Sustainable management of globally significant endemic ruminant livestock in West Africa: Guidelines for the replication and improvement of the N'Dama cattle breeding program of The Gambia

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(Sustainable Management of Globally Significant Endemic Ruminant Livestock in West Africa)

Sustainable management of globally significant endemic ruminant livestock in West Africa: Guidelines for the replication and improvement of the N'Dama cattle breeding program of The Gambia

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1 Purpose of this document

This document is designed to assist countries partnered to the project 'Sustainable Management of Globally Significant Endemic Ruminant Livestock in West Africa' (PROGEBE www.progebe.net) in the development of plans for N'Dama cattle within breed improvement programs, following the 3-tier (nucleus/multiplier/commercial) model of The Gambia. The document proceeds as follows. First some background information is given including the broad steps to developing an animal breeding program (based on FAO 2010), as well as a basic overview of a 3-tier breeding program. Second, The Gambia breeding program is described from both a historical perspective and in terms of its current activities. Third, detailed guidelines are given in relation to the replication/improvement of the breeding program, with a number of specific recommendations made. Finally issues which will be critical to the success of the program—including human capacity, breeding program sustainability, and scale of operation—are discussed in some detail.

It should be noted that underlying assumptions to this document are that a) within-breed genetic improvement of N'Dama cattle is an appropriate livestock development intervention within the PROGEBE countries, and that b) the 3-tier model of The Gambia is the most appropriate genetic improvement and dissemination model to implement. This document does not discuss these issues further, as it is understood that the PROGEBE country partners are already committed to establishing such breeding programs.

It should also be stressed that this document does not replace the need for country-level capacity in terms of trained people for genetic improvement programs to design and oversee their N'Dama breeding activities. Instead this document should be considered reference material, from which the country-level animal breeders/quantitative geneticists and other stake-holders can draw on in designing their specific breeding plans.

2 FAO guidelines on animal breeding strategies

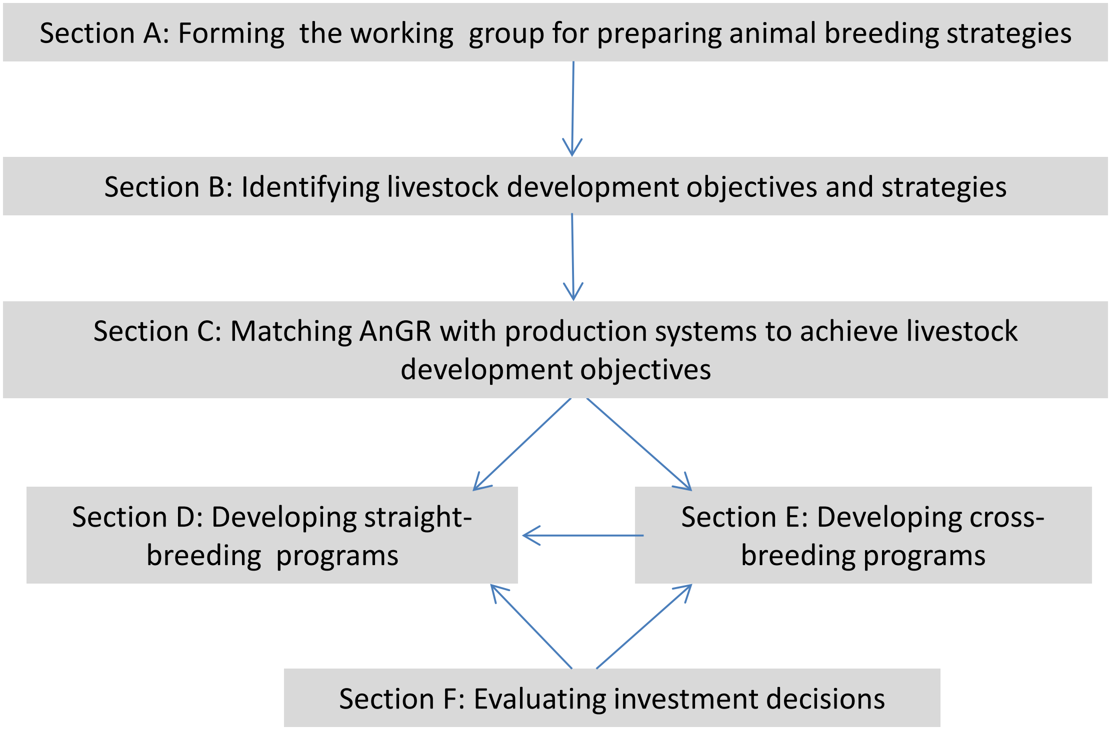
In designing the country level breeding plans, it is strongly recommended that the FAO guidelines 'Breeding strategies for sustainable management of animal genetic resources' (FAO 2010; available on-line at http://www.fao.org/docrep/012/i1103e/i1103e00.htm) are consulted. This section provides a brief overview of these guidelines, and describes the 'fit' of the information given within this document.

The basic structure of the FAO breeding strategies guidelines is given in Figure 1. All sections of the guidelines, with the exception of Section E which deals with cross-breeding, are relevant to the breeding activities being implemented under PROGEBE. The specific objectives of the relevant sections are as follows (FAO 2010):

- Section A: Establish a working group to formulate a livestock breeding strategy. Set the working agenda and assign responsibilities. Develop an inventory of stakeholders and other potential contributors to the development and implementation of the breeding strategy.
- Section B: Identify achievable livestock development objectives and design a livestock development strategy to achieve to the livestock development objectives for all important production systems within the country (region), placing particular emphasis on assessing whether there is a need for a breeding strategy and what its role might be.
- Section C: Define the overall breeding goal. Describe locally available breeds and possible alternative ones. Provide arguments on the basis of which decisions can be taken regarding which breeds should be used and what type of breeding program should be developed.
- Section D: Develop a sustained straight-breeding program by using the genetic variation within the breed(s) being targeted.
- Section F: Provide the investor (government or private) with a clear indication of the benefit of investing in animal breeding programs.

The information provided here (i.e. this document) mostly deals with the more technical details of implementing and optimizing the N'Dama breeding programs, and fits to Section C of the FAO guidelines, in relation to defining the breeding goal, as well as Section D, in relation to aspects of within-breed improvement. It is presumed that the objectives in Sections A and B of the guidelines have been met, and that action towards the objective of Section F is, or will be, undertaken.

Structure of the guidelines



Source: Reproduced from FAO (2010).

Figure 1. Basic structure of the FAO 'breeding strategies' guidelines

3 Overview of 3-tier (nucleus–multiplier–commercial) breeding programs

The basis of a 3-tier breeding program is shown in Figure 2. The first tier is the breeding nucleus, where efforts to genetically improve the animals are concentrated. For example, a breeding nucleus may entail a group of animals on a research station with animals selected to be parents of the next progeny crop based on their estimated genetic potential, evaluated from trait and pedigree records. The second tier is the multiplier tier which often comprises a number of individual livestock units. This tier receives animals from the nucleus and then mates them to their own animals to 'multiply' the number of genetically improved animals. Finally the third tier is the commercial tier, which receives animals from the multiplier tier, to mate to their own animals producing progeny for the final (possibly commercial) purpose. The basic advantage of this structure is the concentration of expensive trait and pedigree recording to a limited number of animals (those in the nucleus and, in some cases, selected herds from the lower tiers). A disadvantage, however, is that there is a genetic lag (difference in mean genetic value of animals) between the nucleus and multiplier tier, as well as the multiplier and commercial tier.

There are numerous variations to the above theme. For example the breeding nucleus may be closed (animals from the lower tiers do not move into the nucleus), or open (animals from the lower tiers can enter the nucleus); germplasm from the upper tiers can be passed to the lower tiers via live animals or through the use of reproductive technologies (such as artificial insemination); the nucleus may be in the same production environment as the commercial population of animals or in a different production environment (in which cases issues related to genotype by environment interaction may need to be taken into account). It is beyond the scope of this document to describe all such possible variations and the effect they have in relation to overall genetic progress, as this is the subject matter of many quantitative genetics text and manuals (for example, Simm 1998). Further details of issues relevant to these guidelines are, however, given in the appropriate sections below.

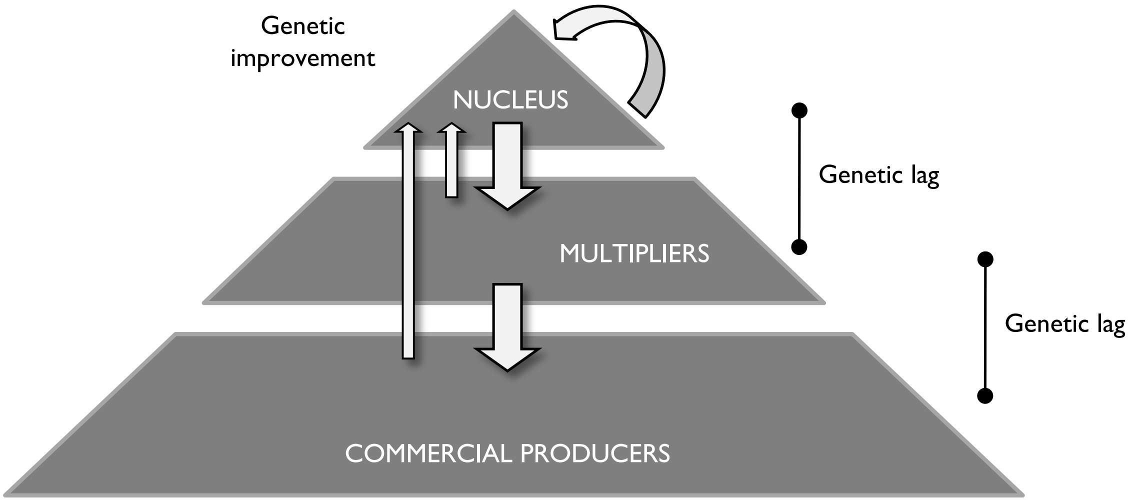


Figure 2. A 3-tier breeding program. Genetic improvement occurs in the nucleus, with the best animals retained in the nucleus as breeders (curved arrow). Genetically improved animals are disseminated from the nucleus to the multipliers to the commercial producers (downward arrows). In an open nucleus, competitive animals can also move from the multiplier or commercial tier into the nucleus tier (upward arrows). Many variations on this theme exist.

4 Overview of the N'Dama cattle breeding program of The Gambia

This section gives a general overview of the N'Dama breeding activities within The Gambia, with additional information and technical details given in Section 5 of this report.

Chronological development. The N'Dama cattle breeding program of The Gambia was initiated in 1994/1995 by the International Trypanotolerance Centre (ITC) with funding from the Bundesministerium fur Wirtschaftliche Zusammenarbeit (BMZ) of the Federal Republic of Germany. Financial support continued to about the year 2000, but was limited thereafter resulting in a down-scale of operations (Dempfle 2008). An overview of the chronological development of the N'Dama breeding program until 2003 is given in Table 1. Following 2003 there have been no major events, until the recent (2010/2011) re-activation of breeding activities under PROGEBE.

Table 1. Chronological development of the N'Dama cattle breeding program, until 2003

Event	Period
Inception of ITC	1984
Food and Agriculture Organization (FAO) consultancy mission conducted at ITC	1990
Need for a coherent and comprehensive improvement program expressed	1993
Proposal to support the organization of the herd into an open nucleus herd	1993
BMZ agree to financially support the proposal	1993
Launch of the program	1994
First derivation of selection index weights	1994
Screening for purchase of replacement animals (animals bought 1995)	1994
Records on performance	1995
Screening for purchase of replacement animals (animals bought 1996)	1995
Workshop organization for the breeding goal & agreement on qualitative goal	1996
Screening for purchase of replacement animals (animals bought 1998)	1996
Screening for purchase of replacement animals (animals bought 1999)	1997
Introduction of an animal model BLUP evaluation	1997
Screening for purchase of replacement animals (animals bought 1999)	1998
Project PROCORDEL: enhance dissemination	2000
Introduction of mechanism to disseminate genetic progress	2001
OPEC-FID: screening operation	2002
Establishment of two livestock multiplier associations	2002
Survey of farmer acceptance	2003

Adapted from Bosso et al. (2007).

Overview of the program. The program aims to genetically improve N'Dama for meat and milk, without the loss of disease resistance and other adaptive traits (Dempfle and Jaitner 2000). It operates as a three-tier scheme comprising an open nucleus, multiplier tier, and commercial tier (village herds).

The nucleus is based at ITC research stations called 'Keneba' and 'Bansang' situated approximately 80 and 200 km from the Atlantic Coast, respectively. Whilst Keneba is classified as low to medium for tsetse challenge, Bansang is classified as very high for tsetse challenge (Watcher et al. 1994). When fully operational the nucleus comprised about 400 breeding females and five to six breeding males, with a total of 1000 to 1100 animals (Dempfle and Jaitner 2000; Bosso et al. 2007). The females with their suckling calves, as well as the breeding bulls, are located at Keneba, whilst animals from 12 to 36 months of age are located at Bansang. The relocation of young animals to Bansang is to allow for growth traits to be measured under high disease challenge, and thus indirectly act as a selection criteria for disease resistance.

All animals within the nucleus are performance tested for daily weight gain (DWG) from 15 to 36 months, and the females additionally performance tested for milk yield (MY) for the first 100 days of lactation. Animals are selected to be the parents of the next progeny crop based on high ranking for an index combining estimated breeding values (EBVs) for DWG and MY, calculated from an animal model using best linear unbiased prediction (BLUP) methodology. Within the index the EBVs are weighted by the economic values of the traits (0.215 for DWG and 0.934 for milk yield) as calculated by a bio-economic model (Dempfle and Jaitner 1999). The program operates as a young sire program, with sire selection taking place at the end of the performance test for DWG. In addition, the nucleus is open and animals can enter the nucleus based on screening of village cows for milk yield (whilst envisioned as an annual activity funding restrictions meant that village animals only entered the nucleus once, in 1996). Figure 3 (reproduced from ITC 1999) shows the annual movement of animals.

Source: Reproduced from ITC (1999).

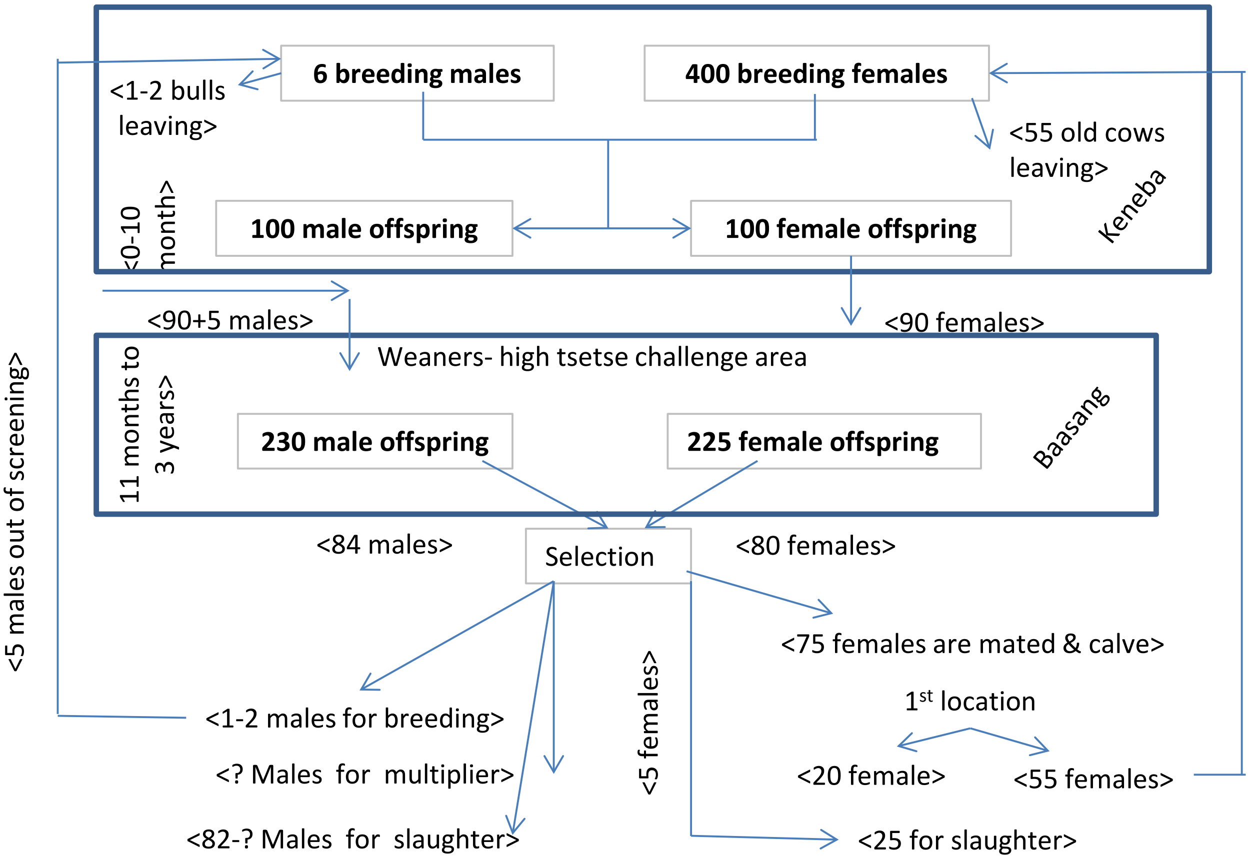


Figure 3. An overview of the N'Dama nucleus breeding scheme. <…> is the number of animals moved annually, other numbers are stock numbers.

Dissemination of genetically improved animals occurs from downward movement of selected sires to the multiplier herds, and in-turn to other village herds. Two livestock multiplier associations were established to assist this dissemination, the Gambian Indigenous Livestock Multiplier Associations (GILMA) of Saloum and Fulladu. As of 2004, 44 nucleus bulls had been distributed to multipliers in 26 villages, with 169 offspring registered in these multiplier herds (Bosso et al. 2007).

Over recent years the program was scaled down due to funding restrictions. The number of breeding females present in the year 2008 was about 280, transportation of animals to/from the Bansang testing station was delayed hindering execution of the program, and distribution of animals to GILMA had ceased. Presently (July 2011), the number of breeding females remains at about 280, efforts (supported by PROGEBE) are underway to ensure proper execution of the program, and distribution of animals to multiplier herds within PROGEBE sites has commenced.

Key personnel. The key personnel involved in the design and implementation of the breeding program are as follows:

- Leo Dempfle [Leo.Dempfle@t-online.de]: Former Director General of the ITC, and founder/designer of the breeding program. Involved in the implementation of the breeding program from its inception to the present.
- Jutta Jaitner: The main implementer and manager of the breeding program from 1995 to 2000. Credited with implementing a state-of-the art recording system (for that time) which has resulted in the very high quality data now available.
- Nerry Corr [keba_corr@yahoo.com]: Joined the breeding program in 1996 with responsibilities around data management and farmer relations. Responsible for managing the breeding activities since the departure of Jaitner (in 2000). Holds a Masters degree in International Animal Health. Current coordinator of the breeding activities.
- N'Guetta Austin Bosso: Related PhD degree completed in 2006 (Bosso 2006)

5 Recommendations for replications of the N'Dama cattle breeding program of The Gambia

In this section various aspects of the breeding program are discussed under the headings 'background', 'details of the N'Dama breeding program of The Gambia' and 'recommendations'. The recommendations relate to both replication of the breeding program as is, and further advancement of the breeding program. In line with the FAO breeding strategy guidelines (FAO 2010) it is, however, suggested that countries start with a simple breeding program then move to a more advanced program.

Note that in 2008 Dempfle produced a consultancy report on the status of the N'Dama breeding program of The Gambia (Dempfle 2008). Within this report a number of very valid recommendations were made, most of which are yet to be acted upon. Many of these recommendations are thus repeated here.

5.1 The breeding objective

Background. A breeding objective defines 'where you want to go' i.e. which traits you wish to improve. Defining a breeding objective is a key first step of any breeding program. A breeding objective can be simple (one to a few traits) or more complicated (ten or more traits). It is usual for the breeding objective to evolve over time, both as the breeding program itself becomes more sophisticated, and also in response to changing market demands. Two points to note are a) that there must be within-breed genetic variation associated with the breeding objective traits for genetic improvement to occur, and b) that traits genetically correlated to those in the breeding objective will also be selected upon.

Details of the N'Dama breeding program of The Gambia. The breeding goal was addressed at an ITC organized workshop in December 1996. In attendance at this workshop were, amongst others, the Directions of the Livestock Veterinary Services and of the Research Organizations dealing with livestock of Senegal, The Gambia, Guinea Bissau, Guinea and Sierra Leone. Here the following statement was issued in relation to cattle in low-input systems: 'The N'Dama will remain the cattle breed of choice for the low-input systems from The Gambia southwards. Throughout the region the breed is regarded as triple-purpose (for meat, milk and traction) and emphasis for improvement will be for milk and meat without the loss of disease resistance and other adaptive traits'. Thus, in-short, the breeding goal can be said to be defined qualitatively as 'improvement of milk and meat without loss of disease resistance and other adaptive traits'.

In the same year that the breeding objective was formalized, a Participatory Rural Appraisal (PRA) study was undertaken to determine the production objectives of cattle owners in The Gambia (Bennison et al. 1997). This study found that 'cattle are primarily kept as a means of savings', that 'farmers placed a value on manure that equalled domestic milk consumption and exceeded that of milk sales', and that 'bull, and cows in one district, were important for draught and transport'. Alignment of the breeding objective to the results of this study is discussed in Dempfle and Jaitner 1999. They indicated that manure was not considered in the objective since it is unlikely that there are economically important differences in manure production between the animals. Further draught aptitude was not included because it was felt there were sufficient animals to select appropriate oxen from (figures given were the need to select 7000 new oxen annually from 29,000 male candidates). Disease resistance was considered important to include, as animals must produce whilst under heavy disease challenge.

Recommendations

- The breeding objective was developed 15 years ago and should be reviewed by all relevant stakeholders, including farmer representatives (also recommended in Dempfle 2008). In doing so the results of the PROGEBE baseline survey in relation to the assessment of livestock production objectives should be taken into account.
- Given that selecting for milk yield will reduce the protein content of milk, and in the longer-term the fat content (Dempfle 1998), it is recommended that maintenance and/or improvement of milk protein and fat content be included in the future derivations of the breeding objective.
- A note of caution in relation to including improved reproductive ability in future derivations of the breeding objective: N'Dama run under typical low-input management conditions show strong lactation anoestrous (i.e. do not return to heat whilst suckling the calf). Thus whilst shorter calving intervals could be obtained by reducing the suckling period of calves and/or breeding, this would result in a shorter milking period and the need to feed calves with concentrates, which may not be economical. Further investigation of this requires modelling studies and this could form part of a PhD project (see Appendix 1 for a list of reproductive traits that could be evaluated during this exercise).
- The four PROGEBE countries could choose to have a single regional breeding objective, or each country could choose to have their own breeding objective. Regardless of this choice, it is strongly recommended that the trait recording scheme is harmonized across countries (in terms of trait definitions and recording protocols). This would allow for standardized breeding values to be estimated, and countries could (if necessary) use different weights (economic values) to combine these into a selection index value. Harmonization of the recording scheme from the on-set will help facilitate regionalization of the breeding programs, as is recommended as a longer-term goal (see section 6.6).

5.2 Economic values of the breeding objective traits

Background. The economic values of the breeding objective traits need to be estimated, as they are used to weight EBVs within the selection index (see section 5.3). Changing the economic weights of the breeding objective traits will alter the response to selection, for individual traits as well as the overall selection index, and additionally the economic returns from the breeding program (which is maximized when the true economic weights are utilized). One common way of calculating the economic values of the traits is to determine the marginal profit associated with increasing each trait by one trait unit, using parameters relevant to an average herd. Note that it is the relative ratios of the economic values that are important, not the absolute values.

Details of the N'Dama breeding program of The Gambia. The traits of interest to The Gambia breeding program were defined as daily weight gain (DWG, from 15 to 36 months) and milk yield (MY, first 100 days of lactation), with disease resistance accounted for indirectly through DWG (as the animals are producing under a high trypanosome challenge environment). The economic values of DWG and MY were determined using a biological-economic model, as described in Dempfle and Jaitner (1999). This model assumed that the amount of metabolizable energy for a herd (or region) is fixed. The model took into account the size and composition of the herd, the average performance, the metabolizable energy needed, the average cost, and the average revenue. The profit per year was calculated, and then the marginal profits of increasing DWG, and separately MY, by one unit determined. The final economic values reported in the ITC biennial report (1998/99) were 0.215 for DWG and 0.934 for MY (units were Gambian Dalasi). It should be noted that this model required a considerable amount of biological and economic data as inputs, and it is likely that these input parameters are now out of date.

Recommendations

- That the economic values be (re)calculated using current economic and biological data, using the same approach as outlined in Dempfle and Jaitner (1999) (also recommended in Dempfle 2008).
- Given the need for a considerable amount of biological and economic data (such as the prices of inputs and outputs) it is suggested that the exercise be first undertaken for The Gambia, with other countries following suit once there is a better idea of the exact data requirements (also recommended in Dempfle 2008)
- That the up-to-date country-specific economic values be utilized in the calculation of selection index values as soon as they are available.
- That the economic values are re-evaluated at regular time periods (e.g. every 5 years), using either the approach outlined in Dempfle and Jaitner (1999) or other appropriate methodologies.

5.3 Selection index

Background. The selection index is the sum of weighted EBVs: if using EBVs derived from BLUP the selection index is equal to economic value$_{\text{trait 1}}$ x EBV$_{\text{trait 1}}$ + economic value$_{\text{trait 2}}$ x EBV$_{\text{trait 2}}$ etc. Under truncation selection schemes, breeding animals are selected on the basis of high selection index values.

Details of the N'Dama breeding program of The Gambia. A selection index is calculated for each animal as 0.215 x EBV daily weight gain (15 months to 3 years) + 0.934 x EBV milk yield (0–100 days part lactation) (ITC 1999).

Recommendations

- That the newly calculated economic values associated with the breeding objective traits be used within the selection index, as soon as that information becomes available (see section 5.2)

5.4 Selection criteria

Background. The selection criteria are the traits that are measured to achieve the breeding objective. There need not be a one to one relationship between breeding objective traits and the selection criteria (i.e. several selection criteria may provide information on one breeding objective component, or conversely an individual selection criterion may provide information on more than one breeding objective component). In defining the selection criteria it is important to consider 'which traits should be measured on which animals and when'.

Details of the N'Dama breeding program of The Gambia. Daily weight gain (DWG). To provide information on DWG from 15 months to 3 years, monthly weight records of all animals within this age range are recorded. The animals are weighted in the mornings, between 8 am and 9 am, before being taken for water. Weights are measured and rounded to the nearest kg.

Milk yield (MY). To provide information on MY, weekly milk offtake measurements are taken for all lactating cows (with data for the first 100 days of lactation used to calculate the MY EBVs). Milk offtake is considered the additional milk not consumed by the calf. The milking procedures are as follows. Cows are milked once daily, in the morning. The calf is allowed to suckle its dam for about a minute for milk let-down, the cow is then milked by hand, and finally the calf allowed to suckle for feeding purposes (the calves are not bucket-fed any milk). Milk measurements are taken using a 1000 ml measuring cylinder, with 1 ml graduations, and the measurements recorded to the closest ml. Note that whilst milking occurs daily, milk offtake measurements are taken on only one day of the week.

Recommendations

- That replicating countries follow the same trait measuring protocols, so the recording scheme is harmonized across countries.
- That personnel taking measurements within the replicating countries are appropriately trained, inclusive of a visit to the N'Dama breeding program of The Gambia to observe measuring activities first-hand.
- That, in the medium term (next few years), a change is implemented to the calculation of the MY EBVs from being based on 100 day lactation data to be based on 180 day lactation data plus calf weight gain (as calf weight gain is from suckling it is also an indicator of milk production). This involves estimating the genetic parameters for these traits (sufficient data from The Gambia program is available for this), and altering the models used in the EBV calculation. This will result in more accurate MY EBVs and thus higher rates of genetic gain.
- That, in the medium term (next few years), modelling exercises be undertaken to optimize the selection criteria in terms of balancing genetic gain vs. the cost of obtaining the information (which traits are measured on what animals and when). Available software to do this includes Z-plan (Willam et al. 2008). This is a substantial exercise and could form part of a PhD project.

5.5 Other recorded information

Background. It can be useful to measure traits in addition to those included in the selection index as this will result in an accumulation of data for future analysis (such as the effect of selection on these traits, estimation of genetic and phenotypic correlations between traits etc.). It will also facilitate inclusion of these traits within the selection index, should this be considered warranted.

Events , such as matings, calvings, animal movements, entries, exits, and health treatments, must also be recorded. This information can be used for monitoring and management purposes, and may be fitted as an effect in the data analysis of other traits.

Details of the N'Dama breeding program of The Gambia. Weights. Weights of all animals are recorded monthly, from the animals entry into the nucleus (by birth or purchase) until the animal leaves the nucleus. Birth-weights (recorded to the nearest 100 grams) are recorded on all calves born, including those still-born. Note that the monthly weight records on adult animals serve a management purpose, allowing body weight loss in the late dry season to be monitored.

Milk quality traits. The protein and fat content of milk, as well as its conductivity, is recorded at two-weekly intervals. (Note that this occurred for a period of time but then ceased due to lack of access to an analysis lab. Re-initiation of the milk quality trait recording using field milk testing equipment is considered a high priority, see Dempfle 2008).

Reproductive traits. Additional measurements related to reproductivity include the date and time of the start/finish of the joining period, each time a cow on heat is put with a bull (including for unsuccessful joining), and birthing information (including for stillborn animals or animals that die shortly after birth). Birthing information is comprised of: birth date; birth order (1st, 2nd, 3rd etc. calving); birth type, defined as 'normal gestation time', 'pre-mature (hairy)', and 'abortion (no hair on the calf)'; and birth ease, defined as 'no or little assistance', 'considerable assistance', 'cesarean or worse'.

Packed cell-volume and blood parasites. Packed-cell volume (PCV) is measured in conjunction with weighing animals located at the Bansang station (i.e. between 15 and 36 months of age). Animals with a packed cell volume of <20% are treated for trypanosomosis. Both PCV and treatment information are recorded. At the same time blood smears are examined by light microscopy and the following information recorded: presence of trypanosomes (yes/no), if yes then type and amount (*Trypanosoma congolense, T. vivax, T. brucei, T. theileria*), and presence of microfilaria (yes/no).

Health. Health related records include the animal's symptoms, diagnosis, treatment (drug and dosage) and the dates associated with these.

Other. Other traits/events recorded include: weaning date; animal exit date and reason; animal entry date, price and type (for animals not born into the nucleus); end of milking dates and reason; herd assignment, herd location and associated dates; herdsman name, location, and start and finish work dates; animal sire, dam, breed and sex.

Recommendations

- That replicating countries record at least the set of traits/events listed above, using the same recording protocols, so the recording scheme is harmonized across countries.
- That personnel taking measurements within the replicating countries are appropriately trained, inclusive of a visit to the N'Dama breeding program of The Gambia to observe measuring activities first-hand.
- That field milk-testing equipment is purchased to allow uninterrupted recording of milk quality traits (as recommended in Dempfle 2008). Recommended is a Lactoscan MCC 50 sec., with the conductivity and real-time clock options, from Milkotronic Ltd. (http://www.lactoscan.com).
- That measurement of bull scrotal size is considered, as this is positively associated with a number of fertility traits, including increased semen quantity and quality, as well as earlier age at puberty. Information on how to take this measurement can be found at http://breedplan.une.edu.au/tips/Recording%20Scrotal%20Circumference%20Measurements.pdf

5.6 Trait and event recording protocols

Background. A successful breeding program requires good data recording protocols. The type of data to be recorded included pedigree, trait records, and other information such as health treatments and animal movement. Errors or omissions in data recording can result in less accurate EBVs and thus lower rates of genetic gain.

Details of the N'Dama breeding program of The Gambia. Four books (a mating record book, a calving book, an exit book, and a treatment book) are maintained, with records entered directly into these books immediately the information becomes available. This information is subsequently entered into an electronic database (see sections 5.8 and 5.9). The books are stored in a secure location within an office.

The recording books are structured as follows:

Mating record book

Cow identification	Herd	Service date	Time	Bull identification	Exit date	Time	Remarks

Calving Book

Herd	Dam identification	Calving date	Calf identification	Sex	Birth weight	Birth weight Date	Remarks

Exit Book

Date	Herd	Sex	Animal identification	Reason

Treatment Book

Date	Herd	Animal identification	Diagnosis	Drug used	Dosage	Remarks

Recommendations

- That replicating countries record data either through the use of recording books or specifically designed forms, capturing at least the set of information described above.

5.7 Pedigree recording protocols

Background. When breeding values are estimated by an animal model using BLUP methodology, pedigree information on both the sire and dam side is utilized. Accurate recording of pedigree is thus important. Inaccurate pedigree information result in less accurate EBVs, and thus lower rates of genetic gain. It is also important to record the pedigree of animals that were still-born, or who died shortly after birth.

Details of the N'Dama breeding program of The Gambia. Any animals born (including those still-born or who die shortly after birth) are assigned a unique identification (see below) and the dam identification recorded against this. The sire identification is (or at least should be) known from the joining records.

Recommendations

- That all efforts are made to reduce pedigree errors. It is particularly important that joining (mating) records are accurate.

5.8 Animal identification

Background. A reliable animal identification scheme is needed so that trait records are correctly matched to animals, and so that animals are identifiable at the time of selection. Each animal needs to be assigned a unique identifier, including animals that are stillborn or die shortly after birth (as such events should be recorded). If using ear tags for identifying animals it is good practice to tag each ear.

Details of the N'Dama breeding program of The Gambia. Five digit identifiers are used: the first two digits represent the year of birth (for example, 99 for 1999), the next digit represents the origin of the animal (for example, a 5 if the animal was born into the Keneba herd, and 4 if it is from a village herd), and the last two digits are sequential numbers (for example, 01 for the first animal born that year, 02 for the second etc.). Thus '99501' would be used for the first animal born in 1999 into the Keneba herd, and similarly '87403' would be used for the third animal acquired from a village herd in 1987. The animals are identified by ear-tags in both ears (though tagging of one ear only occurred during some times of funding shortages). Note that the ear-tags remain in place for the life-time of the animal, even if they are sold to multiplier herds.

Recommendations

- That double-identification of animals , for example an ear-tag in both ear, is practised
- That any lost ear-tags are replaced immediately
- That replicating countries use a similar 5-digit identification system, but with their own specific codes for the third digit. Each animal identification must be unique.
- That if breeding programs are regionalized an additional digit is added to the code, representing country of origin.

5.9 Database

Background. All data (pedigree, trait records, events etc.) should be stored in a well-designed database. Designing such a database is not a trivial task, and personnel with database expertise should be utilized. Database options include (but are not limited to) Microsoft Office Access and MySQL. Microsoft Office Excel should not be used as a database, as it does not have database functionality. It is advantageous for the database to be coded to perform a series of automatic checks on data entry, to help reduce the number of data-entry errors (for instance, by setting year of birth to always be a four digit number, or setting minimum and maximal trait values). Writing scripts (code) to automate the extraction of data for the database, for both the genetic analysis and summary reports, is also advantageous. It is good practice to keep at two additional back-up copies of the database, stored in different locations to each other and the original database.

Details of the N'Dama breeding program of The Gambia. The data was originally stored in a dBase database, however it was recognized that this was becoming out-of-date. Thus, in the first half of 2010, with the support of Dempfle, a customized and fully relational database was developed. Access (part of Microsoft Office Professional) was chosen for this purpose, due to the relatively high number of people familiar with it. A number of reports (such as those for weights, milk, matings and events) can be automatically generated (R is used as the statistical environment, Latex for report writing, and Sweave + R + Latex as an automatic reporting tool). An overview of the structure of this database is given in Appendix 2. Transition to the new system is currently (July 2010) near completion.

The database is backed up (copied) whenever data is entered, which is usually weekly. Two additional copies are made onto an external hard-drive, USB stick, or CD, and these stored in separate locations to each other and to the original database.

Recommendations

- Given the highly developed state of the Access database and associated scripts, it is suggested that replicating countries contact Dempfle (as the developer of the database), as well as any other relevant stakeholders, to discuss whether they may be able to access/purchase the database. Note that some country-specific customization of the database may still be required.
- That the database be operational prior to the start of the recording program, to avoid storage of data in a 'temporary' electronic format.
- That a similar database back-up procedure is established and followed.

5.10 Data management protocols

Background. Data management here will refer to data entry into the database and basic data checking.

Details of the N'Dama breeding program of The Gambia. Data entry. Data from the weekly event list is entered into the database weekly (each Thursday). This is performed at Keneba, and the Bansang weekly event list is transferred to Keneba in hard-copy by vehicle. Data is double-entered into the database, either by two separate people each entering the data once (preferable), or by one person entering the data twice. After the double entry is complete, a database program is run to compare the two entry files. It the two entry files match (i.e. no errors detected) one is permanently appended to the database: if an error is detected it needs to be corrected and the error entry program re-run again till the two files match completely.

Data checking. A series of data-checks are performed using several scripts written in R (R is freely available software for statistical computing and graphics, see http://www.r-project.org/). Various data summary reports can also generated at this stage.

Recommendations

- That staff involved in data entry/analysis are appropriately trained, preferably by Leo Dempfle or Nerry Corr (assuming the database constructed by Leo Dempfle is utilized).

5.11 Genetic evaluation

Background. The current best practice is to estimate breeding values using best linear unbiased prediction (BLUP) methodology and an animal model. In this case, breeding values are estimated for each individual using not only the animals own trait records, but also information from relatives and, in the case of multi-trait BLUP, from correlated traits. In addition, measurable environmental factors are simultaneously accounted for. Some features associated with BLUP include:

- BLUP accounts for some animals having more or less information than others, by constructing a customized index for each animal, with each information source appropriately weighted.
- BLUP accounts for potential source of bias, such as culling and selection, and non-random mating, assuming culled animals, non-selected animals and mates are included in the analysis.
- BLUP EBVs are comparable across animals raised in different herds or management groups, if genetic links between the herds or management groups exist (i.e. there are related animals in the different herds or management groups, and this relationship is known).
- BLUP EBVs are comparable across age classes: selecting breeding animals based on EBVs will automatically optimize the generation interval.

- BLUP EBVs can be used to estimate genetic trends: as BLUP separates genetic effects and year effects, genetic trends can be observed by plotting BLUP EBVs over years

It should be noted, however, that BLUP EBVs are associated with a particular accuracy dependant on the data structure (how much and what type of information is available), the quality of the data (accuracy of recording of the pedigree, trait and environmental effects), underlying genetic parameters (such as the heritability), and the appropriateness of the model utilized (all significant genetic and environmental effects should be included). More accurate EBVs will result in higher rates of genetic gain.

The input required for a BLUP analysis includes the animal records (pedigree, trait values, fixed effects, management group etc.) as well as a number of genetic parameters (heritabilities and variance estimates and, for multi-trait BLUP, the genetic covariance between traits). Commercially available software to estimate BLUP EBVs include, for example, ASReml and PEST (with user guides found at http://www.animalgenome.org/bioinfo/resources/manuals/ASReml/UserGuide.pdf and ftp://ftp.tzv.fal.de/pub/pest/doc/pest-manual-Apr-2006.pdf, respectively). Given the complex nature of any genetic analysis, however, it is imperative that the analyst has a strong quantitative genetics/statistical background, and a comprehensive understanding of both the BLUP methodology itself as well as the implementing software.

Details of the N'Dama breeding program of The Gambia. The statistical models used for DWG and MY are as follows:

$$\text{DWG:}\quad y_{ijklm} = \alpha_i + \beta_j + \gamma_k + \delta_l + A_m + e_{ijklm}$$

Where y = daily weight gain, α = sex (male, female), β=year x season of birth, γ=station where the animal was between birth and weaning, δ=herd where the animal was between 15 and 36 months, A=breeding value of the animal, and e=environmental affect (residual). A and e are random effects with E(A)=0; E(e)=0; $\text{Var(A)}=\text{A}\sigma^2\text{A}$ and $\text{Var(e)}=\text{I}\sigma^2\text{e}$. The remaining factors are fixed effects.

$$\text{MY:}\quad y_{ijklm} = \alpha_i + \beta_j + \gamma_k + A_l + Ep_l + e_{ijklm}$$

Where y=100 day milk yield in lactation m, α =herd, β =year x season of calving, γ =lactation number (1 for first lactation, 2 for second and third lactation, 3 for fourth or higher lactation), A=breeding value of the animal, is the environmental covariance between the (part-) lactations, and e=environmental effect (residual). A, Ep and e are random effects with expectations and variances of $E(A) = 0$; $E(Ep) = 0$; $E(e) = 0$; $\text{Var}(A) = \sigma^2_{\text{A}}$ for all lactations; $\text{Var}(Ep) = \sigma^2_{Ep}$ for all lactations; $\text{Var}(e) = \sigma^2_{\text{e}}$ for all lactations and $\text{Cov}(e_{kl}\,;\, e_{k'l}) = 0$, and the remaining factors are fixed effects. The breeding value A is the same in different lactations (repeatability model) whereas the environmental effects of the same cow in different lactations is assumed to be equicorrelated. Note that the use of a repeatability model here assumes that the cow's genotype has the same effect on all lactations.

Genetic parameters used in the analysis are given can be obtained from contacting the International Trypanotolerance Centre.

The software used for the genetic analysis is PEST Version 4.2.3 (Groeneveld et al. 1990) which is a Fortran program for the estimation of breeding values (contact Eildert.Groeneveld@fal.de to obtain a copy of the program). R scripts are used to extract data into the format of the input files for the PEST analysis, and the PEST analysis run using appropriate implementation code. Both the R scripts for data extraction and the PEST implementation code was written by Dempfle.

Recommendations

- That replicating countries similarly estimate breeding values using an animal model and BLUP, and that the person performing the analysis is appropriately trained and further supported.
- That replicating countries obtain a copy of PEST (see contact details above), and also contact both Dempfle and the ITC in relation to use of the data extraction scripts and PEST implementation code
- That in the absence of country-specific genetic parameters, those given in Table 2 and/or from the literature, be (carefully) utilized
- That country-specific genetic parameters be estimated once sufficient data has accumulated (after a number of years). A decision can be taken at that time whether to use the newly estimated parameters in the analysis or not, based on the accuracies of the parameter estimates
- That genetic trends be utilized as a means of monitoring genetic progress in the nucleus (though these need to be appropriately interpreted as input parameters to the analysis, such as trait heritabilities, effect the trends).

5.12 Selection scheme

Background. Different selection schemes exist, such as progeny testing schemes, half-sib schemes and young sire programs. In a progeny testing scheme the selection of parents takes place after progeny information is available (e.g. milk yield on female progeny of test bulls); in a half-sib scheme selection takes place after half-sib information is available (e.g. milk yield on female half-sibs of test bulls); and in a young sire program selection takes place when animals are young (e.g. 3 years). Each of these is associated with different EBV accuracies and generation intervals, both of which affect the annual rate of genetic gain (more accurate EBV and shorter generation interval s are associated with higher rates of genetic gain: see section 5.15). EBVs are most accurate for the progeny testing scheme and least accurate for the young sire scheme, whilst generation interval is longest for the progeny testing scheme but shortest for the young sire scheme.

Details of the N'Dama breeding program of The Gambia. Simulation studies carried out for The Gambian N'Dama breeding program indicate that the half-sib and young sire schemes produced about the same rates of annual genetic gain, which were considerably higher than the progeny testing scheme (Dempfle and Jaitner 1999). A young sire scheme was chosen because it was considered the simplest and easiest to operate (Dempfle and Jaitner 1999).

Recommendations

- In the absence of information to suggest that a different type of selection scheme is more optimal, use of a young sire scheme should be retained.

5.13 Selection and mating of breeding animals

Background. Breeding males and females can be selected based on high EBV or index value (termed truncation selected) and then mated at random. However, as BLUP EBVs are calculated using family information (especially for lowly heritable traits), there is a tendency for selected animals to be related, which may result in high inbreeding rates. An alternate to this is to use 'mate selection' approaches where 'which animals to select' and 'who these animals should be mated to' are simultaneously optimized (see for example, Meuwissen and

Sonesson 1998; Kinghorn 2011). These approaches can results in the same rates of genetic gain with lower rates of inbreeding (or vice-versa) than truncation selection and random mating, and are being applied in a number of breeding programs world-wide.

Details of the N'Dama breeding program of The Gambia. Animals to be used as breeders are selected based on high index value (i.e. truncation selection), though animals with defects are excluded. Further, in order to increase the effective population size, sires are replaced by their best performing son, and no dam has more than one son used as a sire (a simplified type of mate selection). Breeding males are kept in individual pens and cows on heat are bought-in to a bull chosen at random. Cows on heat are detected using a vasectomized teaser bull which is always kept with the herd (to keep away stray bulls whilst herding in the bush). If the cow returns to heat with 21 days of the first joining it is returned to the same bull (to ensure that the sire of any resultant calf is known): however if the cow returns to heat after 21 days of the first joining it is assigned a bull at random. Breeding bulls are typically used for three years (depending on the genetic merit of the bull), and then sold to multiplier herds.

Recommendations

- That 'mate selection' approaches are implemented within the medium term future. This requires the availability of specialized software (such as that freely available through pedigree viewer: http://www-personal.une.edu.au/~bkinghor/pedigree.htm), or the use of commercial companies providing this service (such as the TGRM® Mate selection Service from X'Prime: http://www.xprime.com.au). It also requires single sire mating to be performed.
- That inbreeding coefficient of animals are calculated, for example at the same time as the genetic evaluation, so rates of inbreeding can be monitored. Freely available software to calculate inbreeding rates include pedigree viewer (link given above).

5.14 Nucleus size, age structures and annual movement of animals

Background. The nucleus size, as well as age structure of animals within the nucleus, is important as they affect the overall profitability of the program. In addition, the nucleus size has a large influence on the number of animals available for distribution to the lower tiers, and thus overall impact. These factors are discussed below, together with the annual movement of animals, due to their inter-relation.

Details of the N'Dama breeding program of The Gambia. According to Dempfle and Jaitner (2000) and Bosso et al. (2007) the program (when fully operational) was structured as follows:

- An active breeding stock of 400 females and 5 or 6 bulls, with a total number of animals at any one time of between 1000 and 1100
- Located at the Keneba research station are the breeding females, calves (until weaning at 12 months) and bulls
- Located at the Bansang research station are animals from 12 to 36 months of age, at any one time about 230 males and 225 females (more males than females due to the entry of some males from village screening)
- Each year about 100 males and 100 females are born. About 90 of each sex are transferred to Bansang (at around one year) for performance testing. About 80 of each sex are available for selection at the end of the testing period. Losses throughout this time are from both natural mortalities and culling for various reasons (such as poor structure).
- Each year, about 5 males identified from village screening enter the nucleus for performance testing at Bansang, of which 4 will be available for selection at the end of the testing period (note thought that in practice this did not happen annually)

- Each year one to two of the existing breeding bulls, and 55 old cows, leave the nucleus, to be replaced by better performing animals
- Each year, of the 84 young sires completing the performance testing at Bansang (80 born into the nucleus, 4 from village screening), the highest ranked one or two are selected as breeding bulls, the next highest ranked animals (about ten) are used as multipliers, and the remainder slaughtered.
- Each year, of the 80 young females completing the performance testing at Bansang, about 75 are mated and calved, and 5 slaughtered. Of these 75, about 55 are retained after their first lactation to replace the old cows leaving the nucleus, whilst 20 are slaughtered.
- Females are mated at around 4.5 years (54 months) of age, first calf at 5.25 years (63 months) of age, and have a calving interval of 2 years. Females are kept for as long as they remain reproductive and competitive (for modelling purposes, a maximum of 6 calvings is used).
- Males are first mated at around 3 years of age, and typically used for three years (depending on genetic merit).
- A diagrammatic representation of the above is given in Figure 3
- The animals are run in a number of individual herds to ease their management.

Recommendations

- That countries ensure they have sufficient facilities, resources and capacity to maintain at least these numbers of animals
- That once the program has been operating effectively for some time, and the average performance of the nucleus animals is significantly higher than that of the lower tiers, the number of males annually distributed to the lower tiers should be increased. The actual number of males that is appropriate to distribute will depend on the genetic lag, the important point being that the average genetic merit of the males distributed from the nucleus be greater than the average genetic merit of the lower-tier animals. Distributing the top 50% of nucleus bulls, for example, would mean that about 40 animals are transferred annually to the lower tiers (assuming 84 sires complete the performance testing and two are kept for nucleus breeding). Note that in early years of the breeding program there is little difference in the genetic merit between the tiers, and as such few nucleus animals will be of sufficiently competitive to warrant distribution to the lower tiers.
- That the optimal size of the nucleus, in terms of impact related to number of animals distributed and/or the breeding program profitability, be examined through modelling exercise. This is a substantial amount of work, and could comprise (part of) a PhD project.
- Note that if males identified through village screening are not selected as breeding bulls, then the nucleus is essentially closed, and strategies to avoid high-rates of inbreeding (such as the use of male-selection approaches, see section 5.13) should be considered.
- Animals may be located on one research station (rather than moving between the two) but for growth rate (from 15 to 36 months) to act as an indirect indicator for disease resistance this should have at least a medium trypanosome challenge. Note, however, that keeping all animals in one location is risky in relation to major loss, for example from disease outbreak.

5.15 Issues affecting rates of genetic gain within the nucleus

Background. It is generally understood that rates of within-breed genetic improvement are slow, and at most one to a few per cent of the trait mean per annum. Using simulation, Bosso et al. (2009) predicted that the N'Dama breeding program (with 400 breeding females) would result in an increase in milk yield of 0.46% per year (or

2.09 kg, based on an average annual milk yield of 450.89 kg), and an increase in daily weight gain of 0.25% per year (or 0.23 g/day, based on an average daily weight gain of 126.32 g/day), averaged over nucleus animals.

Factors affecting the annual rate of genetic gain (response per year, R_{year}) are accuracy of selection ($r_{I,A}$), selection intensity (i), generation interval (L), and the genetic variance (σ_A) as given by:

$$R_{year} = r_{I,A} \frac{i}{L} \sigma_A$$

Accuracy of selection is defined as the correlation between the true breeding value/selection index, and the estimated breeding value/selection index. This is affected by a number of factors including:

- the underlying genetic parameters, such as trait heritabilities (higher heritabilities results in more accuracy),
- the appropriateness of the model used in the calculation of the breeding/selection index values, and the accuracy of the input parameters to these models (inappropriate models or incorrect input parameters will reduce accuracy)
- the amount of information used in calculating the estimated breeding values, such as own phenotype, information on relatives, information on correlated traits (more information results in more accuracy)
- the accuracy with which trait, pedigree, other (such as fixed effect) information has been recorded (erroneous information will reduce accuracy)

Selection intensity is dependent on the proportion of animals selected to be parents : the smaller the proportion of animals selected the greater the selection intensity and also the greater the rate of genetic gain. However, selecting fewer animals is likely to result in a higher rate of inbreeding than selecting more animals, and thus a selecting intensity that results in a compromise between the rate of genetic gain and the rate of inbreeding is most often utilized. Increasing the reproductive performance of animals, as well as their survival rate, will increase the number of animals available for selection, and thus (assuming the same number of animals are selected) the selection intensity.

Generation interval is defined as the average age of parents when their progeny are born, and shorter generation intervals result in higher rates of genetic gain. The generation interval is dependent on the age at first calving, the calving interval, and the number of calvings, and decreasing any of these parameters will shorten the generation interval.

The genetic variance is integral to the trait and population under selection. With selection the genetic variance is expected to decrease (due to the Bulmer effect as well as fixation of larger genes).

Details of the N'Dama breeding program of The Gambia. Considerable efforts have been undertaken to optimize the factors influencing the rates of genetic gain, including the use of good statistical models and a young sire program, as discussed above. However recent issues of concern relate to high mortalities (as this has an unfavourable effect on the selection intensity), and high age at first calving (as this has an unfavourable effect on the generation interval).

Recommendations

- That the number of animals available for selection is maximized by ensuring low mortalities and good reproductive performance, through appropriate management (also recommended in Dempfle 2008)
- That the generation interval is as short as possible by decreasing the age at first calving, as well as the calving interval, through appropriate management (also recommended in Dempfle 2008)
- That good weight gain of calves is ensured, as this can result in earlier weaning and thus shorter calving intervals, again through appropriate management. A average weight of 70 kg at 300 days is recommended (Dempfle 2008)

- That the above be done whist still reflecting village management conditions, to avoid issues associated with genotype by environment interaction

5.16 Creating the initial nucleus

Background. Selection of base animals, i.e. those that create the initial breeding nucleus, is an important step in the breeding program implementation. At the very least the genetic merit of the base animals should not be worse than that of the wider population. The selection of unrelated animals is also recommended as this is important in the control of inbreeding rates.

Details of the N'Dama breeding program of The Gambia. In the early 80's the ITC purchased N'Dama animals (mainly females, but also males) from all regions of The Gambia, and located them at three stations, namely Keneba, Sololo/Bansang and Kerr Serign. In 1994/1995 funding was available to support the establishment of the N'Dama nucleus breeding program, and the ITC herds restructured so that breeding animals were located at Keneba and Niamina/Bansang (see Corr 1999 for further details). Limited pedigree or performance information was available on these animals at that time. Breeding activities using these animals as a base started in 1995.

Recommendations

- That countries' develop and document their own protocols for selecting animals to create the breeding nucleus. Animals can be selected at random or based on village screening for traits associated with the breeding objective. Animals should be sourced from a broad geographical area, such that they are reasonably unrelated, and be structurally sound.
- That animals are identified (e.g. by ear tag or tattoo) before leaving the village herds
- That relevant information is recorded on each animal, including owner, location (village or GIS co-ordinate), sex, approximate age, number of parturitions (if female), body condition and purchase price.

5.17 Opening the nucleus—Village screening

Background. An open nucleus refers to a nucleus where competitive animals from the lower tiers can enter the nucleus. The advantage in comparison to a closed nucleus (where animals from lower tiers do not enter the nucleus) is higher rates of genetic gain and lower inbreeding levels, as well as increased farmer participation. The disadvantage in comparison to a closed nucleus is the costs associated with the recording (screening) of the lower tier animals. Screening is most important in the earlier years of a breeding program, as in later years there is greater genetic lag between tiers and the screened animals are less likely to be competitive.

Details of the N'Dama breeding program of The Gambia. Village screening was performed to identify outstanding cows in relation to milk yield. This occurred during and after the main calving season (August to December) with 500 to 1000 cows screened (Dempfle and Jaitner 2000). Following weaning, male offspring of the outstanding cows were purchased and placed with other animals of the same age for performance testing. Screening was performed in 1994 (animals bought 1995), 1995 (bought 1996), 1996 (bought 1998), 1997 (bought 1999) and 1998 (bought 1999): in total 32 male animals were purchased.

A more detailed overview of the screening procedure is given in Dempfle and Jaitner (1999). The most important points are that a) all cows calving between July and October were included, b) the cows were ear-tagged, c) milk-offtake was measured once a month by trained milk recorders, for 3 months, d) milk recorders were from the participating villages, and were contracted and paid, e) the herdsman received incentives to participate (one rope per cow plus animal health-care).

Data recorded included the following (Dempfle and Jaitner 1999):

- Herd data: village, herd, herd owner, name of milk recorder
- Calving data: village, herd, animal, date of calving (to month if the exact day was not known), parity, and sex of the calf
- Milking data: village, herd, animal, date of sampling, frequency of milking, milk yield morning, milk yield evening (if milked), and reason if cow not milked

A linear model was used to calculated 0-100 day part lactation from the monthly milk measurements, taken into account village, herd, frequency of milking (where appropriate) and parity. The deviation of each cow from its herd mean (the residual deviation) was used to identify outstanding cows.

Recommendations

- Optimization of the number of animals to screen, the screening interval (annual, biannual etc.), and the recording protocol, is required through a modelling exercise. This is a substantial amount of work and could comprise (part of) a PhD project.

5.18 Environmental and management conditions

Background. A breeding nucleus is often run under the same environmental (including management) conditions as the commercial tier animals, to avoid the issue genotype by environment (G × E) interaction (where the performance of animals varies across environments). In some cases, however, the breeding nucleus is run in an improved environment, and this can be beneficial if the greater rates of genetic gain (associated with the improved conditions) offset the G × E.

Details of the N'Dama breeding program of The Gambia. The Gambia breeding program is located within the vicinity of herds comprising the multiplier/commercial tiers, and generally follows village management conditions. It is thus assumed that G × E is not a concern.

Recommendations

- That environmental and management conditions be as similar to village conditions as possible
- That, in the longer-term and assuming the availability of G × E information, modelling studies be performed to evaluate the effect of departures from the above, such as feed supplementation to decrease the age at first calving or to increase survival rates. This could be part of a PhD project.

5.19 Dissemination strategies

Background. In broad terms a within-breed improvement program can be said to involve a) improving the genetic merit of animals, and b) disseminating this improved genetic merit. It is thus important that as much attention be paid to optimization of the dissemination strategy as is paid to optimization of the nucleus activities. The average genetic merit of the nucleus animals disseminated to the lower-tiers should be greater than the average genetic merit of the animals in the lower-tiers (else the lower tiers will not benefit). In earlier years of the breeding program the genetic merit of the nucleus animals will only be marginally greater than that of the lower-tiers, and thus fewer animals can be distributed. In later years of the breeding program the genetic merit of the nucleus animals will become significantly greater than that of the lower-tiers, and thus more animals can be distributed.

Details of the N'Dama breeding program of The Gambia. Genetically improved animals were disseminated from the nucleus to the multiplier herds, and subsequently to the commercial (village) herds, though the movement of bulls. Females were not disseminated, mainly due to their lower reproductive capacity. Dissemination started in 2001 (5 years after performance recording started in 1996) and by 2004 44 bulls had been distributed to multipliers in 26 villages, with 169 offspring of these bulls registered in the multiplier herds (Bosso et al. 2007).

Two multiplier associations, namely the Gambian Indigenous Livestock Multiplier Associations (GILMA) of Saloum and Fulladu, were established to support dissemination activities. The main objectives of these associations were to: a) increase awareness of the availability of breeding males, b) purchase male offspring from multipliers and disseminate them to other farmers, and c) increase farmer involvement in the breeding scheme (Bosso et al. 2007). The members of these associations comprise owners of the multiplier herds, and the association officers (including a president, treasurer and secretary) are elected every two years from the members.

Multiplier herds were selected following stakeholder meetings, and needed to meet the following criteria, amongst others (Bosso et al. 2007; Corr 2009):

- at least 40 breeding females above 5 years of age
- the farmer should have the authority to make decisions regarding herd management, and be willing to test innovations
- the person responsible for the bull should be aware that the main role of the multiplier is to sell male offspring to other farmers

It was also agreed that multiplier herds will only have bulls derived from the nucleus (other bulls must be sold or castrated), that the multiplier bulls stay in the herd for about 3.5 years after which it is sold and replaced by another bull from the nucleus (so multiplier bulls do not mate with their daughters), and that the multiplier bulls should not be removed from the herd without the knowledge of ITC or Department of Livestock Services (DLS) representatives.

At present, multiplier bulls are purchased from ITC (the owners of the breeding program) by GILMA, who then sells the bulls to its members. The price that GILMA pays for a multiplier bull is set by ITC and DLS staff, at slightly above the typical market slaughter price. GILMA purchases the multiplier bulls in cash, derived from seed-funds and any operational profits. The price that GILMA will then sell the multiplier bull to its members is set by GILMA. Means by which the members pay for the multiplier bulls include cash up-front, cash with payments over a 6 month period, and in-kind (such as bull exchange). Note that prior to the establishment of GILMA multiplier bulls were sold directly from ITC to the owners of the multiplier herds.

The multiplier association is also responsible for buying progeny of the multiplier bulls, and distributing them to other farmers. The price at which GILMA purchases progeny of the multiplier bulls is agreed by the individual selling the animal and GILMA. The price at which GILMA subsequently sells that animal is set by GILMA, with a mark-up typically added.

Record keeping of events within the multiplier herds (including identification of the breeding male received, date of delivery, purchase price, date of withdrawal, as well as progeny information such as its assigned identification number, sex, birth-date, sale price, date of sale) was planned but only implemented on a small scale due to funding restriction. Similarly, identification (e.g. by ear-tag) of progeny born to multiplier bulls was planned, but not fully implemented.

Recently, and under PROGEBE, multiplier herds have been identified in each of the three primary project sites, and a number of multiplier bulls distributed to these herds (as of August 2011, 5 multiplier bulls had been distributed to Nianija site, 4 to Niamina East and 4 to Kiang West) . Formation of associations similar to the existing GILMAs to support these multiplier units is planned. Recording within the multiplier herds occurs through weekly visits by livestock technicians, who record information onto field forms (based on what farmers have recorded in event books and recall). This information includes an inventory; details of calvings, entries, exits, and transfers; milk measurements and weights; any re-tagging that has occurred; and details of immunizations, deworming and other treatments. This data is then entered into a database developed in Microsoft Office Access.

Recommendations

- That, through stakeholder consultation, a decision is made on a country-basis around whether to use a multiplier association as a 'middle-man' in the distribution of improved animals or not
- That, regardless of the decision above, a multiplier association is formed for purposes such as knowledge sharing, promotion of genetically improved animals, and to give feedback on activities related to the breeding program/dissemination strategy.
- That record keeping within the multiplier herds is established, and means for this to continue long-term set in place. At a minimum, records of the breeding males received should include their identification number, date of delivery, purchase price, date of withdrawal and reason for withdrawal. Records on the progeny of these males should include their identification number, sex, birth-date, sale price, date of sale, and date/reason for exiting herd if not sold. Other relevant information to record is described above.
- That progeny of the multiplier bulls are permanently identified (e.g. by ear-tag or tattoo) so that they can be traced within the village herds.
- That regular workshops involving all stakeholders of the breeding and dissemination process take place, and that this feed-back from these workshops s incorporated into the on-going breeding program/dissemination strategy design.
- That learning lessons between countries in relation to the dissemination strategy are exchanged, for example by regional workshops.
- That each country makes a decision about the proportion of the total breeding-program budget to be allocated to nucleus activities vs. dissemination activities, and that this is continually reviewed.

5.20 Complexity of the breeding program

Background. It is now widely recognized that breeding programs in developing countries are more likely to succeed if kept simple the initial years, and develop over time as capacity and belief in the system builds (FAO 2010).

Details of the N'Dama breeding program of The Gambia. This program was purposely designed as a simple breeding program, resulting in low running costs and relative ease of implementation.

Recommendations

- That replicating countries keep their breeding programs simple, particularly in the initial years
- That the design/ structure of the breeding-program and dissemination activities are continually reviewed, and appropriate changes implemented (it should not be considered a static entity)
- Issues for consideration during these reviews include, but are not limited to:
    a. Extending the selection index to include additional traits (such as milk quality traits, additional disease resistance traits, feed intake)
    b. Refinements of the models/input parameters used in the genetic evaluation
    c. Introduction of mate selection (optimal contribution theory)

d. Optimization of the size of the nucleus, and number of animals disseminated

e. Optimization of the recording schemes

f. Regionalization of the breeding program, which would require the creation of genetic links between the different nuclei (for example, via the use of common sires across countries).

6 Additional issues of major concern

6.1 Capacity and expertise

Due to the highly technical nature of within-breed improvement programs, it is critical that each breeding program is managed by someone with training and experience in this field (i.e. a quantitative geneticist/animal breeder). Trying to do otherwise will undoubtedly compromise the impact of the breeding program. It is thus recommended that each country employ a person with a higher degree and/or considerable experience in animal breeding as their breeding program manager, and that this a full-time position at least for the initial years of the breeding program when there will be many development activities. Capacity building programs should also be considered. For example, similar training programs could be run to what Leo Dempfle has previously delivered, which were an initial 6 week course on animal breeding with a 2 week follow-up course.

6.2 Sustainability of the breeding programs

Difficulties in relation to implementing and sustaining the N'Dama breeding program of The Gambia, as noted at the 2009 PROGEBE breeding workshop, were (a) lack of funding affecting activities within the breeding nucleus and related to dissemination, and (b) lack of human resources, in particular personnel qualified in the area of genetics. Both of these concerns will need to be addressed.

It is suggested that each country develop and document extensive plans to ensure sustainability of the breeding program, under various assumptions (for example continuation/discontinuation of public sector funding). In doing so a useful resource is the FAO guidelines 'Breeding strategies for sustainable management of animal genetic resources' (FAO 2010). An iterative and consultative process, involving all stakeholders, is recommended.

In developing these plans, it may also be useful to consider the reasons why the majority of breeding programs within developing countries have not been successful (in terms of their impact and sustainability). These include, though are not limited to:

- Failure to apply a systems approach
- Lack of proper targeting & stakeholder involvement
- Lack of demand for genetically improved animals
- Lack of impact due to too small scale of operation
- Over reliance on project funding, resulting in cessation of activities at project end
- Lack of capacity, supporting institutions and policies

6.3 Scale of operation in relation to expected impact

The impact of the overall breeding program depends on a number of factors including the importance of N'Dama to livelihoods, the rate of genetic gain achieved in the nucleus, and the number of animals disseminated (both from the nucleus to multiplier herds, and from the multiplier herds to other village herds). As discussed above, Bosso et al. (2009) predicted that the N'Dama breeding program (with 400 breeding females) would result in an increase in milk yield of 0.46% per year (or 2.09 kg, based on an average annual milk yield of 450.89 kg), and an increase in daily weight gain of 0.25% per year (or 0.23 g/day, based on an average daily weight gain of 126.32 g/day), averaged over nucleus animals. The multiplier and commercial tiers will lag behind the nucleus tier in terms of the average genetic merit of animals (the extent of the lag dependant on factors such as the number of animals moved between tiers and the accuracy of selection of these animals). A further consideration is that not all village herds will receive improved animals. The impact of breeding programs for different scales of operation and over different time-lines can be modelled using gene-flow approaches, and this activity is recommended.

6.4 Monitoring and evaluation

Monitoring and evaluation of the breeding program should occur at a number of different levels, with the most basic of these including the rates of genetic gain in the nucleus, the number of animals distributed to multiplier herds, the number of animals distributed from the multiplier herds to other village herds, and the effect of animal distribution on livelihoods. It is recommended that each country develop their own monitoring and evaluation procedures, and that results from monitoring and evaluation exercise are fed-back into the breeding program design.

6.5 Documentation of breeding activities

It is strongly recommended that all activities related to the breeding program are well documented, and that these documents are placed in a central repository. Such documentation is rarely available (the N'Dama breeding program of The Gambia being an exception), and are extremely important in relation to identify learning lessons. An annual report overviewing all activities related to the breeding program and dissemination strategy that have occurred in the last twelve months, with all relevant documents (protocols, agreements etc.) appendixed, would be extremely valuable.

6.6 Regionalization of the breeding programs

Regionalization of the breeding programs, where exchange of animals occurs between the four country breeding nuclei, is recommended as a longer term goal. This reasons behind this recommendation include (a) the expectation of higher rates of genetic gain and lower inbreeding rates , (b) the reduced risk of loss of the genetic improvement through severe disease outbreak or natural disasters such as drought, and (c) the facilitation of cross-exchange of ideas and learning lessons. It is thus suggested that breeding programs are designed now with a view to future regionalization of the program in mind. In this regard it is very strongly recommended that the trait recording schemes be harmonized across countries from the onset.

7 Concluding comments

Development of a sustainable within-breed improvement program for livestock is a non-trivial task, involving considerable planning and the application of various types of expertise over a long time frame. In this regard the need for country-level capacity in terms of people trained in designing and implementing genetic improvement programs, as well as carefully considered sustainability plans for the breeding activities, cannot be overly stressed. It is also extremely critical that other system constraints (such as access to animal health-care, feeds and markets) are simultaneously addressed, as packages of interventions are the most likely to increase livestock productivity and thus benefit the rural poor.

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Appendix 1 Additional information on traits related to reproductive performance/fertility

Trait: Scrotal size

Why important: Increased scrotal size (scrotal circumference) is positively associated with a number of fertility traits, including increased semen quantity and quality, as well as earlier age at puberty. In addition, some female fertility traits (such as age at puberty, return time to oestrous, and days to calving) are favourably genetically correlated to the scrotal circumference of their male relatives.

Description: Scrotal circumference is measured using a tape measure at the widest point of the scrotum for animals of a constant age (e.g. one year). The unit of scrotal size EBVs is usually cm (and higher EBVs are considered favourable).

Required data: Scrotal size of bulls within a particular age range (e.g. 300 to 400 days) recorded in cm to one decimal place. One person should take all the measurements for consistency.

Comments: Measurements should be taken when the bulls are reaching puberty, which may be at a different age range to that given as examples above.

Trait: Gestation length

Why important: Longer gestation lengths are usually associated with higher birth weight and calving difficulties, as well as re-breeding problems.

Description: Gestation length is the time period between the date of conception and calf birth. The unit of gestation length EBVs is usually days, and lower EBVs are considered favourable.

Required data: The date of conception as well as the date of birth. Also type of mating (natural or AI), birth type (single vs. twin), and management group.

Comments: This is mostly used for conceptions via AI where the date of conception is known (which is not always the case).

Trait: Days to calving

Why important: Days to calving is an important indicator of female fertility. It comprises the ability to conceive, time to conception after joining, the gestation period, and the ability to give birth to a live calf. Females with shorter days to calving also tend to reach puberty earlier and more quickly return to oestrous after calving.

Description: Days to calving is the time from the start of joining (when the female and bull are put together) until the subsequent calving. Variation is due to differences in the time period from the start of joining to conception (the main source of variation) as well as from conception to birth of the calf. The unit of the EBV is days, and lower EBVs are considered favourable.

Required data: Joining information on all females (both heifers and cows, and even those that do not calf). For natural mating record the bull the cow was put to, as well as the first and last joining days (even for unsuccessful joining). For AI, record the bull, AI date, and AI type (even for unsuccessful AI's). AI type indicates the broad AI procedure (e.g. insemination of individual animals observed to be on heat, vs. synchronization of all females with individual insemination, vs. synchronization of all females with blanket insemination etc.) and is only required if this is likely to vary across animals / years**.** Cow exit details for any cows leaving the herd, inclusive of reason (particularly differentiating between those culled for not conceiving/calving, and those culled or exiting the herd for other reasons). Calf details including date of birth and whether the calf was born alive or dead.

Comments: Failure to collect all required records (including those on unsuccessful joining, heifers/cows that do not calf, and those on dead calves) will result in biased EBVs. EBVs will be more accurate if single sire mating is performed, however EBVs are still possible to calculate if multiple sire groups are used.

Trait: Calving interval

Why important: Calving interval is generally considered an important determinant of profitability within a cattle herd.

Description: The time period, usually measured in days, between the birth of a calf and the subsequent birth of the next calf, from the same cow.

Required data: Dates of birth of all calves, types of birth (single, twin, dead/alive), management group of cow.

Comments: It should be noted that N'Dama run typical low-input management conditions show strong lactation anoestrous (i.e. do not return to heat whilst producing milk). Thus whilst shorter calving intervals could be obtained by reducing the suckling period of calves and/or breeding, this would result in a shorter milking period and the need to feed calves with concentrates, which may not be economical.

Trait: Birth weight

Why important: Too high calf birth weights are associated with calving difficulties, associated with death of the calf or mother, and/or the need for additional labour or health-care, as well as re-breeding problems.

Description: Calf birth weight is recorded using a weighing device. The unit of the EBV is kg and lower EBVs are usually considered favourable

Required data: Calf birth weight, recorded at or shortly after birth (preferably with 24 hours), on all animals including those born dead. A management group if different groups of females are managed differently prior to calving (e.g. via supplementary feeding)**.** An additional management group if special circumstances are associated with the calf birth (such as sick mother, or being born premature). Also, birth type as single/twin.

Comments: Whilst low EBVs are usually considered favourable, there is an optimal, as too low calf birth weights are associated with poor calf survival.

Trait: Calving ease

Why important: Calving difficulties can lead to the death of the calf or mother, and/or the need for additional labour or health-care, as well as re-breeding problems.

Description: EBVs can be produced for 'direct calving ease' i.e. the ability of a sire's calf to be born unassisted, as well as 'daughter calving ease' i.e. the ability of a sire's daughters to calve unassisted. The unit of calving ease EBV is the per cent of unassisted calving, and higher EBVs are considered favourable.

Required data: Calving difficulty score for the calf (usually on a 1 to 5 scale, or similar). Birth weight and gestation length data can also be incorporated. A management group if different groups of females are managed differently prior to calving (e.g. via supplementary feeding)

Comments: This trait would only be included in the breeding program if calving difficulty is considered a problem and differences between animals in the calving difficulty scores are expected. For N'Dama, calving ease may be of little importance.

Appendix 2 File structure of the Access database for the N'Dama breeding program

This database was developed by Leo Dempfle, who kindly gave permission to reproduce the file structure here.

A. Master Files:

There are 14 master files as follows:

01 Master_BaseAnimal
02 Master_Birth
03 Master_Exit
04 Master_Health
05 Master_Herd
06 Master_Herdsman
07 Master_MilkContent
08 Master_MilkYield1
09 Master_MilkYield2
10 Master_Movement
11 Master_Repro
12 Master_Stop_Milking
13 Master_Weaning
14 Master_Weight

01 Master_BaseAnimal

Name	Type	Length	Indexed
ID_Station_born	Text	3	No
ID_Herd_born	Text	5	No
ID	Text	5	Y-D
D_old	Text	5	No
Name	Text	30	No
Name_old	Text	40	No
Date_Birth	Date	short	No
Sex	Text	1	No
ID_Breed	Tex	1	No
Name_Breed	Tex	6	No
ID_Sire	Tex	5	No
ID_Dam	Text	5	No
Price	number	2	No
Date_Entry	Date	short	No
Type_Entry	Text	1	No
Comment	text	20	No
Input_Date	Date	general	No

02 Master_Birth

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	Y_D
Date_Birth	Date	short	No
Order_Birth	number	int	No
Type_Birth	Text	I	No
Ease_Birth	Text	I	No
n_Offspring	number	int	No
ID_offspring	Text	5	No
Sex	Text	I	No
Fate_Offspring	Text	I	No
Breed_Offspring	Text	2	No
Weight_Birth	number	I	No
Date_BirthWeight	Date	short	No
Comment	Text	40	No
Date_Exit	Date	short	No
ID_Sire	Text	5	No
Date_mating	Date	short	No
Input_Date	Date	general	No

03 Master_Exit

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	Y_D
Date_Exit	Date	short	No
Sex	Text	int	No
Code_Exit	number	1	No
Reason_Exit	Text	Int	No
Weight	number	20	No
Price	number	in	No
Comment	Text	40	No
Input_Date	Date	general	No

04 Master_Health

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	Y_D
Date_Disease	Date	short	No
Symptoms	Text	40	No
Diagnosis	Text	40	No
Drug1_used	Text	20	No
Dose1	Number		No
Drug2_used	Text	20	No
Dose2	Number		No
DOSE	Number		No
Comment	Text	40	No
Input_Date	Date	general	No

05 Master_Herd

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	Y_D
Location	Text	20	No
Date_Entry	Date	??	No
Comment	Text	40	No

06 Master_Herdsmen

Name	Type	Length	Indexed
ID_Hman	Text	2	No
Name	Text	20	No
Name_given	Text	20	No
Location	Text	20	No
Start_to_Work	Date	Short	No
End_to_Work	Date	Short	No

07 Master_MilkContent

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	N
Date_milking	Date	Short	o
ID	Text	5	N
Fat_p	Number	2	O
Prot_p	Number	2	Y_D
Conductivity	Number	2	No
Pro_TITR	Number	2	No
Input_Date	Date	general	No

08 Master_MilkYield1

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
Date_milking	Date	short	No
ID	Text	5	Y_D
am_Milk	Number	int	No
am_Add	Text	1	No
Input_Date	Date	general	No

09 Master_MilkYield2

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
Date_milking	Date	short	No
ID	Text	5	Y_D
pm_Milk	Number	Int	No
pm_Add	Text	1	No
am_Milk	Number	Int	No
am_Add	Text	1	No
Input_Date	Date	general	No

10 Master_Movement

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID_Station_old	Text	3	No
ID_Herd_old	Text	5	No
Date_moving	Date	short	No
ID	Text	5	Y_D
Input_Date	Date	general	No

11 Master_Repro

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	Y_D
Date_mating_Start	Date	short	No
Time_mating_Start	Text	1	No
Date_mating_End	Date	short	No
Time_mating_End	Text	1	No
ID_Bull	Text	5	No
NS_AI	Text	1	No
Comment	Text	20	No
Input_Dat	Date	general	No

12 Master_Stop_Milking

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	Y_D
Date_stop_milking	Date	short	No
Reason_stop_milking	Text	20	No
Comment	Text	20	No
Input_Date	Date	general	No

13 Master_Weaning

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	Y_D
Date_weaning	Date	short	No
Reason_weaning	number	int	No
Comment	Text	20	No
Input_Date	Date	general	No

14 Master_Weight

Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
Date_weighing	Date	short	No
ID	Text	5	Y_D
Weight	number	Int	No
PCV	number	Int	No
MF	number	Int	No
TRYPS	number	Int	No
TC	number	Int	No
TV	number	Int	No
TB	number	Int	No
TTH	number	int	No
Input_date	Date	general	No

B. Synthesised Files:

Stock_All: acquired animals (base animals + screening animals) + animals born into the program

Stock_All			
Name	Type	Length	Indexed
ID_Herd	Text	5	No
ID	Text	5	No
Date_Birth	Date	short	No
Sex	Text	1	No
ID_Breed	Text	2	No
ID_Dam	Text	5	No
Origin	Text	5	No

Stock_Actual			
Name	Type	Length	Indexed
ID_Station	Text	3	No
ID_Herd	Text	5	No
ID	Text	5	No
Date_Birth	Date	short	No
Sex	Text	1	No
ID_Breed	Text	2	No
ID_Dam	Text	5	No
Origin	Text	5	No
Date_moving	Date	short	No
ID_Herd_original	Text	5	No

Pedigree			
Name	Type	Length	Indexed
ID	Text	5	No
ID_Sire	Text	5	No
ID_Dam	Text	5	No
Date_Birth	Date	short	No
Sex	Text	1	No

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