

OPTIBOV: genetic characterization of cattle populations for optimal performance

The Netherlands, Uganda, Finland, Egypt, South Africa and Portugal



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Why OPTIBOV

- Maintain traditional (local) cattle breeds (biodiversity)
- Capture genetic and genomic variation
- Capture adaptation and productive traits
- Capture health traits (resistance to disease)
- Identify selective sweeps related to adaptation
- Use known variation to improve productivity in traditional breeds (marker-assisted selection)
- Train, educate and involve stakeholders to perform optimal breeding (long-term investment) by workshops, app, website.

Aim To characterize traditional (locally adapted) cattle breeds to detect and use genetic variation associated with adaptation to local ecosystems in improving breeding schemes for the future (production, longevity, disease resistance)

Breeds and Phenotypes

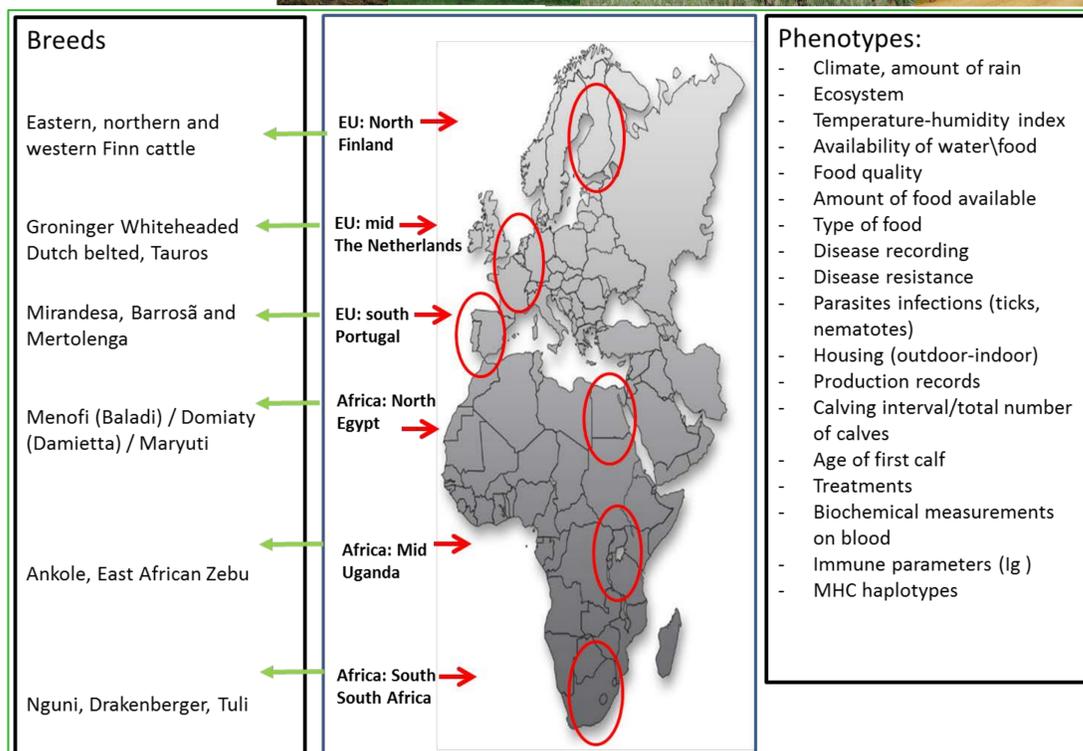


Figure 1. Overview of countries and traditional cattle breeds involved in OPTIBOV including list of potential phenotypes

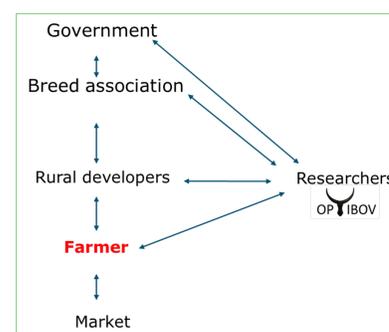
Methods

- Design protocol for phenotyping
- Whole genome re-sequencing
- Selective sweeps
- Deleterious alleles
- Amount of inbreeding

Expected Outcome

- Markers detected for selective adaptation and productive traits
- Phenotype list
- African cattle breed variants
- Traditional/local breed characterisation
- New African SNP array
- Recording system (OPTIBOV: app, database, website)
- Training modules

Opportunities and Challenges



Arrows indicate:

- Information flow
- Data flow
- Knowledge flow

- Training is packaged at all levels

Training

Within the OPTIBOV project training programs will be made for phenotyping and data analysis on different levels as well as workshops for stakeholders.

