ESF GENOMIC-RESOURCES

Standing Committee for Life, Earth and
Environmental Sciences (LESC)

Editorial

Advances in Farm Animal Genomic Resources (GENOMIC-RESOURCES)

The final GLOBALDIV workshop which took place on February 8 and 9, 2011, at EPFL in Lausanne, Switzerland, concluded with a session dedicated to the new GENOMIC-RESOURCES project, a 4 years (2010 – 2014) European Science Foundation (ESF) Research Networking Programme that may be considered as GLOBALDIV's project follow-up.

As high-throughput genotyping is about to be available for all major farm animal species, the availability of a huge amount of genomic data calls for new ideas for the extraction of information and for new methods of data management and analysis in conservation and valuation of FAnGR. Moreover, to make sense of this genetic information in practical conditions, integration and comparison with geo-environmental and socio-economical data is key. GENOMIC-RESOURCES will offer appropriate opportunities to investigate new avenues for research and to address the major multidisciplinary issue mentioned here above.

The main goal of the project is to contribute to the education of a new generation of scientists in cutting edge approaches to the characterization, evaluation, management and conservation of Farm Animal Genetic Resources (FAnGR). Eleven participants from ten different countries will deliver an interdisciplinary research and training programme, covering different branches of genetics and breeding, animal physiology and husbandry, socio-economics and geographic analysis. They will regularly publish calls to fund *Workshops* and *Summer Schools* organised at European level and addressing topics like characterization, economic evaluation, exploitation and conservation of FAnGR. *Visiting scientists* will work and learn novel tools and methods offered by recent advances in molecular technologies, statistical and econometric approaches, GIScience and integrated data analysis.

In 2010, GENOMIC-RESOURCES co-organized with GLOBALDIV a Summer School on Genomics (whole genome sequences, large SNPs data sets) and on conservation strategies applied to wildlife that may be of interest for livestock management. A total of 30 well qualified and motivated graduate students, post-docs and young researchers from 18 different Countries were admitted to the School. GENOMIC-RESOURCES distributed four 350 Euros grants to students from Spain, Italy, Slovenia and Czech Republic and sponsored several lectures. In November 2010, GENOMIC-RESOURCES published a first call for Exchange Grants. The Steering Committee selected 5 applications out of 32 projects submitted. Topics addressed by the winners are the "Application of modern high-throughput molecular technology to characterize sheep genetic resources" (Menghua Li, MTT Agrifood Research, Finland), "Landscape genomics and FST approaches to reveal SNPs under selection in cattle" (Saif Agha, UCSC Piacenza, Zootechnics Institute, Italy), "Novel genomic resources for sole (*Solea solea* L.) breeding" (Eveline Diopere, Katholieke Universiteit Leuven, Belgium), "FAnGR and social values. The conservation of indigenous breeds at green care farms" (Ulla Partanen, MTT, Finland) and the "Assessment of the functional

diversity in the chicken genome based on high throughput genotype data" (Saber Qanbari, University of Goettingen, , Germany). These projects are described in the present newsletter.

Last February in Lausanne, two talks constituted the first GENOMIC-RESOURCES workshop session. One by Stéphane Joost who presented this new ESF action, and one by Dr Panagiotis Deloukas of the Wellcome Trust Sanger Institute (Hinxton, Cambridge - UK) who gave a talk on "Genomic Approaches in Human Genetics" to explain to the participants the current advances in human genomics that should soon become available for application to animal science. Dr Deloukas presented examples of genetic studies of cardiometabolic traits, functional annotation, and gave an overview of next generation sequencing tools and related implications in human genomics.

As regards the latest GENOMIC-RESOURCES activities, a Workshop took place in Iceland between September 7 and 9, and a Summer School was organized in Wien from September 26 to 29. Both events will be described in the forthcoming GENOMIC-RESOURCES newsletter issue next December.

Please keep watching on GENOMIC-RESOURCES websites (http://genomic-resources.epfl.ch and http://www.esf.org/genomic-resources), apply to calls, participate to workshops and summer schools.

Also read the GENOMIC-RESOURCES Newsletter we will publish from September 2011 to continue GLOBALDIV's effort to inform on facts related to GENOMIC-RESOURCES partners and projects, on the field of animal genetic resources in general, and on articles and conferences related to biodiversity conservation.

Stéphane Joost
Chair of GENOMIC-RESOURCES,
Ecole Polytechnique Fédérale de Lausanne

GENOMIC RESOURCES RNP

GENOMIC-RESOURCES is a four year ESF Research Networking Programme (2010-2014). Its main objective is to contribute to the education of a new generation of scientists in cutting edge approaches to the characterization, evaluation, management and conservation of Farm Animal Genetic Resources (FAnGR).

Training is organised at the European level through summer schools and workshops addressing specific interdisciplinary topics and by offering visiting researcher mobility grants and training programs in one of the partner institutions.

Visiting researchers are planned to work and learn novel tools and methods offered by recent advances in molecular technologies, statistical and econometric approaches, Geographic Information Systems and integrated data analysis. Participants from different EU countries offer a structured interdisciplinary research and training network covering all these different branches.

Main research themes comprise i) characterization, ii) economic evaluation and iii) exploitation and conservation of FAnGR.

Emphasis will be placed on training future research leaders to design and manage research programmes in an interdisciplinary perspective by providing complementary skills such as basics of socio-economy to geneticists and vice-versa. Project management skills will also be addressed.

What's new ?

Grants for Exchange Visits - Call for Applications

GENOMIC-RESOURCES contributes to the education of a new generation of scientists in cutting edge approaches to the characterization, economic evaluation, management, exploitation and conservation of Farm Animal Genetic Resources (FAnGR). Target researchers will learn and work with novel tools and methods offered by recent advances in molecular technologies, statistical and socio-economic approaches, GIScience and integrated data analysis. GENOMIC-RESOURCES offers funding for a number of Exchange Visits (from 2 weeks up to 3 months) related to the scientific objectives of the programme, to take place between February and July 2012.
The deadline for submission of applications is November 25, 2011, 17:00 CET. Late or incomplete applications will not be considered.
For application form and eligibility criteria, see http://genomic-resources.epfl.ch and http://www.esf.org/genomic-resources

First Call for Proposals under the Funding Strategy for the implementation of the Global Plan of Action for Animal Genetic Resources

Pleased to announce the decision of the Commission on Genetic Resources for Food and Agriculture, in its Thirteenth Regular Session in July 2011, to open the First Call for Proposals under the Funding Strategy for the implementation of the Global Plan of Action for Animal Genetic Resources:

http://www.fao.org/ag/againfo/programmes/en/genetics/Funding_strategy.html

The Call relates to the FAO Trust Account in support of the Global Plan of Action for Animal Genetic Resources for the biennium 2011-2012 which will invest more than USD 1 Million in projects globally. The Commission has limited the number of proposals submitted under the First Call for Proposals to no more than one per country. It further limited the maximum allocation per project to USD 50'000 for single-country projects and USD 100'000 for bilateral, regional or multilateral projects, and the project length to not more than two years.
The thematic focus of the First Call for Proposals, within the three agreed priorities of the Funding Strategy, is helping to ensure sustainable food security by assisting livestock keepers and farmers in activities on the conservation and sustainable use of animal genetic resources for food and agriculture.
Any governmental or non-governmental organization, including research institutions and gene banks, livestock keepers and livestock keepers' organizations and regional and international organizations, based in developing countries or countries with economies in transition that are Commission Members may apply for grants **until 15/11/2011, 24:00 Rome time**. Applications must be submitted through the national authorities of a country that is a Commission Member or Commission Members, i.e. through the National Coordinator or Permanent Representative to FAO. The text of the Call for Proposals and the Submission Forms are attached in Annexes 1 to 4 to this notification. Concept notes can be submitted in any of the Commission's languages plus a translation in either English, French or Spanish.
For any submission, the competent national authorities of the participating countries are expected to provide their explicit concurrence.
At the opening of the Call, 15/09/2011, FAO express deep gratitude to the

Governments of Switzerland, Norway and Germany who have each made significant financial investments in support of this Call. Details of further investors will be published on FAO website as and when received.

Irene Hoffmann - Chief
Animal Genetic Resources Branch
Animal Production and Health Division

Promoting collaboration between livestock and wildlife conservation genetics communities

Journal: Conservation genetics Resources
Issue: 2011, 3:785–788
Authors: Stéphane Joost • Licia Colli • Aurélie Bonin • Iris Biebach • Fred W. Allendorf • Irene Hoffmann • Olivier Hanotte • Pierre Taberlet • Michael W. Bruford • The GLOBALDIV Consortium

Summary: The collaboration between livestock and wildlife conservation genetics communities has the potential to help promote shared priorities, with respect to emerging technologies and new analytical approaches such as next generation sequencing incorporating adaptive variation.
The GLOBALDIV Consortium recently organized an international workshop held at the Ecole Polytechnique Fédérale de Lausanne (Switzerland) including a whole-day session with contributions aimed at taking stock of the situation regarding the extent of information and methodology exchange between the two communities. Discussions permitted the identification of potential benefits of further promoting cooperation in the context of genetic monitoring
in particular, a central concept to current concerns for both the livestock and wildlife conservation communities.
Link:
http://www.springerlink.com/content/v64m2m562x78l022/fulltext.pdf

Exchange Visits 2010: funded projects

The ESF GENOMIC-RESOURCES RNP decided to fund 5 exchange visit grants in 2010. These projects are presented hereunder. The following issue of GENOMIC-RESOURCES newsletter will present the results obtained.

Project N.1

Application of modern high-throughput molecular technology and a multidisciplinary approach in characterizing the sheep genetic resources in the north

Dr. Menghua Li, From MTT, Jokioinen, Finland, hosted by Università Cattolica del Sacro Cuore, Piacenza, Italy

Previous genetic diversity studies of farm animals have contributed to the conservation (e.g. setting criteria for conservation priorities and optimising in- and ex-situ conservation programs) and management of animal genetic resources, particularly in cattle, sheep and goats in Europe [e.g the ECONOGENE, and the North European Cattle Diversity (N-EURO-CAD) projects]. However, most of the studies were carried out at the local or regional (or subcontinental) scale and the recommendations for conservation and further utilization were proposed from a local perspective (e.g. Cañon et al. 2006; Li et al. 2007). In particular, the breeds in north Eurasia were characterized separately from that of other European breeds of cattle and sheep (see Li and Kantanen 2010; Tapio et al. 2010). To increase the resilience of animal production systems to the effects of climate change, it is necessary to understand the genetic diversity of the species at the continental or global scale by combining the data sets

which include breeds representing different geographical and genetic origins. Moreover, earlier investigation were mostly based on a limited number of the neutral microsatellites (ca. 20-30 microsatellites in sheep and cattle), which have left the genomic information of millions of SNP variation unincorporated. Therefore, with accessibility to the genome-wide SNP data for some farm animals (e.g. cattle and sheep), the integration of SNP variations into previous microsatellite-based genetic diversity studies will give new insights into the conservation and utilization of animal genetic resources. Besides these, an interdisciplinary approach by applying modern geographical and environmental information to identify the environment-induced adaptive selection (e.g. Joost et al. 2007) in farm animals has also been greatly prompted by the experts to characterize farm animal genetic resources.

Our aims are at least two-fold and straightforward: (i) to extend previous knowledge of sheep biodiversity using new molecular technologies (i.e. genome-wide SNPs) and compare the consistency of the results based on different information (e.g. microsatellite, SNPs and pedigree); and (ii) to identify the candidate loci for selection by the classical FST method (e.g. Beaumont et al. 2004) and the SAM (spatial analysis method, Joost et al. 2007) method which combines molecular and environmental or landscape data, and further compare their consistency.

The genome-wide SNP data of 99 Finnsheep animals which were genotyped at the Illumina's Ovine SNP50K Beadchip is at deposit for my use. Also, the microsatellite data of 30 Finnsheep animals genotyped at 25 loci (Tapio et al. 2005) and pedigree information of the 99 SNP-genotyped Finnsheep animals (in a comprehensive pedigree data set of over 300 000 individuals collected over 30 years; see Li et al. 2009) are available for within-breed comparisons. Moreover, the

microsatellite data from the ECONOGENE project and the genomewide 50K SNP data from the Italian Sheep HapMap project are also available for comparisons across breeds.

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Project N.2

Landscape genomics and FST approaches to reveal SNPs under selection in cattle

Mr. Saif Agha, from Università Cattolica del Sacro Cuore, Piacenza, Italy, hosted by EPFL, Switzerland

The recent development of sequencing and marker technologies have facilitated the genome wide analyses of individuals and populations. Among the possible objectives of these investigations is the detection of specific signatures left by natural and anthropogenic selection. These signals are specific and differ significantly from those left by other evolutionary forces, as genetic drift and demographic events. For instance, directional selection fostered by the use of different selection indexes in dairy and beef cattle induces differences in allelic frequencies at selected loci higher than at neutral loci (Stella et al., 2010). At the same time at these loci the diversity within dairy and within beef cattle is expected to be lower than that of neutral loci. These effects can be detected also at loci located in a region around the selected locus, the size of which depends on the level of linkage disequilibrium in the populations

(Maynard and Haigh 1974). Several statistical methods are used to identify genomic regions under selection. Most of these are based on allelic or genotypic frequencies, such as FST, and on re-sampling or Bayesian approaches to identify significance thresholds. The association between selection signatures and specific traits is difficult and can be better searched comparing groups of breeds differing for the same trait, for example dairy vs. beef production - e.g. Stella, et al, 2010, used HapMap data to identify selection signatures for dairy production in cattle - or adaptation to different production conditions. Even if group comparisons facilitate the downstream bioinformatic analysis in search for the gene(s) under selection, this task remains hard to accomplish. Nonetheless the selection signature approach has the potentiality to identify genes very difficult and costly to identify with other methods as those involved in adaptation to different environmental conditions.

A second approach to link markers and environment has been developed by Joost et al. (2007). Their method is based on a Spatial Analysis Method (SAM) to detect associations between markers and environmental variables. Using environmental parameters and molecular genetics, SAM employs multiple univariate logistic regressions to test for association between allelic frequencies and environmental variables. This approach is not based on population genetics models and is independent from methods based on allelic frequency. Also, it detects links between markers and specific environmental variables, rather than detecting signals of selection for traits not defined ex ante. Finally, it seems more sensible than the FST based approach (Joost et al, 2010). A parallel evaluation of the FST and SAM approaches using 30 SNPs in goat breeds has been reported by Pariset et al (2009). The use of both FST and SAM methods reduced the probability of getting false positives and assigned some marker signatures to selection driven by specific environmental variable.

The research project I propose employs the bovine HapMap SNP dataset (37K SNP markers on 19 breeds) to identify markers associated to cattle adaptation to extreme environments. As step 1, I will assign geographic coordinates to bovine individuals involved in the HapMap project. Information will be collected from sample providers. In the case no reliable information will be retrieved, animals will be geographically assigned to the traditional area of origin of their breed of origin. This will permit to link individuals to the precise or approximate environment to which they have adapted. In step 2 breeds will then be clustered according to a principal component analysis of environmental variables, to choose groups to be contrasted with the FST approach. As step 3, I will use existing software (Lositan, BayeScan and SAM) for detecting selection signatures and association between markers and environmental variables. New methods that will become available at the time of my stage will also be tested. After the identification of genomic regions carrying relevant signals, as step 4, I will use bioinformatics to identify candidate genes likely to be responsible for the signals detected.

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Project N. 3

Novel genomic resources for sole (*Solea solea* L.) breeding

Miss Eveline Diopere, from University of Leuven, Belgium, hosted by Wageningen University, The Netherlands

Several commercial marine fisheries have strongly declined or even collapsed in the last decennia (Myers & Worm, 2003; Mullon et al., 2005; Worm et al., 2006). The negative effects of overharvesting can be observed at both the population and individual level, ranging from changes in demography (Hutchings, 2000; Hutchings & Baum, 2005) and genetic population structure/size (Hauser et al., 2002; Turner et al., 2002; Hutchinson et al., 2003), to rapid changes in life history traits (LHTs) over few generations (Law, 2000; Heino et al., 2002). Besides working towards an increased sustainable exploitation of fish stocks through better regulations and protected areas, the development of aquaculture is of key importance to ensure sufficient global food production. The use of genetic molecular tools in aquaculture has only been introduced the last two decades but is highly complementary to traditional breeding programs based on phenotypic strategies (Wenne et al., 2007). By developing genetic markers, such as Single Nucleotide Polymorphisms (SNP) or microsatellites, genetic intervention has been successfully applied for many years to enhance animal and plant agriculture production. These techniques have also been transferred to aquatic animals in an effort to overcome various production challenges. For instance, the management of efficient breeding programs in aquaculture requires detailed pedigree information and marker based relatedness information can be used to avoid inbreeding between close relatives (Blonk et al., 2010). A better knowledge of the heritability and molecular basis of economically important but complex traits, such as growth, food conversion, product quality, stress tolerance or disease resistance, is of pivotal importance to control and improve the success of breeding and domestication of new species. Advances in the use of genomic selection and gene expression technologies – such as microarrays, Q-PCR and proteomics – for the study of these traits can lead to a significant improvement of fish production in the near future as denser genetic linkage maps and a vast amount of EST (Expressed Sequence Tags) based markers become available (Cerda et al., 2010). The marine flatfish sole (Solea solea L.) is a commercial species currently the target of a broad scale genetic analysis, to protect natural populations against overfishing (EU FP7 project FishPopTrace, 03/2008-02/2011). Additionally, this species is the focus of a wellconsidered aquaculture strategy aiming at improving breeding strategies, growth rate, developing sustainable feed and increasing disease resistance in several European countries. The application of novel genomic tools is of great importance to increase production efficiency in this species while maintaining brood stock diversity on a long term. Recently, new genomic data and markers (> 300,000 ESTs and 500 validated SNPs) from natural populations within a EU project framework have accumulated. The first step towards application is to develop a linkage map for these data. Such a map is of paramount importance for further research on sole.

The aim of my visit to the lab of Prof. Martien Groenen, Animal Breeding and Genomics Centre (ABGC) at Wageningen University, is first to gain more insight in bioinformatics and genomics, while performing advanced analyses to construct the first SNP linkage map of sole. The ABGC has developed expertise in three interrelated areas: (1) Animal Breeding: definition of breeding objectives, estimation of genetic parameters and design of selection schemes. (2) Statistical genetics and genomics. (3) Molecular genetics and bioinformatics. Prof. M. Groenen is the head of the Genomics group: Increasing the understanding of genotype-phenotype relationship for complex traits is a major research theme in this group and an important aim of my

early scientific career. I list hereafter the ten most relevant publications of Prof. M. Groenen, as beside poultry and pigs, his group also investigates fish

species like sole (Solea solea), and tilapia (Oreochromis niloticus). Sole is the species of interest of my PhD and also of this project proposal, resulting in a better understanding of selective processes in artificial and natural environments.

The proposed exchange project consists of the following three scientific aims:

1) Testing of inheritance of all 500 validated Single Nucleotide Polymorphisms (SNPs) developed by High Throughput Sequencing of Expressed Sequence Tags (ESTs) at the K.U.Leuven. The genotyping of two families from Wageningen UR breeding facilities has already been done (two full sib families, 96 samples), constituting a strong asset for controlling the inheritance of SNPs validated in natural outbred sole populations.

2) The technological transition of genetic markers from microsatellites to SNPs includes some challenges concerning the statistical power of both markers in specific questions. Pedigree analyses are for instance difficult to perform in marine organisms because of the lack of families. Through the comparative analysis of 100 % pedigreed individuals and several pedigreed individuals with lower accuracy based on SSR markers, we will assess the power of pedigree analysis using SNPs using controlled breeding populations of sole. The minimum number of SNP markers will be defined to reach the highest assignment levels.

3) EST-based SNP genotyping of natural and aquaculture populations gives a broad scan of the transcriptome and as such it is highly relevant for future aquaculture applications in sole (for example to study the genotype-phenotype axis through association analysis). As a first step towards the development of Quantitative Trait Loci (QTL) mapping in sole, we will

perform a linkage analysis using the above mentioned families to develop a novel SNP Linkage map.

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Project N. 4

Farm animal genetic resources and social values. The conservation of indigenous breeds at green care farms

Miss Ulla Mirjami Partanen, from Helsinki University, Finland, hosted by Wageningen University, Netherlands

The multifaceted reasons for conserving indigenous farm animal breeds and political will to carry out the conservation are not necessarily enough to safeguard the farm animal genetic resources in reality. Therefore, it is important to study the governance of their conservation, because there is usually a long period of transition from political will and interests to real implementations of conservation programmes at the grassroots level, which makes the conservation of indigenous farm animal breeds and their genetic resources challenging. In addition, it is now broadly agreed that local cultural values and

practices should be considered in conservation policies, and that the implementation of conservation should include community-based and participatory approaches rather than top-down policies. The bottom-up approach is important for the successful conservation of FAnGR, because in reality global action to conserve FAnGR can only consist of the sum total of actions taken by nation states hosting FAnGR. The concept of governance is thus broad: it includes governmental actions but also includes other processes, formal and informal, that communities employ to decide what is in their common interest, and how to act collectively.

In developing societies, local breeds often play an important role in the primary production and livelihood systems. In those countries the main challenge of the conservation is to find means for preserving local breeds in the changing livelihood systems. The role of indigenous breeds in developed societies is to be components of multifunctional agriculture or sustainable rural development. This is achieved through rural entrepreneurship and provision of social and cultural services, animals representing a form of rural capital.

In the western societies a new argument for the conservation is the therapeutic use of the local breeds. These so called Green Care activities and especially social farming and care farming are emerging all over Europe, and are particularly advanced in the Netherlands. These activities provide a new possibility for the conservation of the FAnGr, which however, needs to be researched into. This is the topic Ulla Partanen will focus on during her stay in Wageningen University, which is a leading research institute in the field of FAnGr and Green Care.

The Animal production Systems group has a long history of studying the social values of animals and animal systems. One line of research is green care farms where people can receive care; day care activities and sometimes activities with a therapeutic goal are offered at farms for a variety of target groups e.g. demented elderly, mentally disabled, former drug addicts, those requiring social rehabilitation. Work conducted for the last year was one PhD project by Simone de Bruin who studied the contribution of green care farms to the health and wellbeing of demented elderly. Presently a range of studies is done to the interaction between animals and people at green care farms. The aim is to learn how animals can best be used at green care farms with as little negative effects on the animal welfare and also which animals can be used best. The latter includes also studies to the possibilities of preserving rare breeds at green care farms.

The Center for Genetic Resources of the Netherlands was mandated by the Dutch government to do research related to genetic diversity and identity of species of importance for forestry and agriculture. Conserving rare breeds at multifunctional farms such as green care farms and hobby-farms is one of their interests.

The Animal Production Systems group and CGN will make an inventory of livestock breeds at the approximately 1000 green care farms in the Netherlands and make the information available to her. This and the information already gathered in other countries will give the possibility to write a comprehensive paper. Her research material will consist of statistical data and interviews concerning the conservation of FAnGR at green care farms in the Netherlands. The interviews will be analysed regarding the arguments and values connected to the breeds. She will use the governance approach in her study in order to present a coherent picture of the different levels and different actors that affect the conservation.

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Project N. 5

Assessment of the functional diversity in the chicken genome based on high throughput genotype data

Dr. Saber Qanbari, from Göttingen University, Germany, hosted by Edinburgh University, United Kingdom

The first draft of entire chicken genome was released to the public in 2004 (Consortium ICGS) with an updated version provided in 2006. This project resulted in the sequence of 1.1 billion bases of the chicken genome. In addition, 2.8 million single-nucleotide polymorphisms (SNPs) were identified by comparing DNA sequences between different breeds (Consortium ICPM). These achievements allowed the development of specific medium-density SNP panels of 36K and 60K tailored to egg layer chicken lines to be developed by industrial groups like Hy-Line, Lohmann Tierzucht and Aviagen working together. These SNP panels allow whole genome scans to be performed on individual chickens as a routine procedure. Advances in high throughput genotyping techniques have opened new perspectives in assessing genomic architecture of the chicken with a higher resolution at the DNA level. In a current collaborative work, academic scientists from Iowa State University and Edinburgh University, the German Synbreed consortium, along with industry partners Hy-Line International, Lohmann Tierzucht, and Aviagen are making breakthroughs in the nextgeneration analysis of the chicken genome. The primary aim of this project is to increase marker density by at least an order of magnitude compared to the 60k chip available so far.

This study is based on the use of genomic data from this collaborative project. About five hundreds birds of different origin (e.g., layer and broiler lines together with exotic breeds and wild ancestors) are screened for a panel of more than 2 million SNPs. In the following I review the emerging opportunities and the objectives to be investigated in this proposal. The expected results will be of high scientific originality and quality and will be publishable in highly ranked international journals.

1. Genome diversity, Breed utilization, genetic improvement, and industry consolidation are predicted to have major impacts on the genetic composition of commercial chickens. Consequently, the question arises as to what extent genetic diversity remains within commercial stocks to address future needs. With the chicken genome sequence and more than 2 million SNPs, it is possible to address this question quantifying the missing alleles. Muir et al. (2008) explored this metric using 2551 informative SNPs and concluded that 50% or more of the genetic diversity in ancestral breeds is absent in commercial pure lines. Further analyses with two parallel 60K and 36K SNP chips suggested a higher degree of fixation in white layers compared to the brown layers (Qanbari et al., 2010). In the planned study, we will explore the allelic diversity within and between commercial vs., non-commercial lines as well as between layer vs., broiler lines using analytical methods that account for inbreeding and SNP ascertainment bias.

2. Linkage disequilibrium (LD) statistics, LD is the structural basis of genomic selection and association mapping studies. The feasibility and efficiency of these approaches depends strongly on the extent, distribution and structure of LD. Several

genetic linkage maps of the chicken genome have been published (Andreescu et al. 2007; Groenen et al. 2008; Abasht et al. 2009; Elferink et al. 2010). The latest map based on 60k markers was recently

published in egg laying chickens (Qanbari et al., 2010). They reported r2 values of 0.73 and 0.32 for SNPs in <25kb apart, respectively, in White and Brown layers with large haploblocks accounting for a substantial proportion of the entire genome coverage (especially so in the white layers). However, the resolution of this map is limited and does not allow the precise identification of recombination hotspots. The availability of larger-scale SNP data (e.g., 2M or 650K chip) allows achieving a comprehensive coverage of the genome. Hence, using a denser SNP panel the large blocks found with a coarse SNP panel may possibly split up in series of small blocks.

3. Selection signatures, 'Selection signatures' delimit regions of the genome that are, or have been, functionally important. Therefore, identifying such regions will facilitate the identification of genetic variation that contributes to phenotypic diversity and helps to annotate the genome functionally. Johansson et al. (2010) analyzed allelic frequency of two chicken lines oppositely selected for the body weight using 60k SNP panel and revealed a dramatic effect of selection on a substantial proportion of the genome. To the author's knowledge, however, there is no similar study using dense panel of SNPs in egg laying chickens so far. In this study we scan the genome of a diverse set of chicken lines including layers using the newly available 650K SNP panel, to examine how various directions of positive selection may have affected the genomic patterns. We use a Bayesian FST metric (Gianola et al. 2010) for exploring the differentiated loci. The procedure has two steps. First, allelic frequencies are assigned a non-informative prior, leading to less

shrinkage of frequencies towards a common value. This step leads to estimates of the posterior distribution of FST which can be used to explore any underlying structure, presumably caused by different evolutionary forces. In the second step the structure is explored by using features of the posterior distribution of FST as response variables in a mixed model.

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