGEN project: whole-genome sequencing for preserving cattle, sheep, and goat biodiversity

Next April, the European FP7 project NEXTGEN will start. The consortium is composed of eleven partners from France, England, Italy, Germany, Switzerland, Morocco, Uganda, Iran, and Australia.

DNA sequencing technologies are currently evolving at a fast pace. Recently, Illumina released the HiSeq sequencer (*www.illumina.com/systems/hiseq_2000.ilmn*). In a single run, for a cost lower than 20,000 $, this sequencer can produce either two mammalian genomes, each with a ~30x coverage, or 8 genomes with a ~7.5x coverage. There is no doubt that sequencing technologies will further improve in the next few years. As indicated in the Editorial of the December 2009 issue of Globaldiv newsletter, computing power and data storage will be the limiting factors.

Thus, in the context of whole-genome data availability, NEXTGEN global objective is to develop optimized methodologies for preserving farm-animal biodiversity.

More specifically NEXTGEN aim to:

- Produce whole genome data in selected populations of cattle, sheep, and goats: comparing and contrasting industrial breeds from Europe, local breeds from Europe, Africa, and Middle East, and sheep and goat wild ancestors.
- Transfer, adjust and enhance the bioinformatic methodologies and infrastructure: transferring methods developed within the 1000 human genome project to farm animals (cattle, sheep, goats).
- Develop tailored methodologies for comparative genome analysis in cattle, sheep, and goats: these will include analysis of nucleotide diversity and detecting signatures of selection along the genome (to distinguish neutral versus adaptive variation).
- Develop genomic methods for the identification and mating of animals to optimize selection response and maintenance of genetic variability: methods will consider genetic gain and genetic contribution of founders and will be developed for both purebred and crossbreeding programs.
- Develop approaches, based on whole-genome data, for the selection of animals for bio-banking: methods will consider various sources of information, including genomic, phenotypic, pedigree and geographic data and their combination.
- Develop new bio-banking technologies: a freeze-drying technology will be adapted to cells and female gametes (oocytes); this low cost methodology will greatly simplify the establishment and maintenance of gene banks, which immortalise cells lines/gametes from rare breeds, compared to current resource intensive cryo-conservation methods using liquid nitrogen.
- Explore new strategies to identify disease resistance genes: integrating and comparing information on the geographic distribution of selective sweeps and the prevalence of target diseases. This approach will lead to the development of new strategies for detecting genomic regions and genes controlling traits, which are very difficult or very expensive to identify with other experimental approaches.
- Design and validate a methodology for studying genome/environment relationships: by sampling sheep and goats using a grid system over an area of traditional breeding (relatively undisturbed by the recent spread of industrial breeds) across contrasting environments, by producing whole-genome data for these samples, and by analyzing the results within a GIScience context.
- Assess the potential of breeds (cattle, sheep, goats) from domestication centres as genetic resources: by comparative analysis of genomic diversity of local breeds from the original centres of domestication with local breeds in Europe, Uganda, and Morocco, and with industrial breeds in Europe; this analysis will clarify the conservation priority that should be given for breed from these "cradles of agriculture".

- Establish the relevance of wild ancestor species as genomic resources: by comparative analysis of genomic diversity in centres of domestication between local breeds and wild populations.

Scientists of the NEXTGEN consortium are from diverse scientific disciplines such as conservation genetics, genomics, bioinformatics, geographic information science, veterinarian sciences, and agricultural sciences. A close collaboration among these disciplines represents an important added value, and is the key to the success of such an integrated project that should have a strong impact on farm animal conservation genetics.

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Article of the month - Livestock and biological diversity: grazing natural and semi-natural grasslands

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Livestock intensification and biodiversity loss

Livestock production plays an important role on the crisis that world's biodiversity is facing. Livestock-environment interactions and in particular contributions of livestock to changes of the environment were assessed a few years ago through the LEAD initiative (Steinfeld *et al*., 2006). Habitat change, climate change, invasive alien species, overexploitation and pollution were identified as important drivers of biodiversity loss. Concerning habitat change, considered the most important category of threat to global biodiversity, livestock production, through colonization of new areas and intensification, has contributed to deforestation, destruction of riparian forests, drainage of wetlands, desertification of overgrazed areas, fragmentation and degradation of habitats of high biodiversity importance.

Grazing abandonment and biodiversity loss

In some areas of the world, traditional grazing through centuries contributed to create and maintain ecosystems of high biodiversity value. Farming systems and semi-natural agro-ecostems have co-evolved, are today strictly dependent each other, with grazing animals playing a unique ecological role. In these cases threats are twofold, livestock intensification leading to habitat destruction and suboptimal grazing or abandonment leading to succession to different ecosystems and consequent biodiversity loss. The process has been reported in particular in Europe, where natural and semi-natural grazed grasslands are important biodiversity and landscape resources. Most temperate grasslands are sub-climax communities, therefore they need periodic defoliation to control succession to scrub and eventually woodland (Rook *et al*., 2004). Rook *et al*. (2004) reviewed the mechanisms by which grazing animals create sward heterogeneity, and related high biodiversity, in these areas. The most important mechanism seems to be selective defoliation linked to dietary choices (Olff and Ritchie, 1998; Bullock and Marriott, 2000). Other mechanisms are treading, nutrient cycle and propagule dispersal (e.g. Bakker, 1998). The relative importance of these four mechanisms depends on grazing pressure, type of grasslands, and type of grazing animals. The effects of livestock grazing on the plant community lead to important secondary effects on invertebrate diversity (e.g. Tscharntke and Greiler, 1995); The abandonment of mountain fields and meadows with a consequent. expansion of shrubs and woodlands has caused a decline in several vertebrate species including the rock partridge (Alectoris graeca) and the cappercaille (Tetrao urogallus) (e.g. Chemini and Rizzoli, 2003). The list of habitats that are considered as being of European importance (European Council Habitat Directive - Annex 1, 1992) include sixty-five types of pasture that are under threats from grazing intensification, but also twenty-six types that are threaten by grazing abandonment.

Sward biodiversity and breed effects ?

Rook *et al*. (2004) analysed the possible effects of the type of grazing animals on sward heterogeneity and consequently on natural and semi-natural grassland biodiversity. Beside the more evident effects of body size (small herbivores require more energy relative to their gut capacity and therefore select higher food quality), species (much literature is available of morphological and physiological differences among grazers, intermediate feeders and browsers) and sex and age (females and young animal often show greater selectivity), it might be interesting within a Globaldiv perspective to review what is known relatively to breed effect. Breed differences in grazing behavior and pasture use received limited attention. Highland suckler cows grazing improved Alpine pastures showed excessive N intakes with respect to Brown Swiss dairy cows, with consequent higher urinary returns rates to pastures, showing a possible breed effect on nutrient cycle. However, absolute levels per area were comparable between breeds, because the higher intake of Brown Suisse dairy cows (Berry *et al*., 2003). Salers heifers were reported to have shorter daily grazing times and higher biting rates respect to Limousine heifers of similar weight (D'hour *et al*., 1994). Higher proportion of bites were taken on short patches with more digestible herbage by Meuse-Rhine-Yssel dual purpose steers with respect to Hereford beef steers (Wallis-DeVries, 1994), however, although both animals were of similar weight, MRY where less mature thus with higher maintenance requirements. S?ther *et al*. (2006a) recorded some differences on grazing behaviour between the high yielding Norwegian Red dairy cattle and the moderate yielding old dairy cattle Blackside Tronder and Nordand

Cattle, where Norwegian Red cows had a higher standing behaviour, but lower walking and playing behaviours. Concerning vegetation preferences (Saether *et al*., 2006b), Norwegian Red cows in low fertile soil selected more nutrient rich vegetation with respect to the old breed. Finally, it should pointed out that some of these comparison somehow fail to separate true genetic effects from other effects, such as prior experience of the animals on the pastures used for comparison.

Conclusions

This short communication points out the need for more research on breed differences in grazing behaviour and use of natural and semi-natural grasslands. Information might be of use in planning the management and conservation of these areas. It also underlines the importance of an interdisciplinary approach for the conservation of both local breeds and natural biodiversity.

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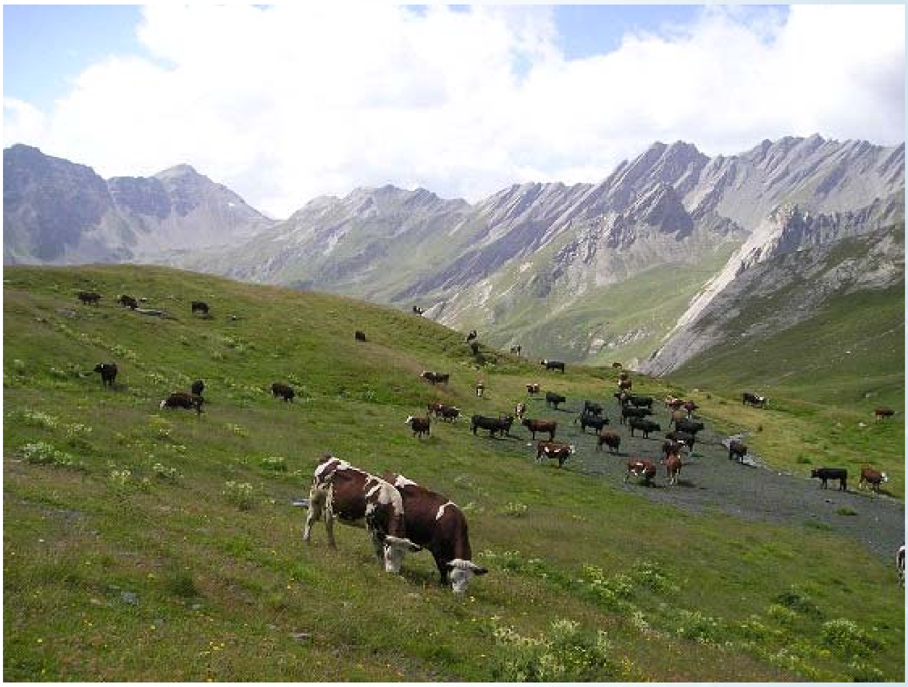

Figure 1. Valdostana cattle on summer Alpine pasture.

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The breed of the month - The Amiatino donkey

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For centuries the domestic donkey (*Equus asinus*) has been used for work and for transportation of people and goods in agriculture and military. But during the 20th century, the European donkey populations started to suffer from a severe reduction in population sizes when technology improvement and growing industrialization progressively affected the management and use of livestock species (Starkey & Starkey, 2000). In Italy, the number of recorded donkeys dramatically decreased by 96% between 1939 and 1996, declining from 790,000 to 27,000 heads. Nevertheless, today Italy still possesses 8 autochthonous breeds, classified by FAO as critically endangered (Asinara, Pantesco, Grigio Siciliano and Romagnolo) or endangered (Amiatino, Sardo Grigio, Martina Franca and Ragusano), while 4 more breeds (Cariovilli, Emiliano, Grigio Viterbese and Sant'Alberto) became extinct during the last century. More recently, some conservation efforts have been made to preserve the remaining Italian autochthonous breeds through the use of donkeys for onotherapy, especially with children, or for the production of meat (salami, stew etc.) and milk to be used in cosmetics industry or for human consumption in cases of food allergies to cow milk.

The Amiatino donkey is named after Mount Amiata (province of Grosseto, Tuscany), the place where the original nucleus of the breed was reared. The presence and exploitation of the domestic donkey in this region is documented since prehistorical times, when the Phoenicians and the Etruscans used this species for the transport of commercial goods, but the recognition of the Amiatino as a breed probably begun only in the 20th century. The selection of a set of breeders and the definition of the standard date back to year 1955, but only in 1974 the Amiatino phenotype reached its present appearance: grey coat (sometimes reddish-grey) with dark shoulder cross, ears with dark borders, blond-white belly, mouth and rings around the eyes. Distinctive zebra stripes are present on the four legs (Figure 1), giving the Amiatino a close resemblance to the Somali wild ass, *Equus asinus somalicus*. Height at withers at 30 months of age is 1.30-1.40 m for males and 1.25-1.35 for females (Baroncini, 2001; Kugler *et al*., 2008). Besides the phenotypic appearance, a relationship between this breed and the Somali wild ass seems confirmed by genetic evidence; in fact, the analysis of mitochondrial control region sequences of 48 individuals showed that Amiata donkeys are characterized by haplotypes belonging to the E. a. somalicus lineage only (Pellecchia *et al*., 2007).

Traditionally used as a working and draught animal, or for riding especially in mountainous regions, due to its rusticity and resistance to diseases the Amiatino can survive also in harsh environments. The last census available on the F.A.O. website (2007; *http://dad.fao.org*) records a population size of about 750 heads, with 30 sires and 275 mares, although the present breed trends are reported as "unknown".

During the last decades, anyway, the Italian public Institutions and private breeders associations made strong and effective efforts to preserve the Amiatino donkey from extinction. In particular, the activity of the breeders association "Allevatori Micci Amiatini (A.M.A.)" (*www.ouverture.it/maremma/associa/ama.htm*) and the Faunistic Park of Monte Amiata (Arcidosso municipality, province of Grosseto) was remarkable. Recently, during year 2009 an innovative project (*www.asinispazzini.net/il-progetto-eng/the-donkey-project*) has been launched by the Municipality of Santa Maria a Monte (province of Pisa, Tuscany) to promote the use of Amiatino donkeys for the door-to-door collection of recyclable waste in an environmental-friendly fashion, which can also contribute to the knowledge and rediscovery of this breed by the general public.

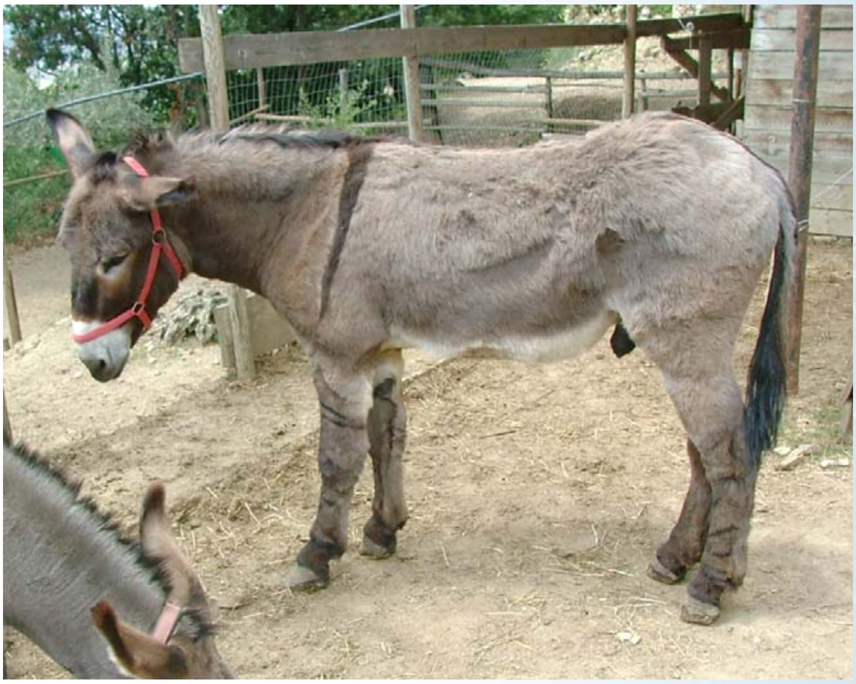

Figure 1. The Amiatino donkey. Photo: Licia Colli.

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GloablDiv Event

Livestock Biodiversity Workshop - FAO, Rome, May 5-6, 2010

Which policies and strategies are required to successfully maintain our European Farm Animal Genetic Resources? What are the opportunities of the latest methodologies to characterize and prioritize livestock breeds? During the past two years, the GLOBALDIV and EURECA projects have been focused on these questions. GLOBALDIV and EURECA are both GENRES projects which are co-funded by the EU AGRI GENRES program. This program aims to contribute to a better characterization of farm animal genetic resources and to strengthening of conservation efforts.

The GLOBALDIV and EURECA projects are pleased to announce a joint 2-days workshop for policy makers, scientists, NGO's and representatives of industry. Outcomes and recommendations from GLOBALDIV, EURECA and other GENRES projects will be presented. Lecture topics will span from genomics to socio-economic issues in biodiversity conservation.

More information is available at:
www.globaldiv.eu/Livestock_Biodiversity_Workshop/index.html

Events calendar

- 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*
- Foot and Mouth Disease International Symposium and Workshop from 12 - 14 April 2010 in Melbourne Australia, *www.fmd2010.com.au*

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Influence of precocious milking of cows on the growth and the health of calves in traditional breeding in the suburban zone of Natitingou (Benin); B G Koutinhouin, A K I Youssao, T M Kpodékon and Y G Gantoli (In French). *www.lrrd.org/lrrd22/2/kout22024.htm*

Participatory analysis of the farming system and resources in Wundanyi location, Taita district, Kenya: A livestock perspective; P M Mwanyumba, A Mwang'ombe, E Lenihan, F Olubayo, M S Badamana, R G Wahome and J W Wakhungu. *www.lrrd.org/lrrd22/2/mwan22026.htm*

Effect of feedlot regimen on performance and carcass characteristics of Sudan Baggara Zebu cattle; S R Fadol and S A Babiker. *www.lrrd.org/lrrd22/2/fado22027.htm*

Artificial insemination in Algeria: Study of some factors of influence among dairy cows; M K Ghozlane, A Atia, D Miles and D Khellef (In French). *www.lrrd.org/lrrd22/2/ghoz22028.htm*

Characterizing and predicting chemical composition and in vitro digestibility of crop residue using near infrared reflectance spectroscopy (NIRS); Dereje Fekadu, Seyoum Bediye and Zinash Sileshi. *www.lrrd.org/lrrd22/2/feka22029.htm*

Growth performance of two African catfishes *Clarias gariepinus* and *Heterobranchus longifilis* and their hybrids in plastic aquaria; G.A. Ataguba, P A Annune and F.G. Ogbe. *www.lrrd.org/lrrd22/2/atag22030.htm*

Contribution of small scale dairy farming under zero-grazing in improving household welfare in Kayanga ward, Karagwe District, Tanzania. J Lwelamira, H K Binamungu and F B Njau. *www.lrrd.org/lrrd22/2/lwel22031.htm*

Productive and reproductive performance of Holstein Friesian dairy cows in Ethiopia; M Tadesse, J Thiengtham, A Pinyopummin and S Prasanpanich. *www.lrrd.org/lrrd22/2/tade22034.htm*

Challenges in milk processing and marketing among dairies in the semi-arid tropical Kenya; D M G Njarui, M Gatheru, J M Wambua, S N Nguluu, D M Mwangi and G A Keya. *www.lrrd.org/lrrd22/2/njar22035.htm*

The effect of harvest stage on the potential nutritive value of kermes oak (*Quercus coccifera*) leaves; C Atasoglu, S Sahin, Ö Canbolat and H Baytekin. *www.lrrd.org/lrrd22/2/atas22036.htm*

Genetic parameters for milk yield, age at first calving and interval between first and second calving in milk Murrah buffaloes; L O Seno, V L Cardoso, L El Faro, R C Sesana, R R Aspilcueta-Borquis, G M F de Camargo and H Tonhati. *www.lrrd.org/lrrd22/2/seno22038.htm*

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