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Genetics and livestock breeding in the UK: Co-constructing technologies and heterogeneous biosocial collectivities

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A B S T R A C T

Cattle and sheep breeders in the UK and elsewhere are increasingly being encouraged to use a variety of genetic technologies to help them make breeding decisions. The technology of particular interest here is 'classical' statistical genetics, which use a series of measurements taken from animals' bodies to provide an estimate of their 'genetic merit' known as Estimated Breeding Values (EBVs). Drawing on empirical research with the representatives of national cattle breed societies and individual cattle breeders the paper explores the complex ways in which they are engaging with genetic breeding technologies. The concept of 'heterogeneous biosocial collectivity' is mobilised to inform an understanding of processes of co-construction of breeding technologies, livestock animals and humans. The paper presents case studies of livestock breeding collectivities at different scales, arguing that the ways in which the 'life' of livestock animals is problematised is specific to different scales, and varies too between different collectivities at the same scale. This conceptualisation problematises earlier models of innovation-adoption that view farmers as either 'adopters' or 'non-adopters' of technologies and in which individual attitudes alone are seen as determining the decision to adopt or not adopt. Instead, the paper emphasises the particularity and specificity of co-construction, and that the co-construction of collectivities and technologies is always in process.

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1. Rural studies and genetic technologies in agriculture

An established tradition of research in rural studies on genetic technologies in agriculture (e.g. Goodman et al., 1987; Kloppenburg, 1990) has been extended in recent years by further research on the political economy and also the gendered dimensions of these phenomena (Bryant and Pini, 2006; Pechlaner and Otero, 2008). A more emergent scholarship has begun to consider the farm level implications of genetically modified organisms (GMO) (e.g. Lane et al., 2007; Lassen and Sandoe, 2009; Oreszczyn et al., 2010) reflecting a wider call within the social sciences for more attention to be paid to "the purchase of… biotechnologies and the discourses and images through which they circulate in social practices…" (Spencer and Whatmore, 2001, pp. 140–141). Given the high profile and on-going nature of the debate about genetically modified (GM) crops within Europe (e.g. Seifert, 2008) it is understandable that popular and academic attention has been focused on genetic technologies within the context of plant based agriculture. However, the corollary is a relative lack, at least until very recently, of rural social scientific interest in the ways in which livestock agriculture is being influenced by genetic technologies (Holloway and Morris, 2008; Morris and Holloway, 2009; Holloway et al., 2009; Twine, 2010). This might be explained in part by the absence of controversy in this context. In the UK, for example, there has been some media interest in cloned cattle and genetically modified pigs and chickens, but debates about the legitimacy of such technologies appear to be largely confined to specialist, scientific arenas (Marris et al., 2001). However, although attracting relatively limited public attention, cattle and sheep breeders in the UK and elsewhere are increasingly being encouraged to use a variety of genetic technologies to help them make breeding decisions with the aim of producing 'better' animal bodies. Such breeding technologies are layered on to and compete with more established breeding knowledge-practices notably visual assessment and the use of pedigree records which remain significant, albeit to varying extents both between and within breed societies, in breeding decisions and in the sale of livestock (Holloway and Morris, 2008, 2012).

The most well developed examples of genetic breeding technologies are: genetic markers, which are identifiable genetic

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material supposedly related to particular phenotypic qualities such as enhanced productivity or reduced disease susceptibility; and 'classical' statistical genetics, used to provide an estimate of an animal's 'genetic merit' known as Estimated Breeding Values (EBVs). The latter technology currently has the most widespread practical impact and relevance to the livestock breeding community and is integral to a geneticising discourse in agriculture (Holloway and Morris, 2008). EBVs thus provide the empirical focus of this paper. EBVs involve the production of a set of figures derived statistically from a set of measurements of the animal body, for example its weight at particular points since its birth, and the depths of fat and muscle in particular places. A statistical algorithm is used to calculate an individual animal's 'breeding value' for each characteristic based on its own data and data from its relatives. These values can be used by breeders to indicate the relative breeding strengths and weaknesses of any animal, and to select animals for breeding in accordance with a particular breeding objective. The calculation of population average EBVs enables new norms or standards to be established because individual animals or herds/flocks can be compared – favourably or not – with these averages. "It can thus be suggested that animals or populations *should* embody particular statistical or genetic characteristics, and their conformity to or deviation from such norms are easily measured" (Holloway and Morris, 2012, p. 65). EBV data are produced by organisations (e.g. publicly funded research institutes and commercial organisations such as breeding companies[1]) typically located 'at a distance' from the livestock animals themselves and the farms on which they are born and reared. Scrutiny of the subsequent results by breeders can take place electronically for example 'on screen' in a farm office where the animal itself is not present. Increasingly, however, EBV data are presented alongside the individual animal they represent at agricultural shows and sales (Holloway, 2005).

The emerging array of genetic breeding technologies has been described by their proponents as contributing to a 'genetics revolution' in livestock agriculture (Bulfield, 2000; Kues and Niemann, 2004; Outlook on Agriculture, special issue: Genomics and Genetic Engineering for the Meat Industry, December 2003). Although mobilisation of the dramatic concept of 'revolution' may indicate the over-hyping that often accompanies the introduction of new technologies (Brown, 2003) it is apparent that active efforts, both within the public and private sectors, are being made to construct a genetic agenda in this field (Holloway and Morris, 2008, 2012). For example, although EBVs have been in circulation for several decades consistent attempts, in the form of articles in the farming press and training events hosted by organisations such as the English Beef and Lamb Executive (EBLEX),[2] are being made to enrol breeders into their use. This entails responsiveness to user needs through the invention of new ways of presenting EBV data to enhance their accessibility and visual intuitiveness. Such promotional activities point to the efforts of technology designers to configure "the identity of putative users" (Woolgar, 1991, p. 59), with livestock breeders who use these genetic breeding technologies being defined as confident, progressive and contributing to the current and future profitability of the livestock industry. On the other hand, those who resist use of the technologies can be represented as problematic obstacles to the modernisation of livestock breeding (Holloway and Morris, 2012).

The purpose of this paper is to move beyond the claims made by those involved in the development of breeding technologies, to try to make sense of what is actually happening 'on the ground' as livestock breeders encounter these technologies within the practices of breeding. As such, the paper is in part a response to the call, by Greenhough and Roe (2006, p. 417), for investigation into "non-expert (sic), micro-scale knowings" of biotechnology as it insinuates itself increasingly in everyday life (see also Michael, 2006), in this case, the lives of livestock breeders and their animals. It is also a response to and questioning of the continuing circulation, within policy and scientific domains, of the notion of 'innovation adoption' that tends to view farmers as either 'adopters' or 'non-adopters' of innovations, i.e. with identities that are coherent and singular in relation to a particular technology or policy initiative,[3] and in which the attributes and attitudes of individual humans alone are seen as determining the decision to adopt or not adopt. More specifically, our aim is to develop a conceptualisation of the use of genetic breeding technologies within livestock breeding that goes beyond a focus on the human 'users' or 'non-users' that is characteristic of past research in rural studies that has a technology focus, including in particular work on innovation-adoption. To do this we work with the idea of 'heterogeneous biosocial collectivity' (Holloway et al., 2009; Holloway and Morris, 2012), relating it specifically to the use/non-use of technologies within this context, exploring also the relationships between and the co-construction of these collectivities and breeding technologies. This paper is distinct from our previous work in that it *develops* the concept of a heterogeneous biosocial collectivity, arguing that particular collectivities associated with different breeds but also identified at different scales within a breed afford different possibilities for the use, and co-construction, of breeding technologies.

In the subsequent sections of the paper we first provide further context by discussing approaches to technology and socio-technical change in rural studies and science and technology studies before elaborating the concept of heterogeneous biosocial collectivity and technology use. The methodology employed to produce data on livestock breeders' engagement with genetic breeding technologies will be described before four illustrative case studies are presented of collectivities associated with beef cattle breeding at different scales. These cases reveal the considerable complexities, ambivalences and ambiguities in engagements with genetic breeding technologies. These are produced because as technologies are encountered on particular farms, by particular breeders with distinct sets of experiences, skills and knowledge-practices, and working with particular groups of animals, a wide range of responses and outcomes are evident. In conclusion we reflect on what our case studies reveal about the co-construction of technologies and heterogeneous biosocial collectivities, both in relation to the specific example of beef cattle breeding but also more widely in relation to technological interventions in agriculture.

2. Rural research, technology use and heterogeneous biosocial collectivities

The study of technology and socio-technical change has a strong tradition in rural studies, notably in the form of innovation-adoption research (e.g. Taylor and Miller, 1978; Rogers, 1983). As Padel (2001, p. 40) explains, the innovation-adoption model

[1] In the UK, Signet is the major company producing EBVs, while ABRI is an Australian equivalent used by some UK breed societies.

[2] EBLEX is part of England's Agriculture and Horticulture Development Board, and is funded by a levy paid on sales of beef cattle and sheep in England. It works to promote the beef and sheep sectors and the more extensive use of breeding technologies such as EBVs is regarded as a valuable means of assisting the development of the British livestock industry.

[3] For example, within the research that provides the empirical basis of this paper, animal scientist members of the project's Consultation Panel were particularly interested in the research producing data that would provide conclusive evidence of the particular types of farmers who adopt EBVs and those who do not, so that more effective extension messages could be designed.

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