

Novel tools to inform animal breeding programs

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Key messages

- Rapid development of novel tools for phenotyping, genetic and genomic analyses, reproduction, and modelling offers opportunities to speed up the genetic gain of complex traits to meet the needs of animal breeding programs.
- Successful application of novel tools depends on a complete understanding of the innovation circle of the particular technology and model, and its associated basic technical procedures and minimal management costs.
- Implementing new phenotyping and genotyping tools requires adequate infrastructure and training of farmers and national agricultural research system (NARS) scientists to enable early participation for enhanced impact in low-income countries.

Circle of innovation

The design of a breeding program largely depends on adequate infrastructure—ranging from efficient collection of phenotypes, development of models, data analysis, program implementation to buy-in from the public and farmers. This key infrastructure is usually lacking in developing countries.

Using novel tools that circumvent these constraints offers many opportunities to developing countries. However, this requires a range of scientific expertise not readily available, underlining the importance of collaboration between advanced universities and research institutes.

Circle of innovation for a breeding program

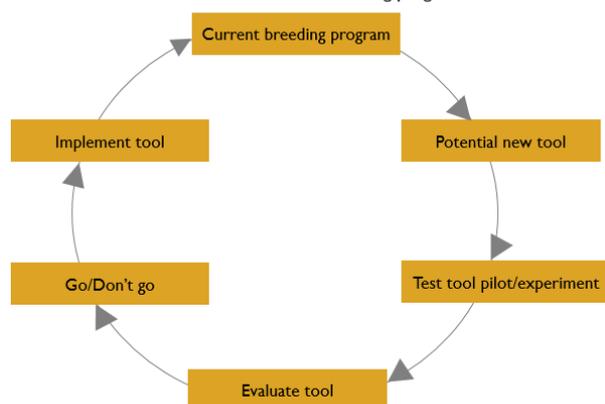


Figure 1 shows a schematic overview of the circle of innovation for a breeding program.

Based on advances in information technology, molecular biology, genetics and statistical methods, these tools are applicable to various aspects of breeding programs ranging from data collection and model design to program implementation. Putting these novel tools into use typically follows a circle of innovation (see Figure 1).

When a new tool has been proposed, the first step is to test its performance in a pilot study or specific experiment. The next stage is to evaluate whether it can make a positive contribution to the breeding program followed by a 'go/don't go' decision regarding its implementation. The pace of innovation depends on the type of tool, the required infrastructure to implement it, the target species, and ownership of different aspects of the breeding program.

Implementing novel tools

The implementation procedures and management costs of tools vary greatly, for instance:

1. While new breeding value estimation models do not, in principle, require any major capital investment, their use may generate additional management costs related to computing capacity or increased data recording requirements.
2. The routine use of genomic tools requires infrastructure to collect samples for DNA isolation, as well as generating additional running costs for genotyping.
3. Information from social economic models and system assessment tools are important to the adaptation of breeding goals but are not constrained by the infrastructure or ownership of the breeding program, unless the new breeding goals require routine recording of additional traits.
4. The requirements for implementing reproductive tools depend significantly on whether the tools are introduced at farm or breeding-nucleus level.

Biological and system constraints

The reproductive capacity of a species can limit or increase the rate at which genetics can be supplied to the market. The level of controlled breeding is informed by both the selection level imposed and knowledge available on pedigree relationships. Genomic tools have only become readily available recently, and, as such, are optimized for the main livestock species. This

can be particularly challenging for some mass-spawning aquaculture species as well as in natural-mating pastoral systems.

Infrastructure constraints

Whether it is access to data recording or opportunities to sample biological material, there is a big difference between breeding at a single-location nucleus or on a number of farms. The ability to keep material frozen at low (-20°C) or very low (-80°C) temperatures can place considerable constraints on using genomic tools and several reproductive techniques. Computing facilities and internet connectivity are also crucial to the delivery of novel methods for genetic evaluation and disseminating the results in a timely manner.

Animal ownership

An important issue is who pays for innovations and who benefits from improved breeding programs. For instance, if breeding animals are centrally owned, by a company or breeding organization, they may be able to sell the improved genetics at a profit. Likewise, the development of new reproductive tools at farm level may directly benefit farmers; they also carry upfront costs. The delivery of improved tools in both examples will be largely influenced by farmers' willingness to pay.

There may also be issues in terms of ownership of data and intellectual property (IP). For instance, milk recording data (for dairy cattle) may be owned by a different company from the one owning the breeding bulls. In other species, crucial data, owned by breeding companies, is never released into the public domain. It is, therefore, important that the scientists take account of IP-related issues to ensure the tools are open access, in line with the CGIAR policy on producing 'global public goods'.

Circle of innovation cases

The usefulness of the circle of innovation approach and framework is illustrated through three cases from the flagship's research in recent years.

Type I circle of innovation

Context: Applying new genetic theories to Nile tilapia

Two PhD projects employed novel quantitative genetic theory to improve the uniformity of Nile tilapia. The first project examined the untested concept of 'indirect genetic effects' in aquaculture where the performance, i.e. growth, of the fish is affected by its own genetic potential and that of those with which it interacts. Quantifying the lack of uniformity among the fish as 'variance heterogeneity', the project estimated the genetic component of the variance. The second project modelled whether the indirect genetic effects could be a source of variance heterogeneity and tested the hypothesis on Nile tilapia.

1. **Tool type:** Quantitative genetic models requiring theoretical expertise and analytical tools for estimation, available at Wageningen University and Research (WUR) and Swedish University of Agricultural Sciences (SLU).
2. **Infrastructure:** Models that estimate indirect genetic effects or variance heterogeneity demand large volume of data structured in particular ways to allow the separation of genetic effects from environmental factors, available at WorldFish.
3. **Species:** Nile tilapia has pedigree based breeding programs with short generation intervals, allowing for full control over mating and facilitating an experimental design with a timeframe which allowed the researchers to go from theory to experiment within a PhD project.
4. **Ownership:** WorldFish ownership of the breeding program facilitated the required experiments and their participation in the research meant they are best placed to interpret the results for their program.

Research partners had full control over all aspects of the circle of innovation, allowing for direct and rapid translation of experimental results into practice.

Type 2 circle of innovation case

Context: DREMS, mobile-based database to enhance community-based sheep and goat breeding programs

Data Recording and Management System (DREMS) helps capture, manage and summarize breeding data from small ruminant production. Developed by ICARDA and EMBRAPA-Brazil, it helps improve recording of breeding and management data using mobile data transfer tools (mobile phones or tablets) from villages to a research centre where it is backed up on EMBRAPA servers. The application facilitates field data collection, storage and transfer to the research and extension staff, which otherwise would have to be done manually by enumerators.

1. **Tool type:** Online mobile application-based database.
2. **Infrastructure:** Given that average flock size was small and farmer participation critical, farmers were organized into breeder groups registered as cooperatives in line with national regulations, and technical backstopping provided to farmers by NARS.
3. **Species:** Sheep and goats. However, the generation interval of the species had no direct impact on the application of these tools.
4. **Ownership:** Though owned by ICARDA, NARS and EMBRAPA, researchers are given access to the data of cooperative members who are required to register their animals. ICARDA and EMBRAPA had full control over all aspects of the circle of innovation, and given the high levels of uptake of tools, farmer involvement can be considered successful.

Type 3 circle of innovation

Context: Application of digital data capture and genomic tools in dairy cattle breeding

Major implementation limitations of efficient dairy cattle recording schemes in developing countries are associated with a lack of organizational infrastructure and prohibitively high costs for farmers. To circumvent these constraints, ILRI developed digital tools to capture dairy cattle performance data. In the East Africa Dairy Genetic Gain project (DGEA) and the ongoing African Dairy Genetic Gain projects, performance was captured using mobile devices developed in the Open Data Kit. The data, automatically fed into a database and analysed, provides feedback to farmers on improving their management and productivity.

Researchers also took DNA samples from the farmers' cows and obtained single nucleotide polymorphism (SNP) genotypic data. Genomic tools were then developed using the SNP data to determine the animals' breed composition and verify parentage, providing farmers with information to realize full genetic potential of their animals. Use of genomic data to assign breed-composition to animals allowed for a breed-comparison based on *in-situ* (farm-based) data, something that has been problematic in the past.

1. **Tool type:** Digital data and genomic tools, developed by ILRI and University of New England, were employed in the studies.
2. **Infrastructure:** The farms and cows, critical to the successful application of these tools, were owned by participant farmers.
3. **Species:** Indigenous and crossbred cows. The relatively long generation interval of the cattle did not directly impact the application of the tools.
4. **Ownership:** While ILRI owned the tools, the cows to be evaluated were owned by participant farmers, some of whom dropped out of the study.

While ILRI and partners only had partial control of the circle of innovation, good logistical support and cooperation with the farmers ensured the successful evaluation and implementation of the tools.

Novel tools for animal genetics

Genetic tools

- a. Quantitative genetic models applied to data, e.g. the application of social genetic effects to aquaculture which account for variance heterogeneity have resulted in more accurate estimations of selection responses.

Genomic tools

- a. Low-density SNP assays for cheap and fast parentage verification;
- b. Second generation sequencing platforms for SNP discovery and validation in unique breeds/populations adapted to different production systems following long-term *in-situ* within-breed selection and/or ongoing *in-situ* crossbreeding programs involving exotic genotypes;

- c. Platforms to identify functional SNPs and/or genomic regions of host species responsible for adaptation to extreme environments—e.g. heat, cold, drought, and high altitudes—and resistance/tolerance to specific pathogens and diseases; and meta-genomic/microbiomic information for enhanced feed conversion efficiency of locally available forage/crop residue resources;
- d. Platforms to develop and apply low-, medium- and high-density, species and/or genetic background specific SNP chip arrays to genotype large number of samples at low cost, helping to determine breed composition following genomic admixture analysis of traditional breeds derived from different genetic backgrounds due to separate domestication and/or local founder events and of crossbreds of indigenous and exotic breeds;
- e. Platforms to develop molecular markers for product authentication, targeting value-added niche markets.

Phenotyping tools

- a. Simplified and optimized recording methodologies and technologies for different species kept in pastoral, low-input and mixed crop-livestock production systems;
- b. Information and communications technology (ICT)-based recording and feedback systems for smallholder farmers and other value chain actors; and
- c. Online databases, such as DREMS, with basic analytical functions accessible to all authorized stakeholders, including NARS partners.

Modelling tools

- a. Combined quantitative genetics theory on heterogeneity and social interactions and test in aquaculture; and
- b. Structured farmers' participation models to ensure their participation in defining breeding goals.

Reproductive tools

- a. Cow side hormone assay for oestrus detection and pregnancy diagnosis;
- b. Preg-Tone for early pregnancy diagnosis in small ruminants;
- c. Ultrasound-based techniques for fertility management in small ruminants which are applicable in the field; and
- d. Protocols for maintaining the semen viability of breeding bulls under room temperature.

System assessment tools

- a. Bio-economic models to assess the effects of selection and management in fish.

Conclusions

The flagship has made much progress in applying novel technologies, including reproductive (cattle, sheep), genetic and genomic (fish, cattle and small ruminants) tools, and application of findings from assessment tools and bio-economic modelling (small ruminants).

The examples above illustrate how the circle of innovation drives the pace at which the tools are developed and applied.

To improve smallholder farmer livelihoods and productivity, the participation of farmers in developing and testing these tools is important to enhance impact. Some of the breeding programs described in this brief illustrate the huge potential of these tools to overcome data recording, model design and implementation constraints typical in low-income countries. Given the current rate of advancement in ICTs, molecular biology and genetics, more novel and cheaper tools can be expected in the near future.

The flagship has improved capacities to generate and analyse data. The availability of ICT tools, the organization of farmers into breeder cooperatives and the participation of NARS scientists guarantee a multi-institutional approach to the use of these novel tools. It will speed up feedback to farmers on data collected and enable them to make faster and better decisions regarding animal management for improved accuracy/efficiency of selection. It will also help ensure that farmer feedback is incorporated in the development and fine tuning of the tools. It will also give farmers a sense of ownership of the tools, making them public goods.

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