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Perspective

Genome-wide selection in poultry

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Abstract. In poultry breeding programs owned by private companies, selection is done within closed populations based on comprehensive phenotypic data recording in both pure and cross line birds under standardised housing conditions. Due to sex-limited data recording, male selection for egg quality and production traits is based mainly on female sibling tests. Early selection of the most promising male within full sib families will improve the rate of genetic progress and can substantially reduce the generation interval. Several past studies, based mainly on microsatellites, have identified quantitative trait loci (QTL) for production and quality traits with only limited use in commercial programs. Genome-wide selection is still in its initial stages in which 10–40-K single nucleotide polymorphism (SNP) chips have been used so far. Due to sequencing of all major pure lines from DNA pools, a customised 600-K SNP chip has been developed for comprehensive genotyping of all commercial lines. Small-scale line-specific SNP chips will be developed afterwards in order to reduce costs for genotyping of male progeny during rearing periods. Only the most promising young males will be transferred to the breeding farm for performance testing and pedigree reproduction. Parental generation will still be genotyped with the comprehensive SNP chip and used for retraining and for imputing. The first results using 30-K SNP chips were obtained from a commercial line used for training, validation and selection, which have shown improved accuracy of prediction at a young age and so resulted in increased genetic gain. Genome-wide marker-assisted selection must prove its advantages over traditional methods including cost benefits.

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Introduction

Feeding the world's growing population with qualitative food is the core aim of agricultural production. As the world's population increases by 80 million people annually, this challenge will continuously become larger. This growth will especially take place mainly in developing countries. The production of eggs or rather, supplying the population with eggs in these regions, will gain great importance. As opposed to poultry meat production, eggs do not enjoy a noteworthy trade between countries outside of Europe. Therefore, provision of the same has to be done by means of local production.

Aside from laying performance, feed conversion and egg quality as well as animal welfare are gaining more importance in Europe and North America. This range of keys require additional and very cost-intensive data recording. Novel recording systems would also have to be developed in order to test chickens in new environments or husbandry systems.

With consistent selection on key traits and more comprehensive phenotyping, ongoing breeding progress, the adjustment of breeding targets with the current genetic pool can be realised.

The laws of diminishing returns are also applicable in poultry breeding. This is why efforts for performance testing, selection and reproduction are becoming bigger although the growth rate should remain stable. By means of other characteristics for the selection criteria, breeding efforts increase for the breeding company without any direct, measurable gain in yield. The breeder is therefore challenged to search for more precise, quicker and economically priced methods.

The science of genomics has advanced exponentially in recent years and there are ongoing discussions on the various models of applications for the different species of farm animals.

Dense genotyping has been implemented in order to find more single nucleotide polymorphisms (SNP), which can be used as markers for selection. With these new tools, the genetic make-up of candidate breeding animals can be determined early and more accurately.

As numerous simulation studies have shown, genomic selection can contribute significantly to the enhancement of breeding progress, mainly by shortening generation intervals.

The certification for the use of these methods in practical breeding, as to when all economically important traits should be simultaneously improved, is not available yet. Only a well balanced selection can improve the entire breeding value of the birds and therefore, increase the revenue of poultry production.

The following discussion will address current status and perspectives of genomic selection in layer breeding in more detail.

Marker-assisted selection

The first successful application of a definitive SNP gene test for a metabolic disorder in brown layers took place ~10 years ago and was published later by Honkatukia *et al.* (2005).

Fishy taint in brown-shelled eggs is caused by a recessive gene (flavin-containing monooxygenases). It is hard to eliminate this defect with traditional challenge feeding programs and subjective scoring of fishy odour. For the first time in poultry, a breeding goal could be completely achieved by looking directly at the structure of the DNA, rather than just phenotypic scoring.

Genome-wide selection

Umpteen theoretical advantages of genomic selection are currently being confronted with substantial expenditure. In addition to launching costs for the establishment of the method in each line/gene pool, there are also costs for ongoing genotyping of candidates in each generation of selection candidates. It must be stressed that at least in the learning process, which has been stretched over several generations, there is no possibility to economise performance testing as the significance of genomic selection is dependent mainly on the complexity of genotyping and the correlation between phenotypic performance and quality parameters to the markers.

The establishment of genomic selection in all lines and families require that performance testing be carried out on all economically relevant characteristics.

The accuracy of these tests and phenotyping decisively defines the success of subsequent genomic selections. It is necessary that the success of these tasks for each line be considered individually as the results from one line to another may not be transferrable. As hybrids for the production stages normally result from 4-way cross breeding, this would mean quadruple efforts. Furthermore, it should be borne in mind that the lines for a white-layer breeding program have no association with a breeding program for brown layers. The global layer market is divided respectively into 2/3 for brown and 1/3 for white layers. The calibration process is therefore to be carried out 8 times. After the application of the first genomic selection and the reproduction of offspring, the real actualised difference in selection will be compared upon completion of the performance testing.

This comparison provides an informative basis for the quality of genome-wide selection. In order to save on the costs for typification, the batch of markers can be readjusted after this phase and if necessary, only the most informative regions should be used.

With a low density line-specific SNP chip, the costs of genotypification in the routine commercial breeding program can be sustainably reduced.

In poultry breeding, there is a priority expectation that the accuracy of genomic selection in broiler breeding be enhanced by genomic selection and at the same time, contribute to the shortening of generation intervals in layers. These two factors contribute to an annually higher progress in breeding.

The advantages are mirrored in better lifetime performance and a lower susceptibility to diseases. Furthermore, genome analysis from the gene pool at hand can be better analysed and the effective population size can be optimised without having to forego selection intensity, respectively, short-termed breeding progress. In simulation studies, it has been calculated that breeding progress can be increased by 20–40% if genomic selection is applied extensively (Avendaño *et al.* 2009; Dekkers *et al.* 2009). The application of genomic data in commercial breeding value estimation has proven increased accuracies for selection at an early stage (Wolc *et al.* 2011).

For several traits like egg production and egg quality, the use of a SNP chip with ~23 000 segregating SNP accuracies of estimated breeding values, could be increased by up to 2-fold for selection at an early age and up to 90% for selection at a later age. For traits with higher heritability, a relatively small number of markers is sufficient to explain most of the genetic variation. These first results in a commercial line indicate that low density chips can be used for pre-selection of males and females, i.e. if phenotypic and genomic data are combined.

In routine breeding programs the application potential of layers lie in the advanced selection of males and the prognosis of persistence data, in terms of egg production and egg quality. At the time of selection, decisions in selection for males are based only on sibling performance and ancestry data. As such, full brothers have identical breeding values although their real genetic potential varies greatly. The pattern of performance in cross-breed siblings, crossed offspring respectively, can vary dramatically. As these data are not available at the time of selection, the selection decision is therefore only based on half-sibling data from commercial field tests. If the entire progeny from the pure line sires are selected, the inbreeding will increase drastically already in the next generation. The objective should therefore be the selection of the theoretical best male for mating out of the large number of up to 15 full brothers.

Potential of application

Unlike other agricultural livestock, the establishment of performance testing of layers in the pure line stages is in fact affordable, but only if the testing phase by means of artificial insemination can also be used for the reproduction of grandparent stocks.

The application of genomic selection is presently calculated to be at ~200€ per bird for a 50–300 000 SNP marker panel. Savings in performance testing on such a large scale is, however, not feasible.

In a conventional breeding program, one pure line male is mated with up to 10 females. As described in Fig. 1, hatching eggs are saved for up to 7 days and the progenies are hatched on a weekly basis. If no DNA markers are available, a random sample of males from several hatches will be grown as selection candidates. All females are used for performance testing in order to deliver the necessary data input for breeding value estimation. Due to variance in sex ratio from hatch to hatch and embryonic development, the number of progenies can vary significantly. Only a limited number of sons per dam are grown.

If DNA markers are available, then the sons with the highest genetic potential within each full sib family will be transferred to the breeding farm. These will be kept as selection candidates to reproduce the next pedigree generation.

As illustrated in Fig. 2, the pre-selection of males will enhance the probability of using the best male per mating group. If all progenies, both males and females, are genotyped, pedigree hens could be mated to multiple sires. The parentage of the progeny has to be verified with low density genotyping. Using this tool, further progress can be generated from the improved population structure.

Pure line pedigree reproduction in layers

Hatch		♂	♀	♀	♀	♀
1	Eggs saved					
	Chicks hatched		♀♀♀	♀♀♀♀	♀♀	♀♀♀
			♂♂	♂	♂♂♂	♂♂♂
2	Eggs saved					
	Chicks hatched		♀♀	♀♀♀	♀♀	♀♀♀
			♂♂	♂♂♂	♂♂♂♂	♂♂♂
3	Eggs saved					
	Chicks hatched		♀♀	♀♀♀	♀♀♀♀	♀♀♀
			♂	♂♂♂	♂♂	—
4	Eggs saved					
	Chicks hatched		♀♀	♀♀♀♀	♀♀♀	♀♀♀
			♂♂	♂♂♂	♂♂♂	♂♂
Females hatched and grown			9	14	11	12
Total males			7	10	12	9
Males grown			2	3	3	3

All females are grown and only a limited number of randomly selected males.

Fig. 1. Pure line pedigree reproduction in layers without marker-assisted selection.

Line-specific high density and low density chips have to be developed. This is most important in brown egg stocks, which represent two-thirds of the world's egg market. Brown egg strains are mainly crosses of Rhode Island Red and White Rock lines with significantly different genetic origins.

Before starting with genomic selection, a line-specific dataset and high density chips have to be applied to these phenotypic data.

Assuming a cost of 200€ for a high density chip and 4000 birds in the training dataset, costs per line for this initial basic step are 800 000€. As shown in Table 1, the total costs for a four-line breeding program will be 3.2 million€. After this starting phase, the first generation of progenies will be genotyped with low density chips for 25€ per test. With 10 000 birds being available, costs per line for genotyping males and females in the growing period will be 250 000€ or 1 million for a commercial product.

To impute further selection candidates, selected pedigree males and females have to be genotyped with the high density chip.

Assuming this scenario and a depreciation value over a period of 5 years for the initial cost of training, 1.2 million per line or ~5 million€ per product are necessary before the initial progress can be generated.

With a worldwide sales volume of 28 million female parents and eight international breeding programs, each program can sell 3.5 million units. With an annual cost of 1.8 million for low and high density genotyping, including costs for training, parent stock prices have to increase by 0.70€, which is more than a 10% increase. If this revenue cannot be generated or costs for training and genotyping cannot be significantly reduced, genome-wide selection is not feasible in layer breeding.

A larger need for further research is still required in the make-up of selection indexes based on a combination of phenotypic and genomic data. Both provide a breeding value estimate, which is regarded as an optimised combination of all traits with various information density as well as to create one for pure breed and cross-breed performance.

Pure line pedigree reproduction with MAS

Hatch		♂	♀	♀	♀	♀
1	Eggs saved					
	Chicks hatched		♀♀♀ ♂♂	♀♀♀♀ ♂	♀♀ ♂♂♂	♀♀♀ ♂♂♂
2	Eggs saved					
	Chicks hatched		♀♀ ♂♂	♀♀♀ ♂♂♂	♀♀ ♂♂♂♂	♀♀♀ ♂♂♂♂
3	Eggs saved					
	Chicks hatched		♀♀ ♂	♀♀♀ ♂♂♂	♀♀♀♀ ♂♂	♀♀♀ —
4	Eggs saved					
	Chicks hatched		♀♀ ♂♂	♀♀♀♀ ♂♂♂	♀♀♀ ♂♂♂	♀♀♀ ♂♂
Females hatched & grown			9	14	11	12
Males grown and genotyped			7	10	12	9
Top males for breeding farm			3	3	3	3

Fig. 2. Pure line pedigree reproduction with marker-assisted selection (MAS).

Table 1. Costs for genomic selection in poultry and the required increase in prices per parent stock sold
HD, high density single nucleotide polymorphism chip, LD, low density single nucleotide polymorphism chip

Genotyping	Cost per chip	Cost/line	Total cost per program of four lines
Training data			
4000 birds	200€/HD chip	800 000	3.200 000
Application selection candidates			
10 000 birds	25€/LD chip	250 000	1.000 000
Selected parents			
1000 birds	200€/HD chip	200 000	800 000
Total:	–	1.250 000	5.000 000
Set-up costs (split over 5 years)		160 000	640 000
Cost/year and program		450 000	1.800 000
Price increase per parent stock sold:			0.70€
Assumption:			
Accessible world market for layer parent stocks			28 million
Four white and four brown international programs			
Sales volume per program and year			3.5 million

This additional effort can only be re-financed with an increase in the prices of parent stocks. As customers only accept a price increase after a traceable increase in performance has been confirmed, all launching costs will have to be pre-financed by the breeding company. Announcements and expected results in the increase of performance in poultry production alone, even with precise and traceable cost-effectiveness, are not sufficient to implement the increase in prices.

First examples of marker-assisted selection in poultry production have already accomplished positive mutual trust.

Examples are the reduced susceptibility to Marek's disease and the infection of viral *E. coli* strains as well as the elimination of fishy odour in brown-shelled eggs caused by the mutation of the 8th chromosome. An example of behaviour parameters can be found in the selection against feather-pecking (Flisikowski *et al.* 2009), which is on the brink of being practically applied.

Practical experiences in genome-wide selection up until now have shown that in normal cases, the time frame until successful practical application is underestimated.

Chips with 40–50 000 SNP are currently available and being used for first selection trials.

Conclusion

Poultry producers recognise the sustainability of breeding progress advantages. The implementation of the same does not require any additional efforts on a commercial level. At the same price for parent stocks, it is very advantageous but for the reasons described above, not realistic. Aside from increase in prices, breeding companies can only balance out costs by selling livestock in large numbers. The concentration process in poultry breeding is already so advanced that lesser than five primary breeding companies share the international market for layers and broilers. The increase in sales is only possible by supercession as the annual reproduction rate for parent stocks and the increase in performance in commercials are sufficient to cover the increasing demands of end consumers.

DNA markers for the genetic profile have to be combined with powerful statistical programs, which incorporate the genomic data into the phenotypic database in order to estimate more powerful breeding values.

Genomics help us to determine which of the day-old chicks have the highest chance of transmitting superior genetics for all traits of economic importance to meet the next generation of pure lines or grandparents, which are the genetic source for all commercials. In layers, mainly improved male selection will contribute to higher genetic progress.

Genomic selection provides precise tools, which can already be used in growing animals without performance testing. This increases the speed and accuracy of selection decisions. The prerequisite for the application is however, upstream performance testing for all traits of commercial interest. Therefore, it is evident that phenotypic performance recording must first be established for new traits before markers can be applied. The molecular-genetic methods do not permit the immediate processing of new traits. They are more of a tool with the potential to achieve a higher breeding effectiveness without manipulating the genome of the birds. The selection target and progress rates have to be realistically predicted so that no false expectancy is possible in the poultry industry. The improvement of husbandry and management conditions in the areas of feeding and hygiene should, therefore, not be narrowed by enhanced expectancy in breeding.

It is therefore assumed in layer breeding that there will be further continuing increase in each generation in the areas of persistency in laying rate and egg quality, feed efficiency, animal health, animal behaviour and adaptability to different housing systems. Animal welfare-related aspects will influence selection strategies even more. Layer breeding is far from a selection plateau as performance testing and selection tools are being constantly further developed. Testing and selection in different housing systems and challenge situations are the basis for the further development of genomic selection, which is increasingly aligning itself to company-specific DNA chips. Therewith, the selection process can be optimised and refined according to the respective products.

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