Combining Pure-Line and Cross-Bred Information in Poultry Breeding

N.P. O'Sullivan*, R. Preisinger[+], A. Koerhuis[Ŧ]

Introduction

Poultry breeding continues to evolve rapidly, as new methodologies are developed in quantitative genetics, they are tested, and if efficient, they are rapidly applied in practical global breeding programs (Arthur, 1986; Hunton, 1990). To deliver products which perform to stringent commercial competitive standards requires evaluation of individuals for large numbers of traits with pureline populations and in sibs housed in field type environments. Estimates of breeding values using Best Linear Unbiased Predictions (BLUP) are generated (Gilmour et al, 2006) combining phenotypes, evaluated for animals housed on research farm environments, and under field conditions, along with their pedigree relationships. To deliver product improvements (Laughlin, 2009) these cycles are repeated as quickly as evaluation and reproduction will allow, to optimize rates of genetic gain. The medium heritable traits, body weights, growth rate, egg size, egg quality, feed conversion, and the low heritable traits, egg production, livability, fertility, mating ability, gait scores, behavior trait need different evaluation environments to obtain optimum trait expression for breeding value estimation. Additive genetic merit is cumulative, and with long term selection in very large populations, has resulted in significantly reduced importance of heterosis for almost all traits under selection today. Cumulative progress due to selection on additive genetic variance shows no indication of demised rates of genetic gain (Smith, 1985).

The Evolution of Breeding Programs.

Up until the third decade of the 20th century genetic evaluation was done on individual nucleus poultry populations (Hutt,1949), the surplus stock from these populations was sold as the final product. These were essential pureline breeding programs. Early 20th

_____

*Hy-Line International, Dallas Center, USA, [+]Lohmann Tierzucht GMBH, Cuxhaven, Germany, [#] Aviagen Limited, Newbridge, UK.

century developments in maize breeding with the use of two , three , and four way crosses was adapted and applied to transformed poultry breeding methodology by mid 20th century. The small breeders with single pureline breeding programs were replaced by larger breeders with hybrid products (Gyles, 1989). This was also the point in which specialized meat and egg laying stocks completely replaced dual purpose stocks. In some companies hybridization first utilized partially inbred lines, the use of inbreeds was quickly abandoned, and selections were there after performed in large closed nucleus populations with controls put in place to minimize rates of inbreeding.

Specialized male and female lines were developed in both meat stocks (Chambers, 1990) and egg stocks (Fairfull and Gowe, 1990). These specialized male and female lines usually have very different foundation genetic sources. Chicken meat type stocks rely on Cornish Game breeds as male lines, and White Plymouth Rock lines as female lines. Brown egg layers use predominately Rhode Island Red and New Hampshire breeds in the brown egg male lines. Plymouth Rock lines are used either, white, barred, or columbian patterned as female lines. White eggs varieties use mainly White Leghorn as both male and female lines. The Mount Hope White Leghorn strains are used only as female lines, and are a characteristically distinctive sub variety of the White Leghorn breed. Many modern commercial lines are now a composite of the founding breeds with minor contribution from numerous other breeds used to contribute variation not found within the founding breeds.

As more use of crossbreeding was introduced into breeding programs, systems such as reciprocal recurrent selection (Comstock, et al., 1949) were used to structure evaluations, and from this developed the widely adopted and still common practice of sib testing. This was built upon Lush's (1947) development of statistical procedures to combine individual and family information. Statistical tools continue to evolve and their improvements have been a hallmark of the continued success of genetics applied to animal breeding (McKay, 2009). The sib testing is done either on commercial farms or in low hygiene environments but never on the same farms as the pedigree birds are housed and evaluated. These cross line sib data are combined with the data collected from pure line pedigreed birds evaluated on high hygiene research farms. In layer breeding sib testing is usually done in a typical commercial environment to evaluate low heritability traits, livability, temperament, feather cover and egg production. Some low heritability traits, such as morbidity and mortality due to disease challenges, are not expressed in high hygiene environments of research farms on which the purelines are evaluated and where the focus is mainly on moderately to highly heritable traits. The use of disease challenges also can't be done on research farms thus requiring sib testing

either for routine evaluation for resistance to Marek's Disease (McElroy et al, 2005, Heifetz et al, 2009) , E. Coli resistance (Leitner et al, 1992), and Salmonella resistance.

Current Breeding Procedures.

The classic antagonism between artificial selection and random drift , with the latter being due mainly to inbreeding depression, are still a focus of modern breeding programs. Modern programs rely on breeding value estimation with animal model BLUP. Large effective population sizes are kept with selected parent numbers far larger than required for production of the desired offspring numbers. These large effective population sizes can protect the erosion of genetic variance and with controls in place to limit inbreeding depression. The surplus production, above that needed to reproduce the selected parents, allows rapid propagation of the purelines to produce directly both grandparent and in layer line even male parent stock due to their highly fecund nature. Each breeding program has four fundamental steps. The first is a clear product profile defined by a product steering process for each product the breeding company wishes to market. Secondly is an assessment of the available genepools and their respective crosses for best fit to the product profile. Third is to use the variance component data on each genepool to define within genepool breeding goals for each trait under evaluation and to design the optimum evaluation procedures and rates of progress in each trait under evaluation. These goals will shift with market changes. The fourth step is to take the genepools under evaluation and to efficiently reproduce, multiply the crosses and deliver the hybrid to the customers in a health status required by the modern industry (Collett, 2009).

The current most efficient selection method is BLUP and this needs a combination of individual's phenotype data, and all family information in a pedigree matrix, which is robust enough to handle data collected on individuals in different environments, such as research farms and sib progeny tests housed on different commercial type farm environments. This does place a restriction on the family structures used in current breeding schemes. Females nested under single sires, restricts genetic variance contained in top hens which are unfortunate enough to be mated to selected but inferior males. However males mating with multiples females have a higher probability of being mated to a broad cross section of the selected population of females. Some top ranked females will not contribute significantly to the next generation as they were mate with an inferior sire. This erodes genetic variance in the population as a whole and contributes to accumulation of inbreeding. A system to allow dams and sires to be mated

to multiple individuals, regardless of sex, will address this limit to rates of genetic gain. However it must be done with maintenance of highly accurate relationship information. Every zygote in a full sib family that is fertilized today under conventional breeding systems is a repeated sampling at the pedigree level of the same sire and dam. With the ability to genotype all progeny and assign sires post hatch, every dam will have a similar opportunity to be matched with a complimentary sire. Since each dam can be mated to multiple since when all progeny are genotyped and still maintain accuracy of the relationship in the population. Each sire and dam will have progeny from numerous different mates, with genetic diversity opportunities currently not available without genotyping.

Layer breeders use sib testing to also provide data on competition effects and selection on livability traits under these group environments. Either full or half sibs are placed in group environments and traits such as egg production as well as livability and behavior traits are measured in these tests. This form of family selection has resulted in life time livability in Layers of over 95 % under commercial conditions and over 98% under high hygiene environments. It has also been successful in changing the bird behavior reducing both dominance drive and increasing the birds ability to cope in high density housing environments. The use of these tests has also helped to select for layer hens ability to adapt to larger bird groups now commonly seen in none cage production.

Future Trends

Traits will continued to be added to the selection matrix, many of these traits will involve bird behavior and methods to improve bird well being. Recent examples would involve selection for nesting behavior in Layers (Settar et al, 2006 Icken et al., 2009) and use of range by birds (Icken et al., 2008). The identification of DNA markers and the recent trend to concentrate these markers to the causative mutations will concomitantly allow development of targeted markers for use in genome wide selection. Elite populations will be resequenced to allow targeted development and use of markers to place on SNP Chip panels for genome wide selection. However first will come the phenotype data and the relationship matrix, after which genotypes are used on which to build genome wide selection. The fundamental foundation of animal breeding will not change, however the methodologies will continue to evolve around the use of phenotype data, relationship matrix and genotype data. As these methodologies rapidly evolve they are being tested and incorporated rapidly into breeding programs. These improvements must result in improved rates of gain, and sustainable rates of gain to pay for costs of evaluation, genotyping and analysis.

References

Arthur J.A. (1986). An evaluation of industry breeding programs for egg type chickens. *Proc 3ʳᵈ WCGALP* Vol X Lincoln, NE, USA Pages 325-336.

Chambers J.R. (1990). Genetics of growth and meat production in chickens. *Poultry breeding and genetics*.(ed. R.D. Crawford) Pages 599-644.

Collett S.R. (2009). Managing current disease challenges in breeders. *Biology of poultry breeding.* (ed. P.M. Hocking) Pages 414-433

Comstock R.E., Robinson H. F., Harvey P.H. (1949) A breeding procedure designed to make maximum use of both general and specific combining ability. *Agron. J*. 41:360-367

Gilmour A. R., Gogel B.J., Cullis B.R., Thompson R. (2006) *ASReml User Guide.* VSN Int. Ltd.

Gyles, N.R. (1989). Poultry, people and progress. *Poult. Sci*. 68:1-8

Heifetz E.M., Fulton J.E., O'Sullivan N.P., Arthur, J.A., Cheng H., Wang J., Soller M., Dekkers J.C.M., (2009).Mapping QTL affecting resistance to Marek's Disease in an F G advanced intercross population of commercial layer chickens. *BMC Genomics* 10:20.

Hunton P. (1990). Industrial breeding and selection. *Poultry breeding and genetics*.(ed. R.D. Crawford) Pages 985-1028.

Hutt F.B. (1949). *Genetics of the fowl.* McGraw-Hill Book Company, Inc. New York.

Icken W., Thurner, S., Cavero, D., Schmutz, M., Wendl, G., and Preisinger, R. 2008. Analysis of the free range behaviour of laying hens and the genetic and phenotypic relationships with laying performance. Br Poultry Sci. 49:533-541

Icken, W., S. Thurner, D. Cavero, M. Schmutz, G. Wendl, and R. Preisinger. 2009. Analysis of the nesting behaviour from laying hens in a floor system. Archiv für Geflügelkunde. 73:253:257.

Laughlin K. (2009). *Temperton Fellowship Report No. 15*, Harper Adams University College, Newport, Shropshire, UK.

Leitner G., Uni Z., Cahaner A., Gutman M., Heller E.D., (1992). Replicated divergent selection of broiler chickens for high and low early antibody response to E. Coli vaccination. *Poult. Sci.* 71(1):27-37.

McElroy J.P., Dekkers J.C.M., Fulton J.E., O'Sullivan N.P., Soller M., Lipkin E., Zhang W., Koehler K.J., Lamont S.J., Cheng H.H., (2005). Microsatellite markers associated with resistance to Marek's Disease in commercial layer chickens. *Poult. Sci.* 84 (11):1678-1688.

McKay J.C. (2009). The genetics of modern commercial poultry. . *Biology of poultry breeding.* (ed. P.M. Hocking) Pages 3-9

Settar P., Arango J., O'Sullivan N.P., Arthur J.A., (2006). Evidence of genetic variability for floor and nest egg laying behavior in floor pens. Proc XII European poultry Confernece, Verona, Italy.

Smith C., (1985). Rates of genetic change in farm livestock. *Research & Development.* 1:79-85