

# NSIP EBV Notebook

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## The NSIP Maternal Wool Breeds Index: Derivation, Interpretation, and Expected Changes in Component Traits

The NSIP “Maternal Wool Breeds Index” was originally derived to predict EBVs for weight of lamb weaned per ewe lambing in NSIP Polypay flocks. The name was changed to recognize that breeds other than Polypay are now represented in the NSIP “Maternal Wool Breeds” analysis. However, the index did not change and, despite its name, no EBVs for wool traits are included. The index is designed to predict breeding values for maternal performance as indicated by genetic differences in weight of lamb weaned per ewe lambing. It is not a comprehensive breeding objective; EBVs for postweaning lamb growth, ultrasound scanning traits, and wool measurements are not included in the index. However, given the role of the Polypay as a maternal breed, we believe that improvement in ewe productivity should be a primary production goal for the breed.

The Maternal Wool Index is defined as a function of EBVs for weaning weight (WW), maternal weaning weight (MWW), number of lambs born (NLB), and number of lambs weaned (NLW) as:

$$\text{Index} = 0.583 \times \text{WW} + 2.639 \times \text{MWW} + 0.406 \times \text{NLW} - 0.035 \text{NLB}.$$

Positive index weightings for WW, MWW, and NLW are obvious, as these are all clearly positively related to the total weight of lamb weaned. The negative weighting for NLB is less intuitive, but allows ewes that weaned large litters without lamb losses to have a slightly superior index compared to a ewe that weaned a litter of the same size, but lost one or more lambs. Thus a ewe that weaned two lambs from a twin litter would have a slightly higher index than a ewe that had triplets but weaned only two lambs. Proper interpretation of index weighting involves viewing them as the effect of a 1-unit change in each EBV holding all other EBVs constant. Thus at the same NLW EBV, a ewe with a higher NLB EBV would require birth of more lambs in order to wean a comparable number, which is undesirable.

Genetic correlations among traits in the Index are all assumed to be zero except for a positive genetic correlation of 0.5 between NLB and NLW, so effects of weaning growth, maternal weaning weight, and prolificacy (NLB and NLW) are essentially independent. Genetic correlations between the Index and each of its components are shown below:

Component trait	Genetic correlation with the Index
Weaning weight	0.07
Maternal weaning weight	0.31
Number of lambs weaned	0.94
Number of lambs born	0.40

The table shows that the Index is dominated by NLW, which is not unexpected, because the most efficient way to increase the weight of lamb weaned is to wean more lambs. Despite its negative weight in the index, NLB still has a positive genetic correlation with the Index, by virtue of its positive relationship

with NLW. Thus, we want to avoid increases in NLB that do not yield corresponding increases in NLW. However, increasing NLB still, on average, results in increases in NLW and, therefore, in the Index. The Maternal Weaning Weight has a modest positive impact on the index, but its effect is much smaller than that for NLW, and the direct effect of the Weaning Weight EBV on the Index is small.

Index values are reported by LAMBPLAN as “ratios” to the mean index value, but, in fact, are derived by simply adding 100 to the Index shown above. The 50<sup>th</sup> percentile for the USA Maternal Wool Index from the June 2013 Percentile Report at [www.nsip.org](http://www.nsip.org) was 107.6, which corresponds to an average value for the Index shown above of 7.6 kg. Index values can thus be derived simply from the component EBVs.

Changes in EBVs for component traits associated with selection on the Index are shown below as the expected change associated with a 5-unit change in the Index, which approximately corresponds to the expected average difference in each trait between animals in the upper 10<sup>th</sup> percentile or the 50<sup>th</sup> percentile for the Index (corresponding to average Indexes of 113.0 and 107.6, respectively, for the June 2013 Percentile Report). The table confirms that selection on the Index will mainly emphasize NLW and will improve NLW more rapidly than NLB.

<b>Component trait</b>	<b>Expected change in breeding value associated with a 5-unit change in the Index<sup>a</sup></b>
Weight of lamb weaned per ewe lambing	5.0 kg = 11.0 pounds
Weaning weight	0.05 kg = 0.11 lb
Maternal weaning weight	0.19 kg = 0.42 lb
Number of lambs weaned	11.5%
Number of lambs born	5.5%

<sup>a</sup>Based on the June 2013 Percentile Report, this difference approximately corresponds to selecting animals in the 10<sup>th</sup> versus 50<sup>th</sup> percentile for the Index.

### **Potential for Genetic Improvement**

Prediction of possible rates of improvement in the index will depend on the accuracies of estimation of the component breeding values in potential replacement lambs, on the mix of proven sires and ram lambs in the breeding rams, and on the replacement rate for the ewe flock. Accuracies of estimation of breeding values will, in turn, vary with the specific traits that are recorded and with the average age (and therefore number of records) of the parents. The following table shows heritabilities and phenotypic variances for each trait in the index and approximate average accuracies for the 7- to 8-month-old lambs that would be available for selection as replacement rams and ewes. Average accuracies were derived as averages of elite male and female progeny (i.e., ram and ewe lambs) from the June 2013 Elites Report.

<b>Component trait</b>	<b>Phenotypic variance</b>	<b>Heritability</b>	<b>Average LAMBPLAN accuracy for replacement lambs</b>	<b>Average accuracy for simple mass selection of replacement lambs</b>
Weaning weight	13.24 kg <sup>2</sup>	0.09	0.57	0.30
Maternal weaning weight	13.24 kg <sup>2</sup>	0.08	0.42	0.17 <sup>a</sup>
Number of lambs weaned	4330 % <sup>2</sup>	0.11	0.35	0.17
Number of lambs born	3930 % <sup>2</sup>	0.13	0.39	0.18

<sup>a</sup>Assumes 65% twins and 35% singles.

In simple mass selection based only on a single direct measurement of lamb performance (i.e., on the lambs' own weaning weights), accuracy of breeding value estimation is equal to the square root of the heritability, which would be 0.3 for weaning weight. For reproductive traits, simple mass selection based

on a single litter size of the dam would have an accuracy equal to  $0.5 \times$  the square root of the heritability (since the lamb is being evaluated based on a record for its dam), which would equal 0.18 for number born and 0.17 for number weaned. For maternal effects on weaning weight, simple mass selection based on the average weaning weight of the litter in which the lamb was born would generate accuracy values of  $0.5 \times$  the square root of the maternal heritability for single lambs and of approximately  $0.64 \times$  the square root of the maternal heritability for twin lambs. For a maternal heritability of 0.08 for weaning weight, these would correspond to accuracies from simple mass selection for maternal weaning weight of 0.14 for single births and 0.18 for twin births. The differences between these expected accuracies from simple mass selection and those shown in the table above represent the additional accuracies obtained by using all records on parents and sibling in the NSIP data base.

Given the accuracies in the table, the accuracies of the Maternal Wool Index for lambs in the current lamb crop would be approximately 0.38, which is similar to that for number of lambs weaned, as expected from the large impact of that trait on the index. This level of accuracy leads to an effective “heritability” of the index of approximately 0.15. In a flock of 100 ewes and four rams weaning 160 lambs per year, with retention of the top 2 of 80 ram lambs and the top 25 of 80 ewe lambs, we would expect the average genetic merit for the index in the replacement lambs to exceed the average of the parents by 5.4 kg of lamb per ewe lambing. With a generation interval of 2 years for rams and 4 years for ewes, this would translate into an expected genetic trend in the ewe productivity index of 1.8 kg (4.0 lb) per year. With an average weaning rate of 1.60 lambs per ewe and an average weaning weight of 55 lb per lamb, the resulting genetic trend from intense single-trait selection on the Maternal Wool Index would equal 4.5% per year. However, in most flocks, supplemental selection on traits related to soundness, body type, and other performance traits such as postweaning weight would reduce this expected genetic progress. Thus if we consider the 2 replacement males to come from the top 10 (rather than the top 2) ram lambs and the 25 replacement ewe lambs to come from the top one-half of the 80 available ewe lambs, the anticipated genetic trend in the Index would be reduced to 1.3 kg (2.9 lb) per year, but would still equal approximately 3.2% of the mean.

These potential genetic trends seem high for an index that is dominated by number of lambs weaned, which is relatively lowly heritable. However, the predicted rate of genetic improvement is a function of both the accuracy of the genetic evaluation and the variability in the trait, which is high for most reproductive traits and, therefore, for the Index. Unfortunately, the high level of genetic variation in the Index also means that selection of an individual ram lamb will carry considerable levels of risk. For an accuracy of 0.38, the prediction error of the Maternal Wool Index EBV will be approximately 7.85 kg. If we select 2 ram lambs from the top 10 ram lambs in the current lamb crop with this accuracy, their expected average EBV for the Maternal Wool Index would be approximately 5.2 kg above the flock mean, but the prediction error for their mean EBV would still be nearly 4 kg.

We also know that there are differences among flocks in management of lambs born in large litters, and these differences can affect the expression of genetic differences in the Maternal Wool Index. For example, differences among EBVs for animals produced and evaluated in flocks that allow their ewes to raise all the lambs born in the litter may not be fully expressed in flocks that foster or artificially rear some of the lambs from triplet and larger litters. The genetic merit of the sheep can thus interact with the flock management. These interactions can affect the rate of genetic progress in the breed as a whole and the expected magnitude of differences among breeding animals, but are not expected to cause major changes in the relative performance of breeding animals used in different flocks.

Despite these limitations, selection for the Maternal Wool Index in large flocks is expected to result in substantial genetic improvement. However, selection of individual rams for use in small flocks will be associated with considerable variation in the true EBVs of selected rams. Achievement of high accuracies for individual rams for the Maternal Wool Index therefore requires progeny testing to directly evaluate daughters of promising rams, but at a cost of increasing the generation interval. Optimal breeding

programs thus involve use of a combination of high-accuracy proven sires to ensure reliability of Index EBVs and promising young ram lambs to take advantage of anticipated genetic trends in the Index. Choices regarding the mix of proven sires and ram lambs will depend on flock size (with larger flocks better able to accept the risk associated with greater use of ram lambs) and the owners' preference to embrace or avoid risk in the breeding program.

### Genetic Trend in the Maternal Wool Breeds Index

Genetic trends in EBVs for the Maternal Wool Index between 2004 and 2013 are shown below for NSIP Polypay flocks. The average rate of genetic improvement was 0.61 kg/yr (1.34 lb/yr), corresponding to an increase of 1.5%/yr. This value is below the predicted maximum, but still substantial, corresponding to a total increase of 5.5 kg (12.1 lb) in ewe productivity over this 10-yr period. While the observed genetic trend is below the predicted maximum, that outcome is not unusual. As a comparison, the genetic trend in milk production in Holstein cattle is commonly held up as the gold standard for genetic improvement of a maternally influenced trait but generally does not exceed 1%/year. Also, over the past 10 years, the U.S. average lamb crop (number of lambs marketed per breeding ewe) has averaged only 110% and has shown no positive trend. By contrast, the rate of genetic improvement in ewe productivity in Polypay sheep has accelerated, equaling 0.87 kg/yr (2.2%/yr) for the 5 yr since the NSIP-LAMBPLAN merger in 2009. NSIP producers are thus in the enviable position of making substantial and documentable genetic improvement in a key economic trait, with additional opportunities for even more rapid genetic improvement.

