Practical aspects of utilising gene bank stocks in commercial dairy cattle population

Background

Farm animal genetic variation needs to be conserved for

- risk management for changes in the future market demands or production conditions
- opportunities for development of unique local products
- ecological, socio-economic and cultural values
- extreme deviants useful research material.

Gene banks formed by animals and conservation herds with backing by cryopreservation.

In Finland the native Finncattle (FC) is too small for progeny testing. The conservation program has tools to constrain inbreeding. The three breeds within FC are Eastern (E) and Northern(N) and Western (W).

Urmeli ET from MOET program ASMO. Photo by Tiina Tahvonen.

A calf of Eastern type of Finncattle. Foto by Sanna Lohenoja.

Objectives

Consideration of practical aspects of introgressing desirable traits or characteristics from a gene bank population to a commercial population - with breeds having a wide difference in economically important traits.

Results and discussion

- FC-populations differ significantly from FAY in genetic level of protein production (Fig.1)
- The genetic trend of protein yield in Finnish Ayrshire bulls shows no sign of deceleration (Fig. 2).
- Well established candidate genes (milk quality) with desirable alleles in the gene bank population (FC)
- Marker assisted introgression with several backcross generations.
- Main emphasis on introgressing the candidate gene, other economically important traits follow the mean response of selected FAY bulls (Fig. 3)
- Important to use large number of unrelated and best possible mainstream bulls (FAY)
- Utilization of genome-wide marker sets in recovering
- Compromises inevitable in introgression and recovery
- Use of genomic selection:
  - speeds up the genetic response in recipient (mainstream) population
  - not usable to select crosses for quantitative traits
  - very low accuracy if used for genomic evaluation in gene bank population
  - blindly selected marker alleles could be different from mainstream population
- Direct gene transfer in the future?

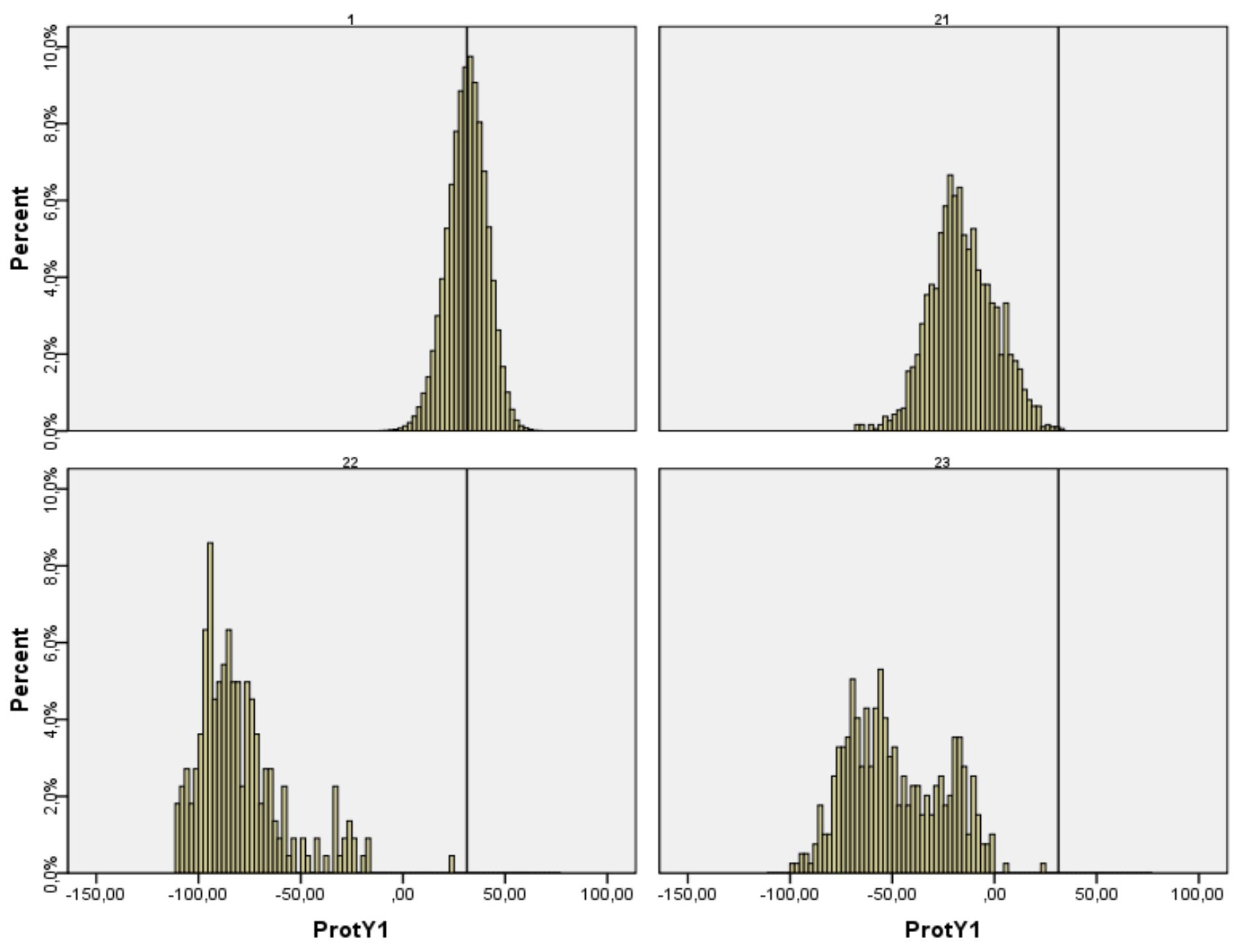

Fig.1: Histograms of the estimated breeding values of first lactation protein yield(kg) for FAY[1] with mean â = 31,3 kg, FC-W[21] with mean â =-15,4 kg, FC-E[22] with mean â =-79,4 kg and FC-N[23] with mean â =-48,5 kg for cows born in 2004-2006.

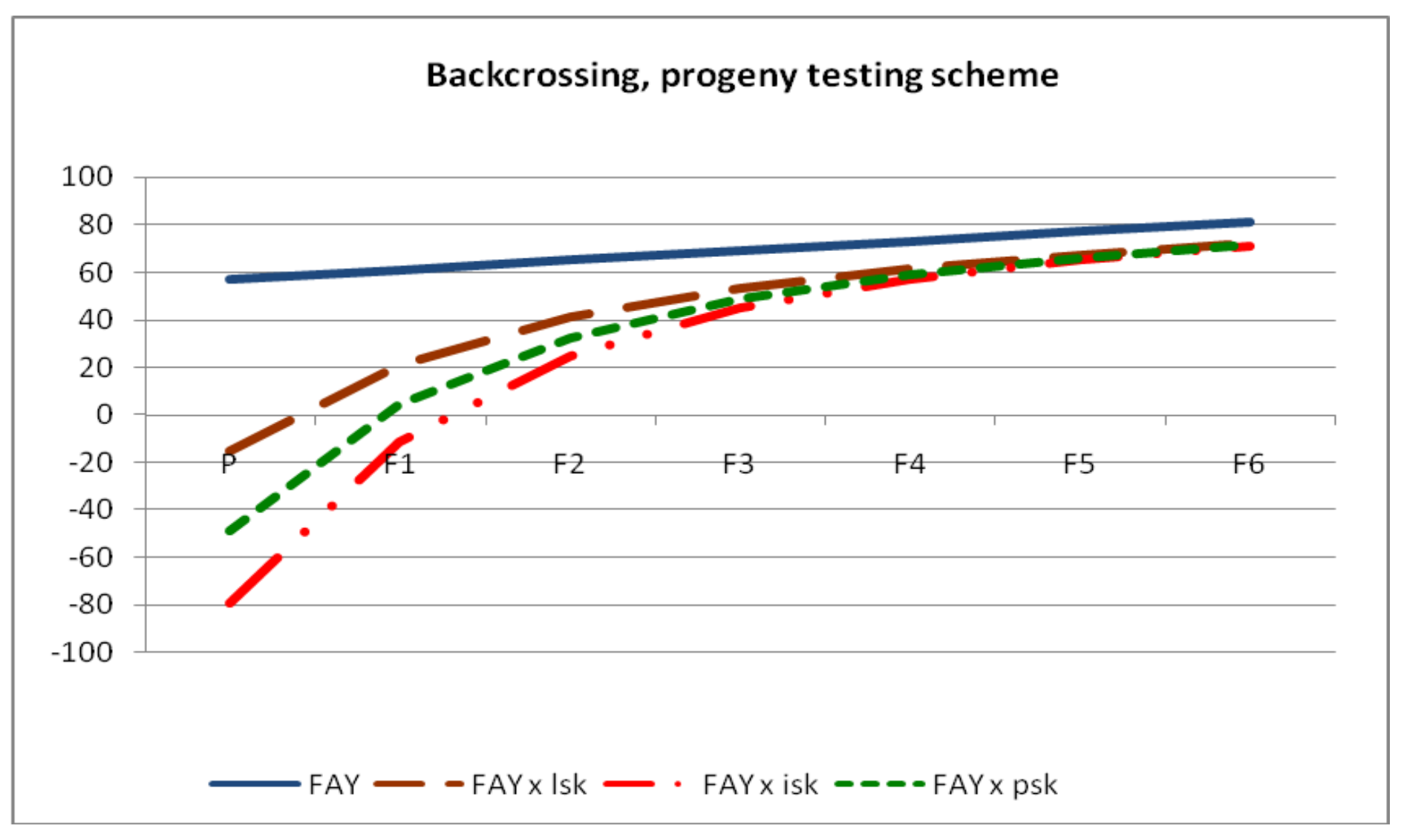

Fig. 3: Genetic change in protein yield when backcrossing the FAYxFC cows with FAY bulls to produce the new AI bulls with a novel trait or gene. lsk=FC-W, isk=FC-E and psk=FC-N subpopulation of Finncattle. F1-F6 are backcrossing generations.

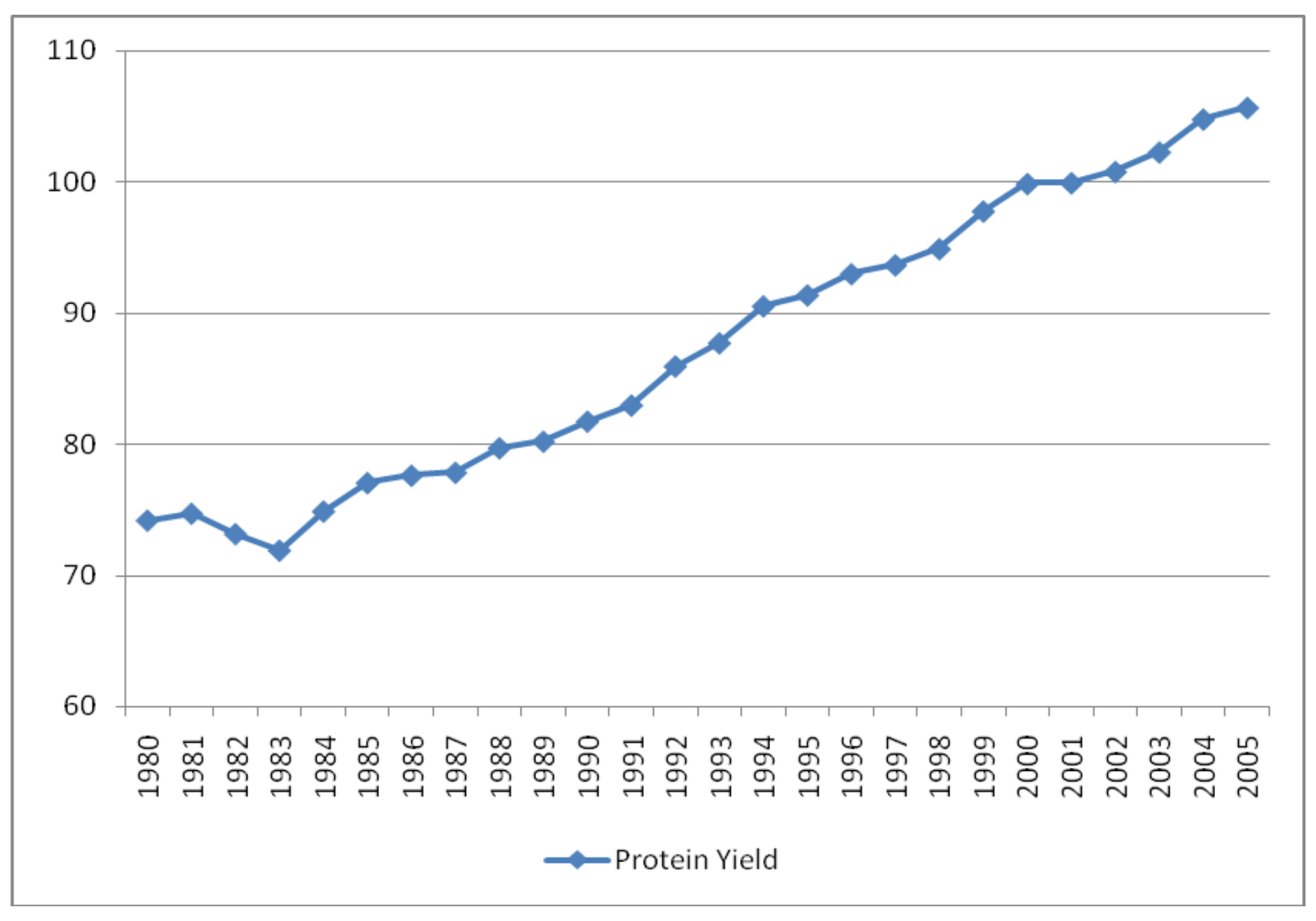

Fig. 2: Genetic trend in protein yield in index points (s.d.=10 = 12,85 kg) for Finnish Ayrshire bulls

Conclusions

- Efficient improvement of mainstream breed should be based on sustainable selection with a broad breeding goal and proper management of genetic variation.
- Introgression schemes with lengthy backcrossing schemes and genome-wide marker sets very costly.
- The new characteristic has to be of extreme economical importance and not available for selection in the mainstream population.
- Utilization of across breed variation not feasible for mainstream breeds.
- The justification for conservation programs of non-mainstream populations arise mainly from other reasons than risk management of mainstream populations.

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