

## Summary

The potential of calculating a unique genetic evaluation simultaneously for all dairy bulls progeny tested in countries of the European Community was investigated. Black-and-White bull pedigree information and national evaluations containing daughter yield deviations from Italy, France, Netherlands, and Germany were obtained. Pedigree data from Canada and USA and national evaluations from USA were included to improve connections among European countries. Traits considered were milk, fat yield, fat %, protein yield, and protein %. The final data sets consisted of 188134 pedigree and 48865 national bull evaluation records from the above countries.

Daughter yield deviations were first standardized within country and then analyzed across countries with a linear model considering all known male genetic relationships. Two separate analyses were performed; one with all data and another with data only from the country where bulls were first sampled.

Results indicated biases in national evaluations which were based on imported semen. Therefore, bull proofs based on daughters resulting from imported semen should be excluded from an international evaluation scheme. Currently used conversions of foreign breeding values are often based on such evaluations.

Results also indicated differences in estimated average change per year in bull evaluations using European Community proofs and pedigree indices based on sire and maternal grand-sire in various countries. Although this could merely reflect differences in maternal grand-dam selection, it could also be associated with biases in estimation of average bull evaluation change in some national evaluation systems. Further investigation on causes of these discrepancies is needed.

In conclusion, a unique ranking of dairy bulls across countries of the European Community can be produced by a linear model combination of data from the country of bulls' first sampling. Checks on result consistency should be made prior to an international evaluation; individual countries should validate their genetic progress estimation and be content with results from their national genetic evaluations. Harmonization of national evaluation systems would further improve international comparisons.