

Prioritization of livestock genetic resources in relation to neutral and selected genetic variation

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Why develop methods for prioritization?

- Is there any evidence that molecular genetic work is actually being used in prioritizing breeds?
- There are probably some examples of genetic work being used for deciding whether a breed should be supported; these examples are more likely to be based on pedigree than on molecular genetics
- In practice, priority lists are probably based on numerical criteria and other assessments of demographic risk

Marketing the concept

- Before investing too much time in developing scientific prioritization methods it would be advisable to ask the policy makers what they actually want
- Scientific papers on prioritization can be very difficult indeed to explain to policy makers – and to non-specialists generally
- Only big breed societies can afford to employ consultants

Reasons for prioritization

- Economic rationale for allocating limited resources – should a few breeds be given large resources or should many breeds be given limited resources?
- Optimization algorithm developed by H.P. Possingham and colleagues:

$$P(b) = P_o \div \{[\Phi(B-c_f)/c_m] + 1\}$$

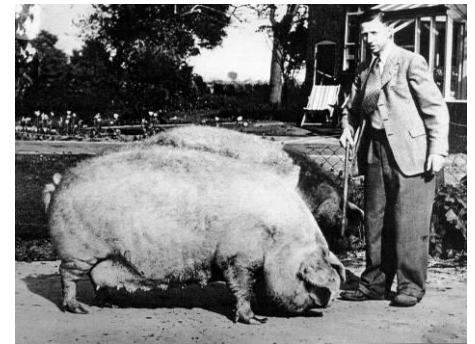
Conserv. Biol. 22, 656 (2008)

$$P(b) = P_o \div \{[\Phi(B-c_f)/c_m] + 1\}$$

- $P(b)$ probability of extinction in planning period b
- P_o probability of extinction if no management applied
- Φ measure of management efficiency
- B budget
- c_f average annual fixed cost of management
- c_m average cost of a specific management intervention

Optimum number of breeds to be managed

- Applying sample data and many assumptions, this leads to the conclusion that a £1 million budget would halve the extinction risk for 30 livestock breeds
- The point is that a rationale needs to be agreed not just for the prioritization process but also for the application of the results of that process



How direct state support for breeds actually operates in England

- Under agri-environment support, farmers who are in Higher Level Stewardship schemes can also get support (about £70 or €83 per hectare per year) if they keep a “Native Breed at Risk” – called “option HR2”
- Currently in England there are 616 10-year contracts under HR2, covering 30,635 hectares, annual cost approx. £1.8 (€2.2) million
- Only grazing livestock are eligible
- No record is kept of what breeds are kept, or of how many animals are involved – a serious omission making it impossible to audit success
- In practice this is the kind of easily-administered support system that appeals to governments

However, let's assume a rational system is requested ...

- Conservation biology has debated prioritization over the years. One theme has been the identification of two different approaches for species conservation –
 - (1) Historical legacy (= evolutionary history)
 - (2) Functional diversity (= ecological exchangeability)
- Their livestock equivalents might be –
 - (1) Neutral genetic variation
 - (2) Selected genetic variation

Do genetic distances from supposedly neutral markers correlate with phenotypic distances?

- If they do, then maximizing neutral genetic variation should also maximize useful genetic variation (Hall, Lenstra et al (2011) JABG 129,218)
- Published data from beef cattle; 4 sets of traits; 3 marker systems (biochemical / immunological markers, microsatellites, SNPs)
- Correlations calculated between genetic distance between each breed and every other breed, and absolute difference in performance between each pair

Correlations calculated between genetic distance between each breed (x) and every other breed, and absolute difference in performance between each pair (y)

A

B

C



A



B



x: Distance A-B
y: |(trait A-trait B)|

C



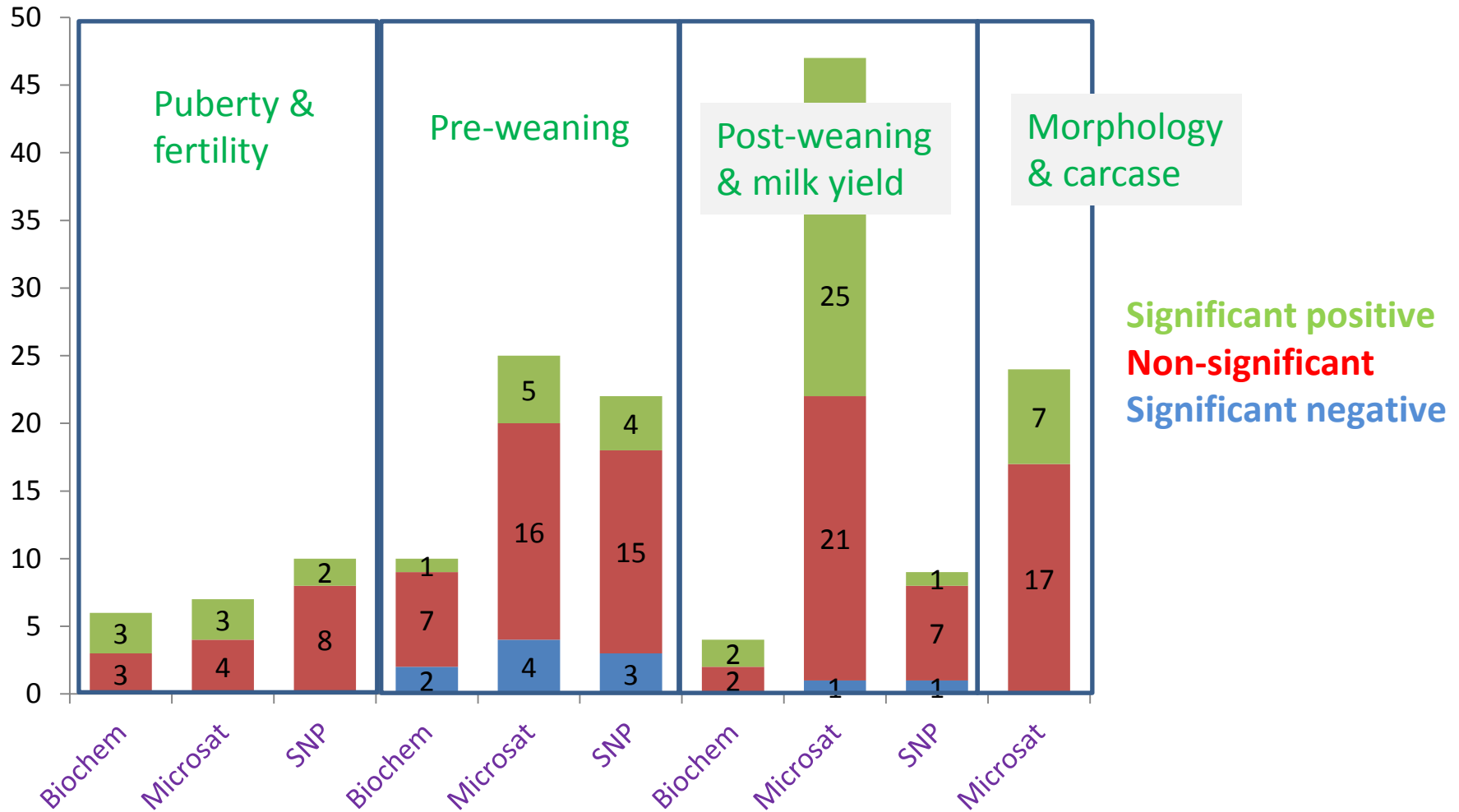
x: Distance A-C
y: |(trait A-trait C)|

x: Distance B-C
y: |(trait B-trait C)|

Phenotypic traits

Puberty & fertility traits	Pre-weaning traits	Post-weaning & milk yield	Morphology & carcass
Age at puberty Weight at puberty Pelvis width 365 days Cow fertility	Gestation length maternal Calving ease direct Calving ease maternal Birth weight direct Birth weight maternal Birth weight Birth weight direct Survival to weaning maternal Preweaning growth rate direct Preweaning growth rate maternal Weaning weight	Weight 120 days direct Weight 210 days direct Weight 120 days maternal Weight 210 days maternal Live weight 365 days Weight 400 days Weight 365 days direct Weight 365 days maternal Withers height 365 days Average daily gain Maintenance efficiency Slaughter weight Slaughter age Mature weight Weight 600 days Milk yield Milk fat%	Girth at weaning Girth 400 days Girth 600 days Carcass weight Length of hind limb Blockiness index Muscularity at weaning

Numbers of correlations for each **group of traits**, using each **distancing method**



- 165 correlations calculated of which 64 were significant ($p < 0.05$)
- Of these 64, 53 were positive
- So, for some traits, maximizing marker diversity should maximize diversity of adaptive variation
- Negative correlations were prominent among pre-weaning traits
 - Maybe genetic architecture of these traits is different, for example there may be non-additive interactions among loci
- Neutral variation doesn't necessarily correlate with adaptive (functional, selected) variation

Index of priority among breeds

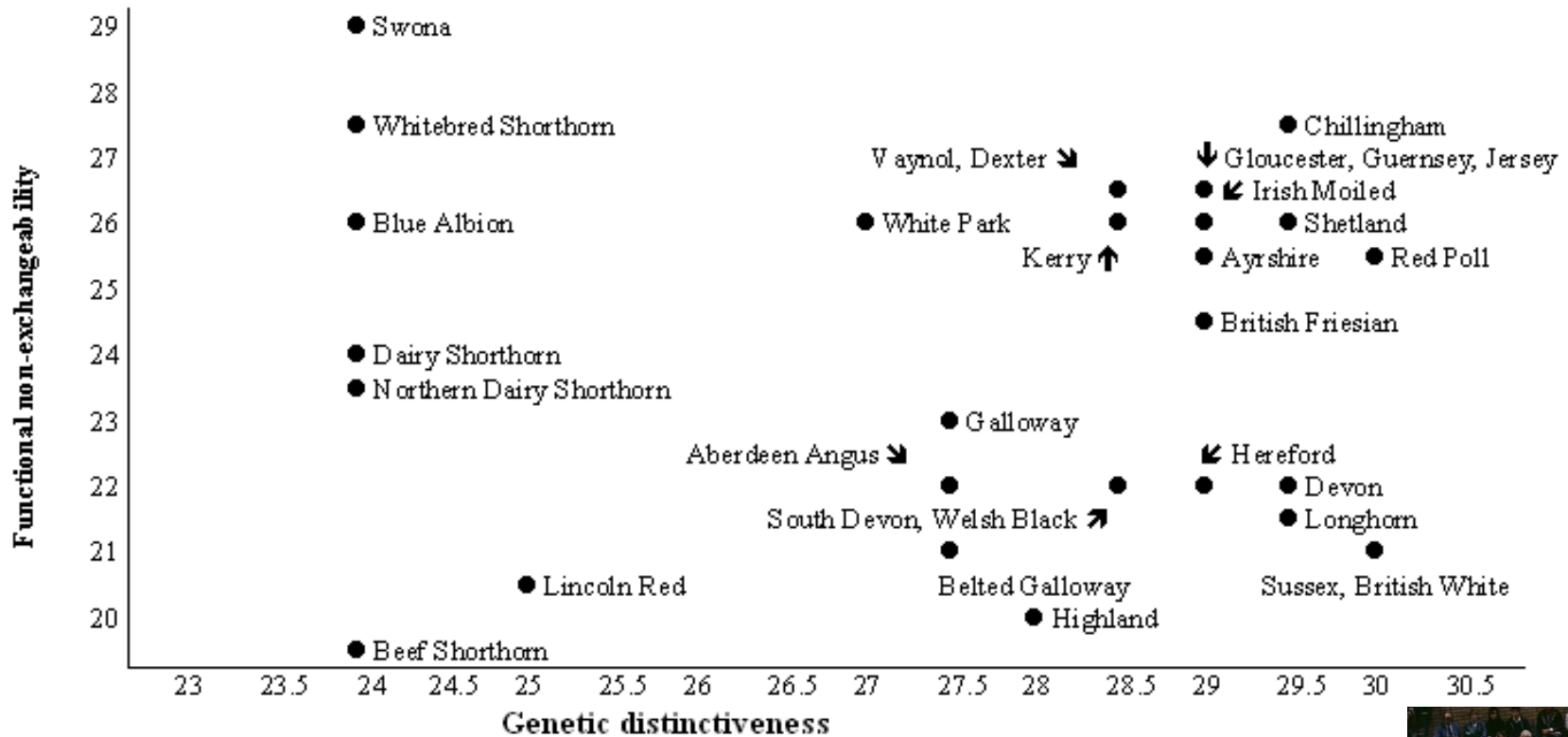
- An obvious course is to score breeds for different criteria of conservation importance and add these to give an index (J. Ruane, 2000, *Conserv. Biol.* 14,1385)
- Problems – subjectivity, weighting of different attributes, dependence on expert committee
- However, it is easily understood, and flexible

Another approach

- Possible solutions – plot scores against each other
- Subjectivity is then reduced to setting the boundaries for the breeds to be included on the priority list
- Here are two examples – Irish and UK cattle and British sheep



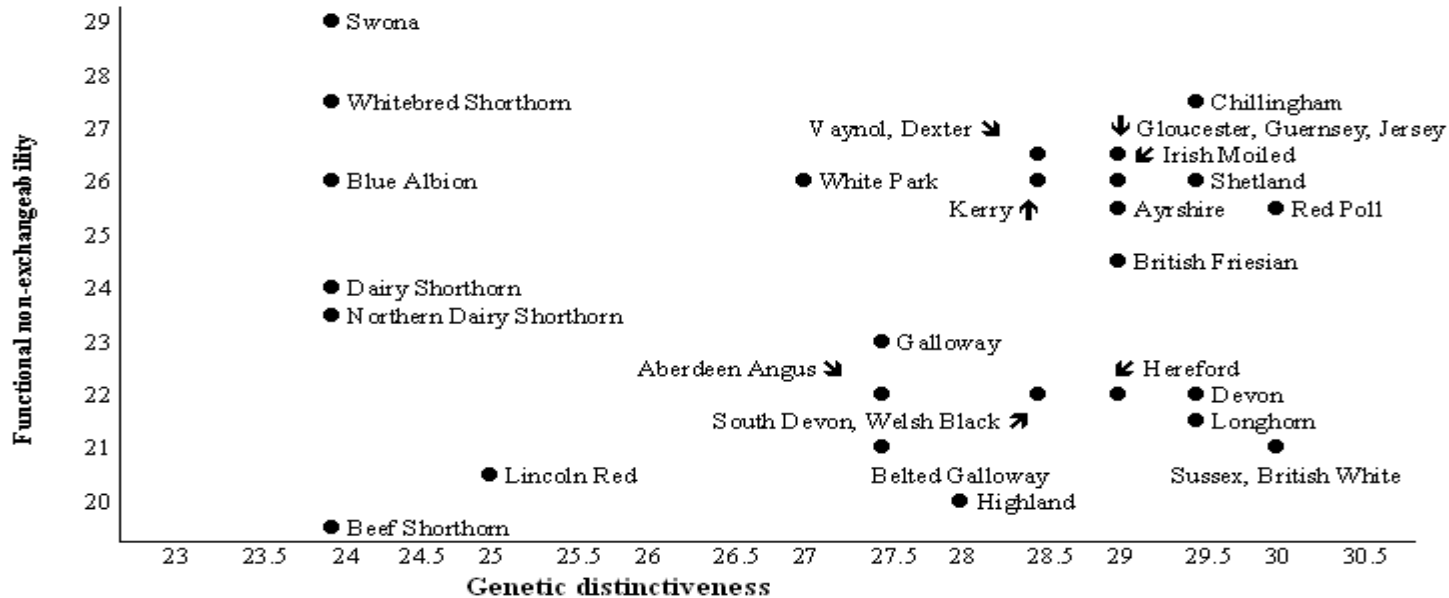
Prioritization plot: breeds with high genetic distinctiveness and high functional non-exchangeability have high conservation priority



In principle a multidimensional plot could be generated – in this case the obvious third dimension would be degree of endangerment



Some details – and cautions



- Highest priority: Chillingham, Red Poll, Shetland, Gloucester, Guernsey, Jersey, Irish Moiled, Ayrshire, British Friesian. BUT some of genetic distinctiveness of Red Poll & Ayrshire might be due to introgression
- Lowest priority: Beef Shorthorn, Lincoln Red, Northern Dairy Shorthorn, Dairy Shorthorn BUT their genetic distinctivenesses are low because they are all Shorthorn derivatives
- It would be essential to refine this model. For most if not all of these breeds, location on this chart can be debated!

Another example – UK sheep

- Problems – lack of national study of sheep biodiversity
- The only phenotypic character that has been studied across a large number of UK sheep breeds is wool fineness
- The only genetic character that has been studied across all UK sheep breeds is the PrP “scrapie” gene

- Bradford Count – measure of wool fineness
- The number of 560-yard hanks of single strand yarn that a good spinner can make from a pound of clean, combed wool
- The finer the wool, the higher the Bradford Count
- Bradford Count is typically given as a range

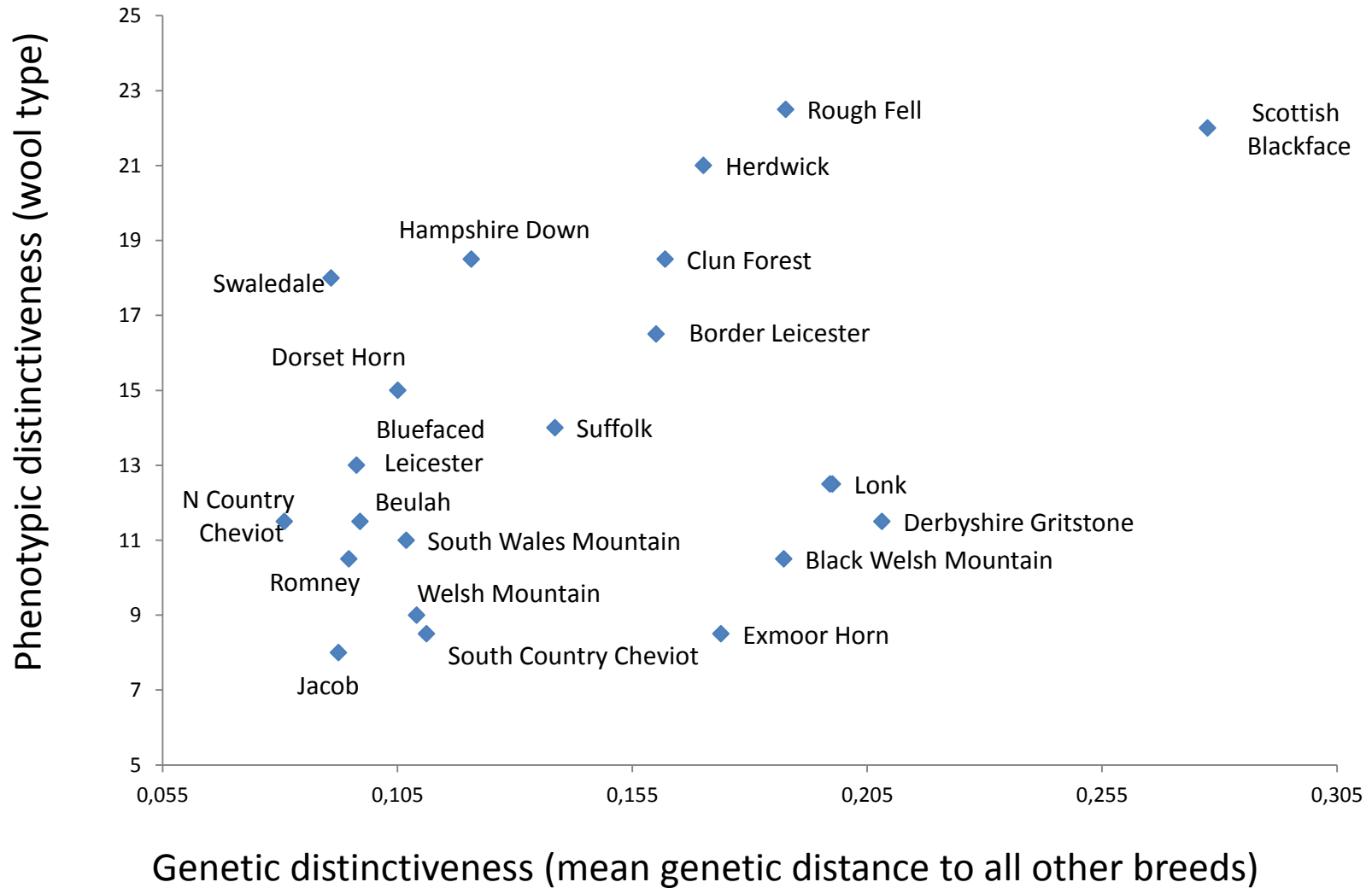


Herdwick wool is 28-32 (very coarse)



Clun Forest wool is 56-58 (quite fine)

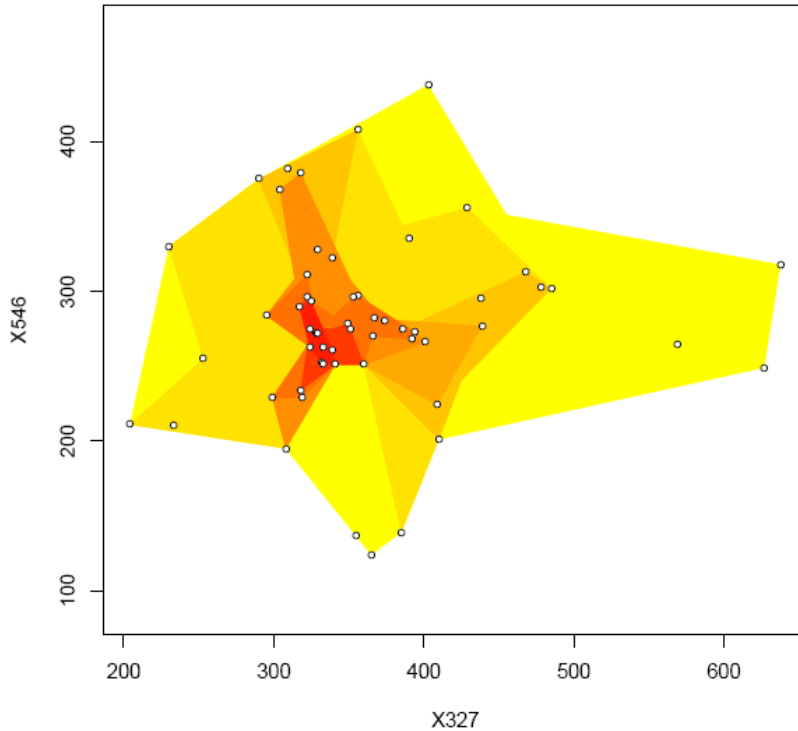
Plot of genetic distinctiveness of UK sheep breeds against the distinctiveness of their wool type



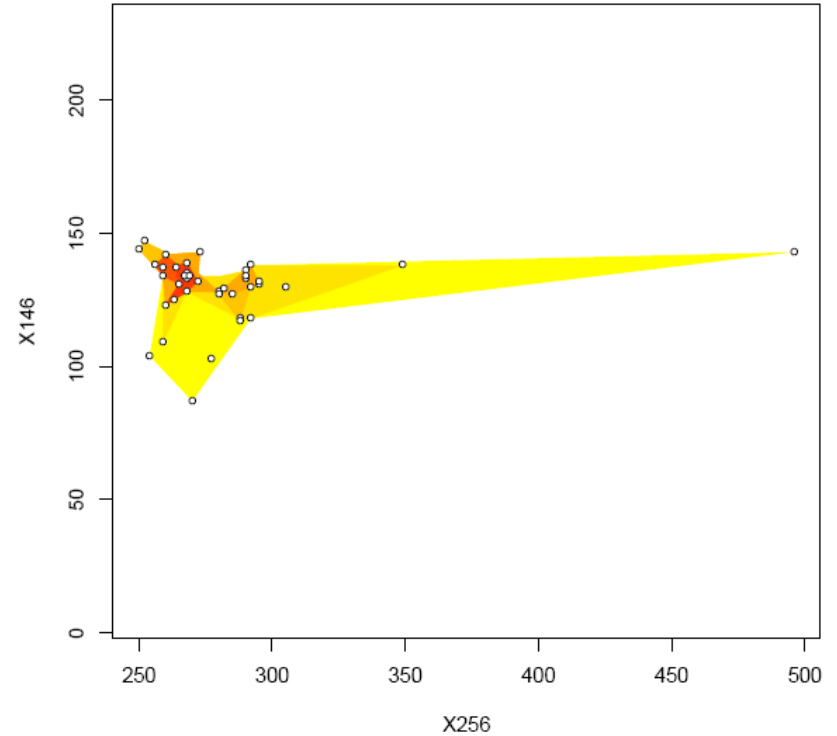
Broadening the discussion – (non-genomic) aspects of prioritization that need to be taken into account

- Geographical confinement – can put even numerically strong breeds at risk of extermination through culling, if they are very localized
- Poses problems of defining flocks/herds of particular conservation significance
- A relevant criterion for prioritization within breeds (identifying significant nuclei)

Kerry Hill sheep (~ 2550 ewes)



Devon Closewool sheep (~ 4340 ewes)



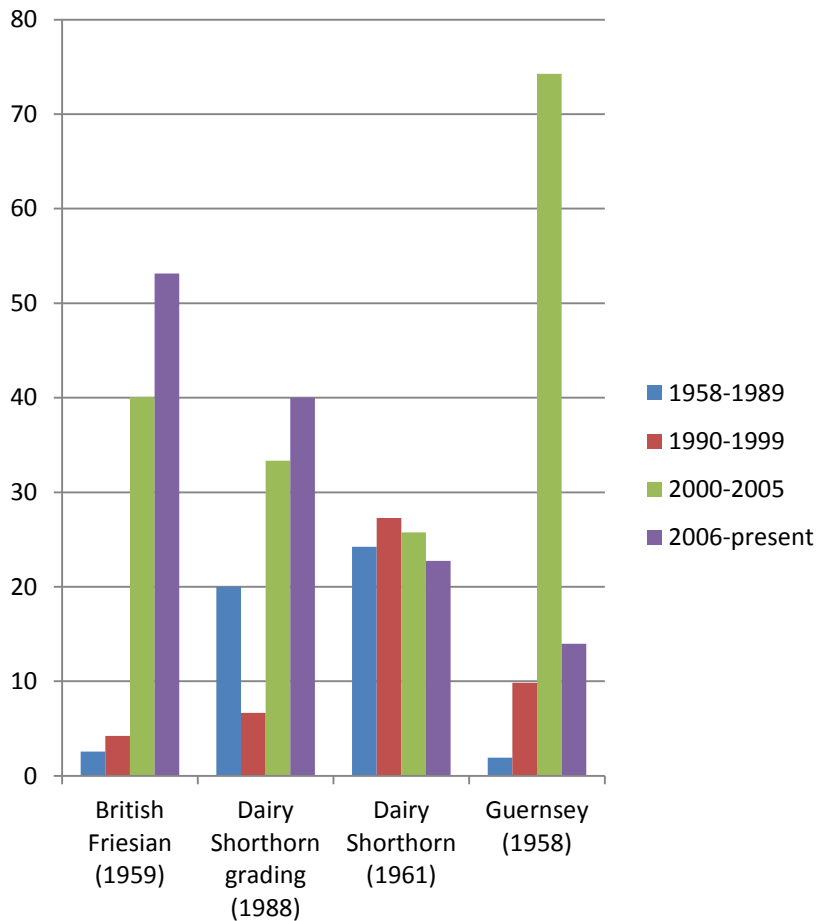
These are the results of applying a home-range (radiotracking) program to map references of locations of sheep flocks. The coloured polygons indicate the areas enclosing different proportions of the total breed.

For a complete picture this needs to be superimposed on a map (GIS process). As it is, the x and y coordinates indicate km distance from a point off the far southwest coast of England

Prioritization within breeds

- Prioritization approaches need to take account of how breeders make decisions
- British minority dairy cattle illustrate this (similar situation for beef cattle)
- Consider the ages of the sires of recent calf crops (in most cases the sires are dead but their semen is still available)
- Possible scenarios – old sires are used if the traditional characteristics are needed, very young sires if there is a young bull proving scheme, “middle aged” sires may be attractive because they have been thoroughly progeny tested and are not yet “obsolete”

Percentages of calves sired by bulls (semen) of different ages



Total numbers of calves:

2588 1230 771 971

- These are the dates of birth of the sires of the 2011 calf crops for British Friesian and Guernsey, and the 2008 calf crops for purebred and grading Dairy Shorthorn
- Note the use of “vintage” semen (year of birth of oldest sire in brackets)

Conclusions

- Prioritization is a complex issue involving the interaction of quantitative and qualitative factors
- Genomics has a part to play but cannot be the only criterion
- Reference must be made to what breeders and policy makers actually want