Market and technology trends

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Poultry breeding, as a profession is around 100 years old and the first specialised poultry breeding companies were founded in the 1940s. As time progressed and competition between breeding companies intensified, methods used in the genetic selection process were increasingly based on science and use of advanced technologies. Today both poultry breeding and poultry meat and egg production are largely in the hands of a small number of highly specialised operations.

Technologies of all sorts have facilitated this development and the main driver of the process has been the reduction of cost price of poultry meat and eggs.

At present key technologies for breeding such as genomics and information technology are developing at an even faster rate. At the same time agriculture, especially in developed countries, is changing rapidly from cost price driven to demand driven. In the USA farmers now only receive 7¢ of every dollar that is spent on food by consumers, whereas in 1950 this was 50¢.

Thus the specifications of the primary product which make it more or less suitable for value addition in later parts of the supply chain, for example, further processing and branding, are becoming more and more important.

In this article we will speculate on the impact of these developments on poultry breeding.

Genomics technologies and our knowledge of the chicken genome have developed extremely fast over recent years.

Markers and maps

Traditional breeding techniques, inspired by quantitative genetics, treat the animal as a black box with an indefinite number of genes influencing the expression of all characteristics of the animal. Since the 1980s we have been slowly opening this black box.

The first development that had an impact on poultry breeding was the discovery of genetic markers.

Genetic markers that form the most widely used category were small anonymous repeat sequences of DNA (microsatellites) that are scattered across the entire genome and can be used as landmarks to construct a map of the genome.

After initial, less detailed, maps had been constructed by several research groups a consensus linkage map was published in 2000 that contained almost 2,000 such genetic markers. The 'practical' use of genetic markers was in the establishment of linkage between these landmarks on the chromosomes and the genetic variability of traits of interest.

QTL mapping

Linkages were established through extensive 'QTL mapping' experiments. Essentially these experiments quantified the co inheritance of genetic markers with variance of traits of interest and thereby were able to localise the sources of significant amounts of genetic variability to a certain region of a chromosome, called a Quantitative Trait Locus.

The first study of this type was done on Hybro birds and was reported by Van Kaam et al (1998). A review of all QTL mapping experiments in chicken by Hocking, shows that up to the end of 2004 well over 100 statistically significant QTL were discovered and these covered all major production traits.

Although this result was better than expected, practical breeders mostly chose not to exploit QTL findings. Practical selection for QTL would involve the genotyping of many animals for many markers as the linkage phase between QTL and marker has to be established in every family. Moreover, the cost of such marker assays is prohibitive as the procedure for microsatellite markers is not suitable for high throughput genotyping systems.

Gene discovery

QTLs however do indicate the presence of one or more major genes on a marked position in the genome. This information can be used in attempts to identify a major gene by what is called positional cloning. This has proven a major hurdle to most research groups.

The confidence intervals for the locations of QTL in the studies reviewed by Hocking, ranged from 30-150 centiMorgans and therefore contain hundreds of genes. Indeed there are very few examples of successful attempts to identify the causative sequence for major gene effects mapped as a QTL.

One of the best is that of the research groups of Georges and Andersson at the Universities of Liège and Uppsala who found a mutation in the IGF2 gene to be responsible for major variation in muscle growth in pigs. The cost of such projects amounts to several millions of euros and if the probability of success is only limited, this is not an attractive proposition to a breeding company. Information on QTLs may however be used in what is called the 'candidate gene' approach. This approach uses prior and external information to hypothesise that a certain gene (the candidate) may be responsible for a known major genetic effect.

Research then focuses on identifying that gene through prior information on its sequence (for example, through information from other species), identifying sequence variation in that gene in poultry and finally associating the various alleles with phenotypic variation of the trait in question. A recent example of success with this approach in chickens may be found in a publication by Gunnarsson et al (2006) on plumage colour.

The full genome sequence

The use of comparative genomics is extremely useful in the candidate gene approach, but the added value of the genome assembly of the chicken that resulted from the efforts of the International Chicken Genome Sequencing Consortium cannot be overstated. Since March 2004 we have the first draft of the chicken genome assembly and its quality is constantly being upgraded.

The latest version predicts some 24,000 genes in the chicken genome. Although more than 50% of these have a known homologue in another species, only a minority of these (around 1,000) have been studied in any significant detail. Nevertheless, the genome assembly of the chicken is an enormously rich resource and it is the major opening to the 'black box' that contains all information on the genetic basis of poultry traits that are relevant to commercial poultry breeding.

The only limitations to the full opening of the black box are time and money. Fortunately, the chicken is regarded as the main avian species for general and medical research, and therefore, the investments in poultry genomics do not depend on the poultry industry alone.

In fact the sequencing of the chicken genome was fully funded by the United States National Institutes of Health (NIH), who provided US$50 million for this effort that led to the chicken being the first agricultural species to be fully sequenced. Nevertheless, the challenge now to poultry researchers is to exploit this rich resource for breeding purposes. One way of using the genome information on the chicken is to study candidate genes in the way described above.

Another way could be to use an intermediate ('gray box') approach by exploiting the information on huge numbers of genetic markers that was indirectly derived from the sequencing effort.

SNP markers

A Single Nucleotide Polymorphism (SNP) is a DNA sequence variation occurring when a single nucleotide – A, T, C or G – in the genome differs between members of the species.

Partial sequences of a broiler chicken, a layer chicken and a Chinese Silkie chicken were compared with the full sequence of the Red Jungle Fowl. Millions of SNPs were detected in this exercise and by themselves, these are a rich

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resource for genomics applications in poultry breeding.

The value of SNPs for breeding is mainly in their use as genetic markers. Genetic markers can be used because of their linkage to genomic locations that explain a significant share of genetic variance. However, the practical usefulness of a marker depends on its degree of linkage to the relevant genomic location and on the effort and cost that is associated with the marker assay. On both criteria SNP markers score particularly well: firstly, SNP markers are so abundant (1 in every 200 base pairs of DNA) that, theoretically, an SNP marker can be found for every unique allele at every locus, and, secondly, the cost of SNP marker assays is relatively low.

The cost may be as low as cents per marker per sample in novel high throughput genotyping technologies. Therefore, experiments can now be done in the human field where as many as 500,000 SNP markers are being used to identify those that are closely associated with genetic variance of a trait of interest.

In poultry breeding research, the previous QTL mapping exercises can now be greatly improved by using SNP markers and major genes may be much more precisely localised by a relatively small set of markers. In fact, this new generation of QTLs may be mapped down to such narrow genomic areas that a few markers can be safely used for further selection for the major genes involved without the need to re-establish the linkage phase on a regular basis. Finally, a whole genome marker approach is now slowly becoming a realistic option.

This approach was first proposed by Meuwissen et al (2001) and its rationale is that the genetic value of an individual animal can be obtained by estimating the effects of all genes or chromosomal positions simultaneously.

To do this, we would require a number of genetic markers that is of the order of magnitude of the number of genes and these would have to be assayed in all breeder candidates. This is an enormous effort and the computational problems to handle all the resulting data are not trivial, but the latest technical developments do bring Meuwissen's visionary option within reach.

Applications of genomics

We expect that over the coming years we will see a growing number of major genes being directly selected for in poultry breeding programmes. We also see aspects of genome wide marker coverage by SNPs being applied for selected purposes. Taken together, we predict that within 10 years from now selection procedures based on genomic information will be an essential part of every poultry breeding programme. We believe that such selection procedures could well turn into the core of the breeding programme. After all, the genome is the core of genetic variability, the livelihood of breeding companies.

A further speculation would be that, if indeed the core of the selection programme changes over time, the structure of the programme, which is very much connected to the selection system, will also change. This will increase genetic progress and indeed, maintenance costs of the programme, but may also provide means of specifically directing the flow of genes to poultry production companies.

Through that route molecular breeding techniques will eventually impact on the working relationship between breeding companies and production companies. Thus, molecular breeding technology contains all aspects of what is called a breakthrough development.

With the assembly of the chicken genome a major step towards the full elucidation of all gene structures of the chicken has been made.

The black box will, however, not be fully opened until we walk the full path – from gene structure through gene function, gene expression, protein interactions, biochemical and signaling pathways, cellular function and cell-cell communication – towards a complete understanding of how phenotypic performance of the chicken is regulated.

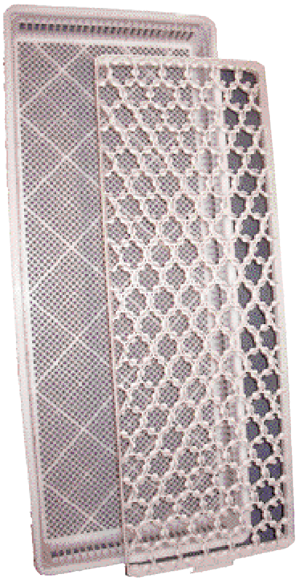
To do this takes an effort that cannot be imagined today. Nevertheless, through current and future research efforts in proteomics and metabolomics, knowledge of this entire field will increase exponentially as new technologies become available.

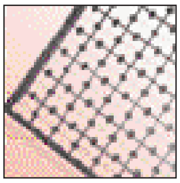
Genetic modification

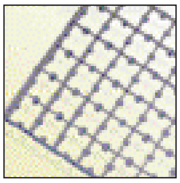
Therefore, it is safe to predict that over the coming years many isolated, critical pathways from gene structure all the way to phenotype will be understood. Once such knowledge is available, its exploitation through directed manipulation of gene structure and function is a natural next step.

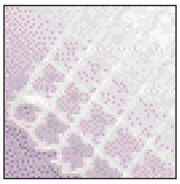
For directed gene manipulation to be workable, we also need effective and efficient technology for genetic modification of birds.

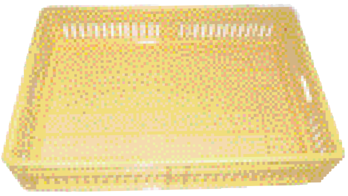
This has proven to be a major hurdle in avian systems and especially











the delivery of a transgene or gene construct to an avian embryo is much more complicated than in a mammalian system. However, perseverance for more than 20 years in this area by several research groups has created definite progress and recently breakthrough successes have been claimed by at least two academic private partnerships.

Although current transgenics are focusing on applications in the pharmaceutical domain, these achievements do open the way to exploitation in poultry breeding for agricultural purposes.

However, this will take a lot of time. Firstly, much more knowledge on gene action in the chicken is needed to come up with a sound proposal for genetic modification of a chicken for agricultural use. Secondly, genetic modification systems for the chicken still need major improvements.

After these two steps have been taken, the establishment of a genetically modified breed, from idea to introduction, takes at least another five years.

Therefore, we expect the first genetically modified chicken with commercial potential in agricultural production to be 'achievable' some 15-20 years from now. However, it is more difficult to predict if such a genetically modified chicken will really be marketed at that time.

Currently, public acceptance of such technological advances applied to animal food production is extremely low and commercial companies – including Hendrix Genetics – are deliberately and explicitly choosing not to embark on research for such applications.

Information technologies

ICT developments have already had a large impact on poultry breeding. Each breeding company now maintains large computer databases with enormous numbers of bird records containing information on a wide range of traits for each individual bird, as well as their full pedigree for many generations.

Breeding values are, therefore, calculated on many measurements not only on the bird itself but also a large number of pure line and hybrid relatives both in the nucleus farms and in a range of locations where pedigreed birds are evaluated in a variety of field conditions.

Data collection is largely automated but new technologies will offer new options in the future.

Advanced breeding programmes no longer use paper recording: all data are recorded through automated systems often using wireless technology and web based solutions for remote locations. Breeding values are calculated from all this information through advanced statistical programmes. New generations of such programmes not only include phenotypic information but also genotypic information provided by DNA based testing of large numbers of birds. Furthermore, the actual selection of the best individuals and the design of the best matings between selection candidates will be guided by devoted optimisation modules that are all computer operated.

The work of the poultry geneticist will be reduced to further improving the breeding and selection systems and programmes and most importantly, to controlling the entire process down to the level of individual breeding birds. After all, machines cannot fully replace the judgement of the professional poultry man ('hands on selection').

A significant increase of annual genetic progress can be obtained through these further sophistications of the breeding and selection process, but also these new tools will allow an increased degree of complexity such as required for product diversification.

Changing market demands

Up to the end of the 20th century the requirements of most clients of breeding companies were straightforward and simple: highest production rates of white meat and eggs at the lowest cost with good liveability and easy to handle birds for standard production environments.

Similarly, the clients of egg producers demanded eggs of the right size at the lowest price and poultry meat consumers looked for their favourite cut of chicken at the lowest available price.

Slowly but steadily consumer preferences are now changing, most clearly in developed countries but also in developing countries. Sales price of a food product is still very important but with the cost of food becoming an ever smaller part of consumer spending (approaching as little as 10% in the most wealthy countries), the importance of primary product price is losing ground against other factors.

With consumer preferences being quite different especially between Asian countries and the rest of the world, the increase of poultry meat consumption in Asian countries relative to the rest of the world is also beginning to affect the price ratio between white and dark meat.

Consumers demand attractive and easy to use products. The food industry is trying to exploit this demand by developing an ever increasing range of processed food products that appeal to consumers.

The consequence of this is that an increasing share of total egg production goes into egg breaking and from thereon into the manufacturing of a wide range of egg derived products.

With the further development of this growing industry there will be increasing pressure on the egg production industry to produce to certain product specifications rather than to low cost price only.

Such specifications could be related to processability of the eggs and their content but also to egg composition. Similarly, further processing of poultry meat is taking an ever larger share of poultry meat production. The range of functional foods targeting at specific nutritional or health requirements of groups of consumers is growing rapidly and broiler and layer breeders will be pressed to offer novel options to producers in this respect.

Food safety is a critical issue for the entire industry from primary production up to retail sales. Layer breeding is urged to play its own role here. This role in the first instance is in guaranteeing the production and delivery of breeding stock which is absolutely free from food poisoning agents. The list of such agents will be growing longer for years to come.

Tracking and tracing is a critical part of contingency plans of food production and distribution organisations. Breeding may play a role here through providing flock information but with each animal's DNA being unique by definition, breeding companies may also play a role by managing or providing DNA based systems for tracking and tracing of animals and animal products.

With primary production units (farms and companies) becoming larger and market requirements becoming more diverse, there is a trend for clients of breeding companies to demand their 'own' genetic specifications.

The availability of a large gene pool and devoted breeding programmes are essential to meet this demand. Fewer breeding companies tend to expand their product portfolio upon this growing demand for tailor made breeding solutions.

Technological tools

New genetic technologies may offer novel technological tools to genetic diversification and novel information technologies may even supportive of systems for in-house product evaluation and breeding in large production companies.

Changing demands of a different nature have to do with the primary production system as such. Society no longer takes for granted that the primary animal production industries – or any other industry – sets its own rules for how to run their business. A long list of issues brought forward in the first instance by activists and pressure groups is now high on political agendas worldwide and consumer awareness on these topics is being translated into changing buying trends of large groups of, especially wealthy, consumers.

These consumer demands are translated into very strict product specifications set for the primary industry by trendsetting retailers and food service companies.

Such issues are: environmental pollution, animal welfare, sustainability of intensive production systems and biodiversity. Some of these issues, such as, animal welfare (for example, European bans on the use of cages and on beak trimming and rules for bird density in broiler production) have a large impact on breeding programmes.

A very recent item on the international agenda that has a large potential impact is the issue of bio-fuels. Feed prices have been and will be affected very heavily by this competing use of raw materials and clients of breeding companies will be more critical than in the past on feed conversion performance of layer and broiler breeds and on their ability to handle lower quality feeds.

Meanwhile the poultry production industry is still increasing the scale of primary operations, more automation of systems is being applied and less skilled labour is available.

Therefore, the primary industry tends to demand more robust breeds of poultry that are better at coping with husbandry conditions that are less than optimal for highly productive birds.

Some affect breeding less directly than others (pollution) but through their impact on the poultry production sector as a whole, breeding companies must deal with all these issues in a pro-active way.

Conclusions

Genomics and ICT based technologies will dramatically increase the power of poultry breeding programmes both in terms of speed and of flexibility. Genomics tools are especially suited for breeding animals for specific new traits such as related to disease resistance, welfare traits (robustness, reduced pecking), resistance to zoonotic agents (bird flu and food safety), meat and egg composition (functional foods) or traits of interest for specific markets (product diversification).

Changing consumer demands force the poultry industry to adapt accordingly whilst having to adapt to changing economic conditions at the same time.

Breeding is the most efficient option to enable and support such adaptations. New technologies will be instrumental in this process. As a consequence poultry breeding programmes will become more complicated and more costly. Large gene pools and effective and efficient breeding programmes based on up to date applications of key technologies are critical success factors for poultry breeding companies. ■