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The benefits of sheep recording schemes for genetic research

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ABSTRACT

Recording schemes designed to provide genetic evaluations at the individual animal level contain basic pedigree and production records fundamental to genetic research. Accessibility, accuracy and consistency of their information and the flexibility of their database design to incorporate new indicator traits with prospects of providing a more accurate or more cost-effective identification of animals able to leave superior progeny influence their value to research. Much research is also likely to benefit from inclusion or access to industry data on animal products and their processing performance beyond the farm gate. Industry-wide evaluations of animals in different flocks can also identify useful contrasting animals for this research as well as for commercial exploitation.

Examples of research using industry data from recording schemes are presented to demonstrate these features. They include estimates of non-genetic influences on animal performance, on methods of adjusting for their effects, estimates of phenotypic and genetic parameters, of genetic group and gene effects, of the effects of selection and culling and their impact on selection and crossbreeding strategies. Research embracing new molecular technologies is also discussed.

Research of this sort can have high extension impact, especially that geared to early incorporation of results into the animal evaluation procedures of the scheme itself.

Keywords: recording schemes; industry data; sheep genetic research

INTRODUCTION

Recording schemes are designed primarily for breeders to provide them with access to technology for genetic improvement of commercial animals. Scheme development has usually given emphasis to the collection, processing and reporting of data to users, computers being well suited to repetitively handling large volumes of data and providing short turn-round times. As the size and history of the recording scheme increases, attention increasingly turns to the suitability of the database design to each of these purposes, many major reviews of national schemes resulting from emerging inadequacies in this area (Callow *et al.*, 1986). However, to be effective a national scheme must also give attention to all major components, and especially to the way in which each is matched to industry needs and is mutually coordinated (Garrick *et al.*, 1992). These workers discussed six main components of effective recording schemes. Clarke *et al.* (1992) described their interrelationships with respect to the development, extension and commercialisation of animal improvement. While all components have a research requirement and all have important messages to the conduct of this research, the emphasis of this paper is on their impact on genetic research and in particular on the genetic research needed to keep national schemes abreast of modern technology.

COMPONENTS OF NATIONAL RECORDING SCHEMES

Committed buyers: because the aim is to accumulate genetic improvement over time, the long-term driving force of any viable genetic recording scheme is the ram buyers who are committed to the use of superior animals and prepared to pay a premium that reflects the profits expected from their progeny. **Motivated breeders:** breeders must be sensitive to future production, processing and marketing requirements. Both breeders and buyers must keep abreast

of relevant research and trends in the consumption of animal products that provide opportunities for improved genetic progress towards particular goals. Both have an important role in stimulating research relevant to anticipated future needs. **The database:** basic pedigree and production records which are fundamental to animal evaluation and to genetic research, in ways which will be discussed in more detail later. It offers not just the data themselves, but the entire database system - the procedures required to receive, validate, correct, manipulate, store, select, export and report information. These processes must meet the requirements of all alternative uses of the data: flock summaries, animal summaries, breeding value calculations, breeder reports, breeding scheme reports, breed society requirements and research extracts. **Genetic technology:** embodies all aspects of the analytical model and the genetic and phenotypic parameters and algorithms used to evaluate the data, and to predict the relative breeding worth of individual animals and genetically related groups of animals using all appropriate information on the individual and its relatives. **Animal breeding research and development:** to provide new information to allow the scheme to move with the times and allow breeders to take advantage of new market opportunities and scientific discoveries relating to the identification of animals producing superior progeny. Much of it should be an integral part of the scheme to allow breeders and their clients to stimulate new research directions and to allow results to be readily available to industry. **Extension:** because of the genetic technology embodied in it, the scheme itself is an important insidious technology transfer mechanism, and needs to be better recognised as such by many research funding agencies. The extension process however, is much more than this alone. In addition to ensuring that industry has a good understanding of all other components of the scheme and their financial impact, and of encouraging effective two-way communication among them, it has the important task

of ensuring that the animal rankings coming from the scheme are used to develop effective profitable commercial breeding plans. This itself has an important research requirement.

RESEARCH OPPORTUNITIES

Thus, while all components can impact on genetic research, the database provides a key operational foundation of this research. It provides the base pedigree information on which all genetic research is based, as well as the core data on animal productivity for traits directly influencing financial returns and identifies the contemporary groupings of animals with records. Much genetic research is aimed at developing new indicator traits and methods of applying them to allow a more accurate and more cost-effective identification of animals capable of leaving superior commercial progeny.

Unique animal identifiers are fundamental. They enable the collation of records collected over the lifetime of the animal, whether this be in a single or in several different flocks. Pedigree records are also critical to link and relate records collected in different generations. A unified national recording protocol can provide both features, as well as information on non-genetic circumstances affecting the phenotypic expression of an animal's characteristic. These include the flock and management group in which the record was made and other special circumstances (e.g. surrogate dams, foster parents and recognisable environmental effects such as birth-rearing rank, age of dam and age at measurement). Genetic effects associated with breed composition, hybrid vigour, sex and major gene effects are also relevant to both animal evaluation and research protocols. Best Linear Unbiased Prediction (BLUP) is the current method of choice for animal evaluation purposes, such predicted breeding values also being an important prerequisite to genetic research involving the estimation of genetic parameters (heritabilities, genetic correlations) essential to this prediction process, and to research comparing alternative selection criteria and selection and mating policies.

Three other features of the data are also critical to usefulness of the database for both animal evaluation and for research purposes. The first relates to the definition of performance which must be consistent over years and subject to well-defined validation rules for detecting data measurement and recording errors, and for defining categories that indicate non-genetic effects on performance. The second relates to the accessibility of the information. Physical accessibility of recording scheme data for animal breeding research is unlikely to be a problem but has a cost attached to it. Modern evaluation methods are geared to combining information on the same animal at different times in its life, to collation of records on animals in the same management group, and to relating records on animals in different generations and representing different genetic groups of animals. Operational accessibility is, however, another issue that is tied to the ownership, security, confidentiality and commercial sensitivity of the data, and usually intimately tied to the way in which the scheme and any proposed research is funded (Garrick *et al.*, 1992).

Apart from these common ingredients, is the key issue

of the flexibility of the database design. Research on new indicator traits usually requires new measurements to be taken, requiring that the database be open-ended and able to accommodate recording of new characteristics as opportunities arise. Only then can the duplication of data collection, validation and retrieval or the costs of combining information from different databases be avoided (Wickham 1984). There may however, be a conflict between the quality of data required for research and the associated costs of data validation, depending on the emphasis given to data quality by the recording process, especially at the time of data capture. The Sheep Improvement Limited (SIL) database is still somewhat inadequately serviced from this point of view, even in terms of the collection of measured data coming from breeding flocks. It is less well developed in terms of its access to data coming from other sources. These include the performance of groups of animals on commercial farms and animal health, processing and product data coming from meat works and quality assurance programmes. Such information is becoming increasingly critical in attempts to move our animal products from commodity markets and to develop new consumer products. Group data can also be useful for farm monitoring evaluations of the sort discussed by McCorkindale (1999) and Shaw (1999). It is clear from the review of Parker (1999), however, that specific additional database design features are necessary to accommodate effective industry-wide farm benchmarking studies aimed at providing commercial farmers with useful data that can assist them learn why and how superior flock performance is achieved.

The value to genetic research of expanded data sharing capabilities is well discussed by Wickham (1984). In addition to livestock improvement data, he considers data from breed associations, veterinary clubs, dairy companies, stock and station companies and Government departments. As he emphasises, it is important that the objectives of all these organisations be considered in developing the logical data model that defines the database structure if a truly unified database serving all organisations is sought. He describes how such a process provides the mechanism for introducing new data items needed for research, and highlights how such facilities can reduce the costs of data collection for genetic research.

It is important to recognise that a flexible database itself can open up opportunities for research. Genetic research is increasingly aimed at physiological studies seeking to identify the mechanisms and genes giving rise to biological variations among animals, or indicator traits and genetic markers associated with these variations. Many of these studies can benefit from divergent animals that have been identified as having high or low levels of performance for the trait under investigation. A national database, particularly one with good genetic links across different flocks, can be very useful to establishing such divergence, although any specific genetic research design based upon it, or involving special matings for more in-depth genetic analysis, would require special alliances for its achievement. Research studies of this sort, linked directly to the national database, are becoming particularly important as the number of special-purpose flocks for genetic research decreases.

EXAMPLES OF RESEARCH USING INDUSTRY DATA

There exist several good examples of past research using industry data. Many serve to illustrate the ways that the effectiveness of this research depends on recording scheme design and the early and appropriate utilisation of results by industry.

Non-genetic influences on performance

Analyses to identify and quantify non-genetic influences on performance are the most common of those undertaken to date. Examples are provided by Jury *et al.* (1979) and Newman *et al.* (1983). The former work was concerned with estimates of non-genetic effects of birth-rearing rank, sex, age of dam and weaning age on weaning weight using 12 Romney flocks (40,560 lambs) participating in the national flock recording scheme from 1968 to 1973. These effects accounted for 33%, 9%, 3% and 24% of the residual sums of squares, respectively. The effects were found to vary as much between years within flocks as between flocks in different districts. Analysis of logarithmic values did not account for a greater proportion of the variation in weaning weight. Eikje and Johnson (1979) undertook a more detailed assessment of the significance of flock differences in adjustment factors in this same dataset. Only about 10% of the variation in adjustment factors for sex and birth-rearing rank between flocks was explained by the average weaning weight of the flocks. Thus only a small proportion of the variation in these adjustment factors from flock to flock (or from year to year within a flock) could be removed by procedures taking the flock's level of performance into account. Further analyses of the expected sampling variances in adjustment factors suggested that within-flock estimates of adjustment factors for sex and rearing rank are likely to be preferable to general adjustment factors in flocks producing 120 or more lambs each year. Eikje (1979a) also reported adjustment factors for fleece weight and lamb production.

Methods of adjusting for environmental effects

Eikje & Johnson (1985) compared nine different methods of adjusting lamb weaning weight for the effects of age of dam, sex, birth-rearing rank and weaning age. Combined additive and multiple adjustments or multiplicative adjustment alone were slightly better than other methods for all but weaning age effects for which an additive approach was recommended.

Trait variability

Johnson *et al.* (1980) examined the effect of between-flock variations in the standard deviation of hogget liveweight on weighting used to rank animals for growth and lamb production traits. The flocks were chosen to represent Romney, Coopworth, Perendale and Border Leicester breeds over a wide range of geographical locations. The recommendation coming from this study was that in order to reduce the impact of liveweight on breeding value rankings for lamb production, records be standardised using the estimates of the within-flock standard deviation in liveweight by flock x sex x year subgroups as well as by

season (age at measurement). Regional differences in within-flock sources of variation in commercial Coopworth flocks were studied by Rendel *et al.* (1990).

Effect of culling

Johnson *et al.* (1980) showed that the effect of culling at weaning on the variability of later weights in 13 flocks appearing to have the highest culling intensities at weaning reduced variation in later weights by a factor of the order of 0.84. Eikje (1979a) examined the effects of selection and culling between weaning and hogget shearing, the effects of selection of flock replacements and the culling of breeding ewes on the basis of performance.

Animal ranking procedures

Many of the results discussed so far were incorporated into revised animal evaluation procedures developed for sheep breeders in the 1980s (Callow *et al.*, 1985; Johnson *et al.*, 1989). These revisions also included an expansion of characteristics able to be included in animal evaluations and offered options for breeders to receive across-year and across-year animal evaluations using BLUP via an affiliated higher-level processing service. These methods are operationally well suited to combining information on all relatives and of including information on correlated traits in breeding value predictions (Johnson and Garrick 1990; Garrick 1991). They are also able to accommodate data from different breeds, although are yet to be fully developed for this purpose. They are especially useful in providing good retrospective information on the effectiveness of a breeder's past selection decisions for particular breeding goals.

Selection effectiveness and industry structures

Using national performance recording data, Dodd *et al.* (1982) first reported on the efficiency of selection practices in recorded flocks. Dodd and Delahunty (1983) analysed performance records in the central flocks of eight group breeding schemes to examine opportunities for increased rates of progress from more intense selection on performance. They found selection efficiencies of the order of 64-74% for rams and 27-44% for ewes, indicating considerable scope for improvement.

More recently, Garrick (1995) estimated across-year genetic trends in estimated breeding values coming from BLUP analysis of breeding values for 50 flocks using data (50,000 lambs each year) going back to 1988. Average genetic trends were 0.13 kg/year for weaning weight, 0.26 kg/year for liveweight at 8 months and 0.02 kg/year for hogget fleece weight, very close to selection index predictions.

Genetic parameters

Genetic parameters for lamb, hogget and ewe production traits were estimated by Eikje (1979a) and by Rendel *et al.* (1990). Eikje (1979a) reported estimates for lamb growth, hogget fleece weight, wool quality number and ewe productivity traits (number of lambs born and weaned, lamb survival and weight of lamb weaned) for six years' data coming from six large flocks of Romney sheep. Lopez-Villalobos and Garrick (1999) estimated heritabilities and

genetic correlations for direct and maternal genetic effects using underlying scales (probit and logit) for lamb survival (25,874 lambs born), in order to examine new procedures for the genetic evaluation of this trait. Low heritability estimates were found (0.01 and 0.03, respectively).

New traits

As an example of genetic research undertaken on new traits not recorded by scheme itself, Skerman *et al.*, (1988) estimated phenotypic and genetic parameters for clinical footscald and footrot in a pedigree flock of Romney sheep inspected during natural outbreaks over a period of six years. This was the one of the first genetic studies on this disease trait. Increasing worm drench resistance stimulated an interest in faecal egg count as an heritable indicator of resistance/resilience to nematode parasites (NZABT 1994; Watson *et al.*, 1986) and required a new approaches to the incorporation of faecal egg count in breeding objectives for dual-purpose sheep (Amer *et al.*, 1999).

Analysis of carcass dissection data lead to the incorporation of meat traits in breeding objectives (Clarke *et al.*, 1991). Genetic parameters for live animal ultra-sound predictors were provided by data from an industry breeding scheme (Clarke *et al.*, 1998), which was also developed to incorporate computerised tomography data into its breeding programme (Nicoll *et al.*, 1997).

Fixed genetic effects

Industry crossbreeding can provide opportunity to analyse genetic group effects associated with different breeds and strains. An example of this is provided by the results of Clarke *et al.* (1999). They reported an analysis of base breed effects from a research study in which high bulk genes from Texel and Dorset sires were introgressed into high fleece weight Romney ewes and the resulting crossbred rams disseminated to commercial Romney ram breeding flocks. The procedures developed have contributed to protocols for the inclusion of genetic group effects in the analytical models to be used by SIL.

While Lewer and Allison (1980) estimated the repeatability of Merino and Booroola x Merino ewes using research data, studies of this sort could equally well be undertaken in commercial flocks. A feature of this study was the high repeatability found for NLB in Booroola x Merino (0.35) compared to Merino ewes (0.20); an effect now believed to be due to a major gene on fecundity. Davis and Kelly (1983) report evidence of its segregation for ovulation rate in commercial and research flocks. This sort of study could well be undertaken using industry data alone. Analytical approaches using special-purpose analytical software to reveal evidence of genetic segregation using industry data (e.g. Marshall *et al.*, 1999) are likely to develop further in the future, especially if the recording scheme is flexible enough to accommodate such new traits and the effects of individual genes on them. Such approaches provided early evidence for a single gene affecting rib-eye muscling in industry flocks in Australia. Segregation analyses suggested an unusual pattern of inheritance; later work in New Zealand flocks providing evidence of linkage to microsatellite markers (Nicoll *et al.*, 1998).

Biotechnology

The discovery of the Inverdale gene is a good example of finding single genes in industry flocks, initially by screening highly-prolific outliers followed by special matings for more intensive investigative research (Davis *et al.*, 1995 and other papers in that publication).

Dekkers (1999) provided a good recent review of the application of molecular technology to animal improvement, with emphasis on research making use of industry-wide population diversity and some operational aspects of utilising this new technology for animal improvement. He discussed two approaches to mapping genes – locating regions of the genome affecting traits of economic importance (QTL). The genomic scan approach relies on the linkage disequilibrium that exists within families in outbred populations or coming from crosses between breeds, strains or selected lines. It needs large population sizes to be effective, one of the main challenges being the development of research designs able to capitalise on existing commercial population structures. An example is the grand-daughter design (Weller *et al.*, 1990) which utilises the large paternal half-sib families created by artificial insemination. Artificial insemination used to hasten the dissemination of genes from scarce new breeds is likely to be especially important, although further research to identify whether the QTL have an effect within populations of commercial interest may also be necessary. The candidate gene approach using knowledge of the underlying physiological mechanism affecting variation in traits of economic importance and knowledge from species rich in genomic information, can rely more directly on existing commercial animal populations.

The importance of being able to accumulate and collate data from commercial animals for new traits that are of specific interest to the application of marker assisted selection is crucial to both approaches. Recording schemes must be able to handle or have direct access to DNA data that are the results of gene and marker evaluations on individual animals and related groups of animals. They will also be important to maintain a regular on-going review of gene effects to guard against unfavourable associations with other traits and against epistatic effects with the background genotype or environment. Accounting for these uncertainties in animal evaluation procedures remains an important research challenge as does the optimal use of molecular information in purebred and in crossbred selection strategies especially for gene effects showing dominance and for different time horizons and for genes affecting different aspects of profitability (Dekkers, 1999). These developments are likely to be especially important for disease carcass and meat quality traits that are expensive or difficult to measure or evaluate on live animals or at a young age.

Breeding plans

The study of Eikje (1978b) provides a good example of research into breeding plans. It examined factors affecting the efficiency of selection based on performance selection and/or progeny testing for improving lamb growth. The factors studied included flock size, flock fertility, genetic

parameter estimates, selection intensity and generation interval using data coming from industry flocks and industry flock structures. This is an important area of research, which incorporates factors beyond the animal evaluation system itself, in order to develop cost-effective breeding strategies able to make best use of the information that they provide. The inclusion of molecular information in breeding plans will intensify this area of work and strengthen the new to simultaneously consider new reproductive technologies as well (Dekkers, 1999).

CONCLUSIONS

It can be seen from these examples that recording schemes can provide useful data for research. This research has direct benefits beyond the immediate requirements of the scheme itself. It also has high extension impact through better ownership of results and through their incorporation into the genetic evaluation procedures, thereby providing effective transfer of technology to industry.

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