

ZPLAN+

A new software to evaluate and optimize animal breeding programs

H. Täubert^{}, F. Reinhardt^{*}, H. Simianer[†]*

Introduction

The German research project FUGATO+brain (breeding and informatics) was implemented to help improving practical breeding programs. It will provide software tools based on the newest developments in animal breeding and selection theory, which animal breeders can use to improve their own breeding strategies.

Aim of the project

The development of an efficient breeding program and design is a classical problem of optimization, balancing input parameters (i.e. breeding costs, data recording, genotyping) versus output parameters (monetary genetic gain). Due to the complexity of breeding programs, this is a complicated all round task. Theoretical methods for this problem are already developed and have been used for years, but to date there is only one comprehensive software package available at the moment, which offers a detailed deterministic evaluation of complex breeding programs. This software, 'ZPLAN' (Nitter et al. 1997) has been developed during the 1980s at the University of Hohenheim, Germany, and has been used widely. The technical platform used by this program is no longer up-to-date and rather complicated to use. This may also be the reason, why this program has generally been used for scientific purposes only. For practical breeders, it was hardly usable. Other available software tools do only cover small parts of the complexity of a breeding program (i.e. selection index), e.g. SelAction (Rutten et al., 2002)

The central goal of the project FUGATO+brain is the development of a new software to evaluate complex breeding programs (ZPLAN+) which will have at least following characteristics:

- a comprehensive range of functions und consideration of all latest developments, with special emphasis on genomic information

^{*} Vereinigte Informationssysteme Tierhaltung w.V. (**vit**), 27283 Verden (Aller); Germany

[†] Animal Breeding and Genetics Group, Georg-August-University, 37075 Göttingen, Germany

- programming based on modern programming platforms (object-oriented programming, platform-independent software, database driven web-applications which enable the user to work from everywhere)
- user-friendly user interfaces with online documentation and support

Three areas of core competence

Optimisation of breeding programs is based on three functional areas: selection, geneflow and economic modeling. These areas will now be described in detail:

Selection means on the first hand the identification of animals to be used as parents of the next generation. The basic concept here is selection index theory (Hazel and Lush, 1942). The selection criterion for parents is based on information available at the time of the selection decision. This information can be extremely variable, individual measures taken on selection candidates themselves, data recording on progeny or other relatives, correlated traits different from the breeding goal etc.. New sources of information have been added in the last years, like marker or genomic information. Furthermore selection is possible in multiple stages, where animals are pre-selected on early available informative, later finally selected based on fully available information. Multiple stage selection is implemented and will be further developed. New options implemented in ZPLAN+ will be:

- unlimited number of information sources and combination with breeding goals;
- implementation of genomic information;
- consideration of reliabilities of partial breeding indexes, as used in modern BLUP-estimation systems;
- allocation of an optimal use of resources, e.g. in multiple stage selection programs;
- optimisation of side effects, maximizing genetic gain under a constraint, e.g. avoiding too much inbreeding.

Geneflow (Hill, 1974) describes the structured descent of genes from one generation to the following. This is of special interest in a breeding program, because in most cases genetic gain will be realized in later generations or even in different sub-populations (i.e. purebred-crossbred). Geneflow may be very complex in modern breeding schemes, because populations may be split up in different lines to cover antagonistic breeding goals. Breeding animals are used several years with different intensities, overlapping generations will appear and need to be considered by the simulation program. During the development of ZPLAN+ the geneflow method has been further developed to calculate the average development of inbreeding and kinship. Also, an optimal strategy to track allele frequencies of major genes in a complex geneflow was developed and will be implemented (Ytournal and Simianer, 2010).

Economic modeling will be the third area of interest in the development of the optimisation program. Modern breeding programs are assessed based on their economic efficiency, so all economic parameter need to be covered by the program (i.e. discounted profit, interest rates of invested funds). All input- and output-components need to be expressed in monetary terms. In breeding programs the returns in most cases will materialise much later than costs. For a neutral analysis of a breeding program net return has to be discounted. Alternative

optimizations, like restricted selection indices or desired gains approaches will be implemented as well.

A major task of a new software will be the collection of all information needed, independently of species, breeds, specific breeding programs etc. The program has to be flexible enough to cover most of the breeding programs used and should also allow for new developments in the future. The amount of information that is needed to optimise even simple breeding programs is huge. All traits used in a population, as index sources or breeding goals, need to be assigned heritabilities, phenotypic standard deviations, phenotypic and genetic correlations, economic values etc.. Index source groups need to be defined as well as different selection groups. The number of proven and selected animals is required, age of animals while their first use in breeding, the time how long breeding animals are used, survival rates, selection strategies after first and following breeding use etc. For most breeding programs these parameters are not yet completely available. Therefore it is planned to create templates for different species. The underlying database system makes different projects available for all users. Giving demonstration populations as templates simplifies the access to a complex simulation of breeding programs. Otherwise, users need to start from scratch and firstly have to collect a vast amount of information in advance.

Output of the program

The complexity of input parameters will consequently result in a complexity of output parameters. It is necessary to find a way of presenting the result of the breeding program optimisation in a comprehensive way so that the user is able to interpret the results. As minimum output, following parameters will be calculated for each path of selection:

- relationship of selected and proven animals
- selection intensity
- generation interval
- standardized discount factors
- monetary genetic gain for individual traits and complete breeding goal
- total return of breeding path
- reliability of selection
- geneflow of selection group

The program will provide user-defined tables containing the desired output. The results can be converted in different formats to be exported to other computer programs (e.g. Excel, R, Matlab) for visualization or further analysis.

Conclusion

The new development of the software ZPLAN+ will provide a powerful tool to evaluate and optimize breeding programs of large complexity. It is more user friendly than existing programs and implements newest developments, e.g. genomic information. Covering all of the new developments in animal breeding demands for an easy-to-use tool to evaluate breeding programs. The new technologies have to be implemented in the existing infrastructure and lots of question will arise how to combine old and new breeding tools in an economically efficient breeding program.

Acknowledgments

This study was conducted as part of the FUGATO+brain project and was financially supported by the German ministry for education and research (BMBF), Förderverein Biotechnologieforschung e.V., (FBF Bonn), Lohmann Tierzucht GmbH (Cuxhaven), Hannoveraner Verband e.V., Trakehner Verband, Verband des Oldenburger Pferdes e.V., Verband der Züchter des Holsteiner Pferdes e.V. and Westfälische Pferdestammbuch e.V.

References

- Hazel, L. N., Lush, J. L. (1942). *J. Hered.* 33:393-399.
- Hill, W.G. (1974). *Anim. Prod.*, 18:117–139.
- Nitter, G., Bartenschlager, H., Karras, K., Niebel, E., Graser, H.-U., (1997). *User's Guide for ZPLAN Version 2007, University of Hohenheim.*
- M. J. M. Rutten, P. Bijma, J. A. Woolliams, et al. (2002) *J. Hered.* 93:456-458.
- Ytournal, F., Simianer, H. (2010). In *Proc. 9th WCGALP (this conference)*