International Camel Consortium for genetic improvement and conservation (ICC-GIC)

WORKPLAN

1. Background

- Importance of Old World camelids for many pastoral societies.
- Several Old World camel populations are at risk of losing their genetic diversity or even are close to extinction.
- Current limitations in genetic improvement systems in camel-holding countries (animal identification, pedigree and performance data collection, sire and bull dam selection).
- Recent publications of whole genome drafts of the dromedary (*Camelus dromedaries*), domestic Bactrian camel (*C. bactrianus*) and wild Bactrian (*C. ferus*) open the door to extensive genomics studies in Old World camelids.
- No genome-wide screening tool is today available and no population genomics study has so far been published for these species.
- New technologies permit the characterization of the genome at a decreasing cost.
- Recently recognised milk and meat production potential of dromedary camels and their remarkable ability to survive on marginal resources in extreme conditions.
- Camels have not been specifically selected for milk and meat productions and no systematic methods have been applied for genetic improvement.
- Little differentiation among camel populations (breeds) and the distinction is not based on sound quantitative parameters.
- Lack of camel identification and production recording systems are considered to be the major obstacles to develop camel agribusiness.

2. Overall Objectives

a. Enabling camel-holding countries to use genomic tools for the conservation of genetic diversity and for the genetic improvement of camels.

b. Support at various levels the network of scientists and professionals to boost, harmonize, coordinate activities and collaborate on camel genetic conservation, management, animal phenotypic recording and genetic improvement in order to promote sustainable development of the camel sector and food security.

c. Increase the public awareness regarding the advantages of camel products (e.g. milk and meat)

3. Specific Objectives (to be continuously updated)

- To implement animal identification, pedigree and performance recording system in camels.
- To characterize individual animals (sires and bull dams) for whole genome variations, as a basis for future selection.
- To develop a SNP-chip and other genome-wide screening tools for Old World camels.
- To enhance the assembly of the camel genome by developing and characterizing radiation hybrid panels, BAC genomic libraries and/or long-read sequencing.[1]
- Strengthen research capacity among animal scientists interested in camel research. .
- Networking among animal scientists interested in camel research and international research institutions.

4. Expected Research Outputs

- Animal identification system in place and a minimum of 200 phenotype recorded animals from each participating country.
- DNA bank of phenotype recorded animals established in each country (available for potential future genotyping).
- Genetic tool(s) for genetic diversity analysis, whole-genome association studies parentage testing, relationship, admixture.
- Radiation hybrid panels for camel long-read sequencing, BAC genomic libraries and/ or long-reads for an improved genome assembly.
- Performance of different genetic groups in different production systems.
- Publication of Standard Operation Procedures (SOPs), protocols and scientific papers on application of genomic tools for animal improvement.
- Capacity in place in member states to perform genomic data analyses.

5. Expected Research Outcomes

- Genomic tools are applied to improve camel productivity.
- Farmers improve productivity through better access to information about animal performance.

[1]In cooperation with IAEA-FAO joined genetic laboratories, Seibersdorf, Austria

- Standardization of animal identification and data recording procedures (sample collection, testing, and data analyses) for implementation of genetic improvement programmes.
- Improved camel whole genome assemblies to enhance genetic improvement.
- Improved research capacity of animal scientists in camel-holding countries.

6. Action Plan (Activities and Work Packages)

WP1. Preparing tools

1) Prepare ICC-GIC logo and website including links to the available genomic tools and a discussion forum for scientists.
2) Set SOPs for recording of pedigree and performance.[2]
3) Decision on tagging system.
4) Identify a reference population (participating farms) in as many camel-holding countries as possible.
5) Meet farmers to explain tagging and SOPs.
6) Preparing electronic tools for data and record collection.[3]
7) Build customised low to high-density SNP assay(s). Design high density SNP chip for sires and reference animals and low-density SNP panels for population analysis, parentage testing (and admixture).
8) Tracking potential funding organizations (non-governmental and governmental) to collaborate in financial support of developing SNP assay.
9) Preparation of camel radiation hybrids panels
10) Identify and collect reference "pure breed" data/ samples (20 per breed)

WP2. Activity on the farm

1) Track recent reproduction and breeding history (source of animals, crossbreeding)
2) Tagging animals on farm.
3) Collect farm description data and breeding plan/program, if any.
4) Collect blood/hair/tissue/swap samples on farm from females and sires.
5) Collect pedigree and performance data on 1000 lactating females per population (pure breed or pure breeds and their crossbred associated animals) according to SOPs.

[2] according to guidelines proposed by the IAEA
[3] utilize the LIMA database of the IAEA

6) Recording live body weight and conformation considering sex and age classes along with carcass, non-carcass and meat cuts, in case of availability, for 200 pedigreed individuals per country.
7) Record health status (e.g. blood controls, clinical examination) and parasitic load (egg counts) of gastrointestinal parasites in reference populations for resistance studies.

WP3. DNA management and molecular analyses

1) Sample database and storage
2) DNA extraction
3) Use low SNP panel for the analysis for parentage and admixture.
4) GBS or LD-SNP panel analysis of a sample of females (30-50 animals per country to check what's in the female population)
5) GBS or HD-SNP panel analysis of a sample of sires and reference animals
6) Characterization of the camel RH (radiation hybridisation) panel and population diversity.

WP4. Integrated data analysis

1) Diversity, inbreeding, genetic structure analysis of sires and females in combination with existing datasets
2) Paternity reconstruction from low density SNPs
3) Population genetic analysis of females (from low density SNPs)
4) Association between genotype and performance data of females considering different production environments.

WP5. Training

1) Genomics and phenotyping workshops
2) Scientific exchange with international research institutions
3) Participation in Web-based training

WP6. Dissemination

1) First round of scientific papers (animal diversity from SNP assays)
2) Second round of papers (paternity reconstruction and comparison with pedigrees when know)

3) Third round of papers (association between performance and admixture, e,g, if admixed better have a better performance in milk, meat or wool production; camel RH map)
4) Transfer of information and management recommendations to farmers (local extension services)
5) Guidelines and protocols made available to member states

7. Traits and information to be collected

- On sires:

  Compulsory: age, pedigree information, semen quality parameters (exception of sires on farm), morphological defects, libido

  Desirable: conformation, scrotal circumference

- On females:

  Compulsory: age, pedigree information (when available), parity, parturition date, breeding age, IA dates, number of services, health history, days in milk, at least 6 milk yield records per year (simplified LIMA).

  Desirable: BCS, CMT, milk composition, SCC.

- On farm:

  Compulsory: GPS → environmental data, No. of animals in the farm, farm purpose, housing, health, feeding regime, breeding management.

  Desirable: socio-economic data on farm and farmers at the beginning and end of the project.

8. Implementation of Action Plan

8.1. First Year

Resources:

- Participating institutions (PIs; farms or research facilities) have laboratory capable of DNA extraction and storage of samples.
- PIs have facilities/capacity to handle data
- PIs have network/infrastructure/logistics capable of collecting data and samples from farms and AI stations.
- Information available from previous or existing projects that can be used to design low-density SNP panels.

Activities:

- Prepare tools (WP1.1-1.5, and 1.7) including design of systems for providing feedback to farmers.
- Identify PIs (research institutions and farms)
- Identify external funding opportunities to expand project impact
- Choose/confirm target farms for each camel-holding country (if possible)
- Enrol farms, and collect baseline data
- Training in data and sample collection, storage and data quality assurance at a first meeting of PIs' researchers and farmers
- Initiate individual animal geographical data (Include tagged animals and collect samples for DNA)
- Collect/collate samples from breeding bulls
- Initiate feed-back to participating farmers and research institutions
- Build bio-sample repository at each PI lab
- Initiate DNA extraction at PI labs
- Initiate farmer-feedback
- Start with the construction of a low to high-density SNP chip
- Collaborate with a laboratory to build RH panels[4]
- Collect camel fibroblasts (ideally from same animals as used for sequence assembly).
- Initiate RH cell line establishment

Expected results by end of first year:

- SOPs published
- Core (animal ID -system, whole genomes, bio-sample repository) tools made available
- PIs identified
- Training of PIs researchers and farmers performed
- Biobanks in PIs labs established

8.2. Second Year

Resources:

- PIs have laboratory capable of DNA extraction and storage of samples
- PIs have facilities/capacity to handle data

- [4]IAEA-FAO joint genetics laboratories, Seibersdorf, AT

- PIs have network/infrastructure/logistics capable of collecting data and samples from farms.
- Information available from previous or existing projects that can be used to design low-density SNP panels.
- Data, samples and tools from year 1 are used to drive year 2 activities and provide information for decision making.

Activity:

- Continuation of sample and data collection PI farms, including new sires
- Continuation of longitudinal data collection on farm
- Continuation of feed-back to farmers and PI research institutions
- Initiate DNA extraction
- Training (if required) in DNA extraction and possibly also on initial data analyses (distance, web-based training)
- GBS (genotyping by sequencing) of camel populations for molecular characterization
- Continue design of SNP assay(s), (i.e. SNP assay of year 1 will be empowered with additional SNPs) using GBS data
- Establish RH cell lines

Expected results by end of second year:

- DNA extracted
- SNP chip under construction
- GBS data of camel populations available
- Preliminary selection of bull mothers
- RH cell lines established

8.3. Third Year

Resources:

- PIs have facilities/capacity to handle data
- PIs have network/infrastructure/logistics capable of collecting data and samples from farms and AI stations.
- Information available from previous or existing projects that can be used to design low-density SNP panels.

- Data, samples and tools from years 1 and 2 are used to drive year 3 activities and provide information for decision making.

Activity:

- Continuation of data and samples collection in AI stations
- Continuation of on-farm longitudinal data collection
- Continuation of feedback to participating farmers and research institutions
- Test low density SNP assays and initiate LD assays on project samples
- Training on data analyses within the PIs
- Initial analyses of camel diversity data
- Initial integrated data analyses (phenotypes and genotypes together)
- First publications from the project.
- Selection and amplification of informative clones for RH panel

Expected results by end of third year:

- First publications
- Low density SNP assay available
- Additional bull dams identified/bred
- RH panel publically available

8.4. Fourth Year

Resources:

- PIs have facilities/capacity to handle data
- PIs have network/infrastructure/logistics capable of collecting data and samples from farms and AI stations.
- Information available from previous or existing projects that can be used to design low-density SNP panels.
- Data, samples and tools from years 1, 2 and 3 are used to drive year 4 activities and provide information for decision making.

Activity:

- Continuation of data and samples collection in farms
- Continuation of on-farm longitudinal data and sample collection

- Continuation of feedback to participating farmers
- Complete low density SNP assays
- Integrated analyses of phenotype and genotype data
- Characterisation of the RH panels
- Training in complex data analysis, interpretation and decision making

Expected results by end of forth year:

- Fully characterised RH panel publically available
- Initial results of integrated analyses publically released.
- System for parentage and breed composition estimation validated and made available
- Publications

8.5. Fifth Year

Resources:

- PIs have facilities/capacity to handle data
- PIs have network/infrastructure/logistics capable of collecting data and samples from farms and research institutions.
- Information available from previous or existing projects that can be used to design low-density SNP panels.
- Data, samples and tools from years 1 to 4 are used to drive year 5 activities and provide information for decision making.

Activity:

- Final farm survey to assess project impact at farm level.
- Final integrated analyses across whole project.
- Final meeting
- Finalisation of recommendations on data and sample collection within genetic improvement programs
- Finalisation of recommendations on application of genotype and phenotype data for effective improvement of dairy genetics and management
- Integration of camel RH data with sequence assemblies to build a better assembly
- Final reports and publications

Expected results by end of fifth year:

- Improved camel genome sequence assembly released
- Guidelines for data and sample collection and analysis pipelines and recommendations on tools, released publically
- Results on appropriate breed composition for different dairy production systems
- Increased capacity of PIs and their collaborators to support dairy genetic improvement through training and research.
- Better functioning genetic improvement systems in participating countries
- Final project publications

9. Assumptions:

Any factors which are needed for the Work Plan to succeed.

Workshop to identify any key assumptions and ICC-GIC EC team to complete based on details of the Work plan. Examples from a previous project are:

- Institutes which are selected for participation in this Work Plan will have local and/or external support either through funding from other bodies or through agreements with local partners, as well as links with national livestock development authorities.
- The project will integrate with on-going development activities and work closely with farm organizations and farmers.
- The team will have transportation capabilities to field sites and the necessary resources to conduct fieldwork, to perform data and sample collection, and to do computerized data recording and analysis.
- The team will have established laboratories for molecular genetic analyses and basic expertise on DNA base technologies.
- The team will have access to breeds/ populations of camels.
- Close collaboration with the IAEA/FAO

10. Foreseen Participation (PLEASE ADD YOUR NAME, EMAIL AND INSTITUTION)

List of research institutions and farms interested in participating in this Work Plan:

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