

Effect of Direction of Gene Flow on Conversion Equations

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The genetic marketplace is truly becoming a global one. Interest in conversion equations is growing and will grow even more rapidly in North America with the acceptance of semen from European Holstein bulls.

The traditional methods for developing conversion equations from country A to B require relating evaluations of a group of bulls evaluated in both countries. Available bulls may have been originally evaluated in country A, in country B, in a few cases simultaneously in both countries, or through some combination of these conditions. Logic would dictate the use of bulls initially evaluated in A, the exporting country, with bulls simultaneously tested included. However, such bulls may be few or even nonexistent as when country A has not yet had its bulls evaluated in country B; e.g., when European countries are the hypothesized exporter to the United States.

Georgios Banos reported on a simulation study comparing equations from data with or against the gene flow at the 1992 INTERBULL Seminar on Sire Evaluation (1) and subsequently in the scientific press (3). Results with the gene flow, even in the presence of selection of bulls to be used in country B based on results from country A, were as expected from the simulation parameters. However, equations from data against the gene flow had an inflated a-value (intercept) and a reduced b-value (regression coefficient). He emphasized the impact on the a-value and concluded that equations against the gene flow inflated predictions of bulls from country A. However, the highest bulls from country A were actually underestimated because the lowered regression more than compensated for the inflated intercept. Only the top bulls are of real interest.

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The objective of this study was to determine the effect of computing conversion equations against gene flow. In other words, I looked at the results of using bulls initially evaluated in country B and then later in country A to compute conversions from A to B.

Canadian and U.S. data are sufficient to compute and compare conversion equations both with and against the gene flow. Considering bulls born in 1975 or later and with reliabilities and repeatabilities of 75% and above, 153 Holstein bulls from Canada and 158 bulls from the United States also were evaluated in the other country. Equations were computed by the Wilmlink method in both directions for both sets of bulls and by the Goddard method for Canada-to-U.S. conversion. Daughter yield deviations needed for effective use of the Goddard method (4) were not available for Canadian data in January 1993.

BCA → PTA (lb)					
Yield trait	Gene flow	Wilmlink		Goddard	
		a	b	a	b
Milk	With	-66	121	-47	113
	Against	-58	107	-49	106
Fat	With	3.6	4.02	4.4	3.70
	Against	6.0	3.69	6.3	3.67
Protein	With	-1.5	3.62	-2.1	3.33
	Against	-2.2	3.15	-3.7	3.17

As expected from the simulation study, regression coefficients were reduced if computed against the gene flow for both the Wilmlink and Goddard methods. Regression coefficients computed with the Goddard method were lower than those with the Wilmlink method with the gene flow but nearly the same against the gene flow.

Researchers dealing with conversions are accustomed to seeing regression and intercept

values moving in opposite directions; therefore, reduced coefficients would be expected to lead to higher intercepts. Accepting, for the moment, the equation in the direction of the gene flow as correct, going against the gene flow resulted in lower than expected intercepts for predicting U.S. PTA from BCA. The regression coefficient with the Wilmink method was reduced by 14 lb of milk per BCA. Thus, a bull with a BCA of +20 would be converted 272 lb of milk too low.

Notice that while there is some compensation between the intercept and regression coefficient, that difference in intercept is inconsequential. With these sizeable reductions in *b*, the *a*-value would have been expected to have a definite, not marginal, increase. I suggest that the *a*-values with the gene flow are biased upward by preferential treatment of daughters resulting from imported semen. Thus, *a*-values with the gene flow would be too high and against the gene flow too low because of preferential treatment.

PTA (lb) → BCA			
Yield trait	Gene flow	Wilmink	
		<i>a</i>	<i>b</i>
Milk	With	1.46	.00846
	Against	.54	.00824
Fat	With	-.83	.246
	Against	-.94	.257
Protein	With	1.24	.294
	Against	.44	.283

The results for equations to predict BCA from PTA support the same conclusions. The regressions are lower for milk and protein, and the intercepts are reduced for all three traits. This again suggested a bias because of preferential treatment of daughters in the importing country. Going against the gene flow and treating the importing country as though it were the exporter resulted in equations that were conservative, thus underestimating the best foreign bulls.

A study replicating the previously reported data but from subsets in which 90% reliability and repeatability were required showed that *each* regression coefficient and intercept was reduced if going against the gene flow. The regressions computed against the gene flow are reduced because of selection on the dependent variable

(statistical property), whereas intercepts are reduced (at least relative to expectation) apparently because of preferential treatment of daughters in the importing country. Thus, going against the gene flow has negative effects on both regressions and intercepts.

In conclusion, equations should be computed with the gene flow, in the same direction as they will be applied, whenever possible. This has been the practice for the United States and Canada long before there were recommendations to that effect or related studies. Even using data in the proper direction, results may be affected by preferential treatment.

If there is no genotype × environment interaction, it might be possible to develop equations that are reciprocal by assuming that preferential treatment is equal in both directions and by some averaging of equations. A preferable solution would be to use other approaches that combine data that can be assumed to be unbiased. Participants in this meeting are aware of those efforts (2, 5), and this report is supportive of those activities.

References

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