



Understanding Genetic Linkage

One of the most important components of the BREEDPLAN analysis is the ability to compare the resulting Estimated Breeding Values (EBVs) of animals running under different conditions. This is achieved through the use of “genetic linkage”.

Genetic linkage is established by the use of common sires across herds. To compare animals from different environments, herds must have some performance recorded progeny from common animals (typically common sires), which are used to bench mark one herd against another. Genetic linkage is also important within a herd, to compare animals born in different years and raised in different contemporary groups. At the within herd level, link sires provide linkage between contemporary groups and dams can provide additional genetic linkage across years.

As an example of genetic linkage, consider a situation where 3 different mobs of calves (either on the same property or different properties) are compared. There are nutritional differences between the Groups - Contemporary Group 1 (CG1) has relatively poor nutrition, Contemporary Group 2 (CG2) has relatively good nutrition and Contemporary Group 3 (CG3) has average nutrition. The figure below shows the average adjusted performance of progeny in each of these contemporary groups by each sire.

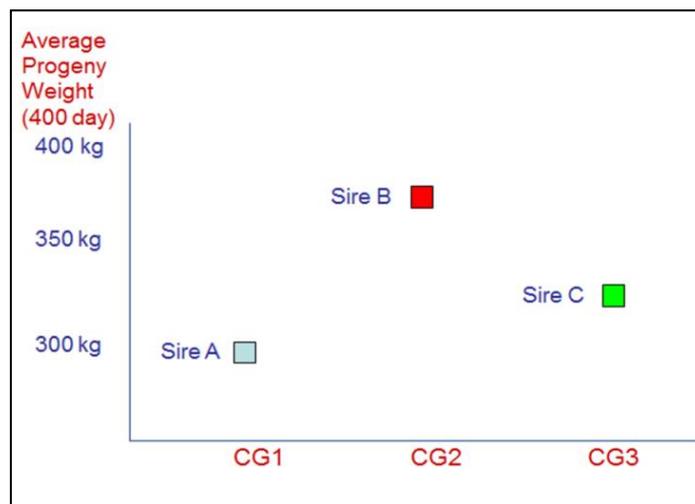


Figure 1. Average adjusted progeny performance in three different contemporary groups by three different sires.

In this example, all of the progeny in each group are by different sires. Nifty is the sire of the progeny in Group 1, Lusty is the sire of the Group 2 progeny and Curly is the sire of the progeny in Group 3. Under such conditions, it is impossible to make valid comparisons about the relative performance of the animals in the different contemporary groups, as there are no “genetic links” between the groups and the groups have been running under different conditions.

If however, progeny from a common sire existed in each contemporary group (for example, an AI sire) then it becomes possible to compare the progeny of the different sires represented in each group. This is illustrated in the figure below where Admiral is the link or common sire.

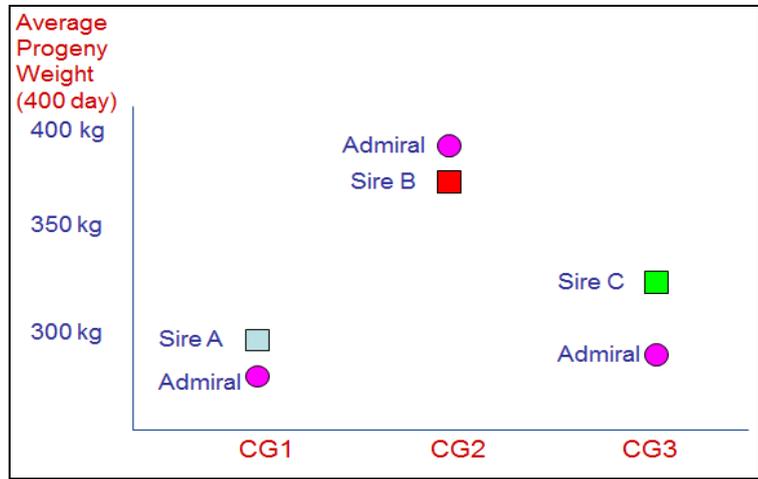


Figure 2. Average adjusted progeny performance of the three different sires compared to the average adjusted progeny performance of the link sire Admiral.

The progeny of the link sire (Admiral) have an average adjusted 400-Day weight of 290 kg, 390 kg and 300 kg in their respective contemporary groups. In comparison, the average adjusted 400-Day weights of the progeny of the other sires are: Nifty: 300 kg, Lusty: 380 kg and Curly: 320 kg. For the purposes of this example, we assume that all sires are joined to cows of equal average EBVs for 400 Day Weight.

In Contemporary Group 1 the progeny of Nifty were heavier than the progeny of Admiral. In Group 2 the average weights are higher than for Group 1 but the progeny of Lusty did not weigh as heavily as the progeny of Admiral. In Group 3 the progeny of Curly were considerably heavier than the progeny of Admiral. These differences in average weights under different nutritional conditions are represented in Table 1.

Direct comparisons	Indirect comparisons
Nifty vs Admiral = +10kg	Nifty vs Lusty (+10kg +10kg) = +20kg
Lusty vs Admiral = -10kg	Nifty vs Curly (+10kg -20kg) = -10kg
Curly vs Admiral = +20kg	Lusty vs Curly (-10kg -20kg) = -30kg

Table 1. Differences in average progeny weights under different nutritional conditions

Figure 3 shows how BREEDPLAN can account for the differences in the environmental conditions for different contemporary groups by using a common or bench mark sire. The differences in average weights of natural sire progeny groups compared to the progeny of Admiral, are shown in the following figure. It shows that

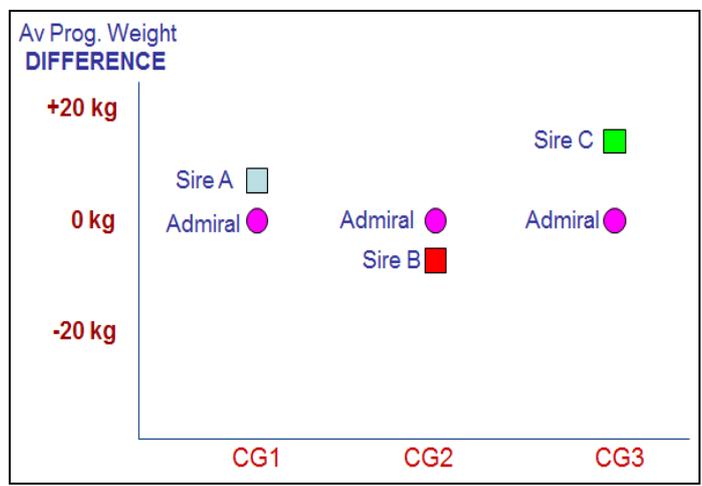


Figure 3. Average adjusted progeny performance of the three different sires benchmarked against the average adjusted progeny performance of the link sire Admiral

while the Lusty progeny had the heaviest average weights of the three home sires they were 10kg lighter than the Admiral progeny. The Nifty progeny outperformed the Admiral progeny by 10kg and the Curly progeny outperformed the Admiral progeny by 20kg making Curly the superior sire for 400 day weight.

Assuming large numbers of progeny, the difference in the sire EBVs will approach twice the average progeny differences. This is because the progeny only receive half of their genes from their respective sires. The other half of the genes comes from the dam.

Ignoring the breeding of each of the sires the resultant EBVs of the sires (twice the progeny differences) are shown in Table 2.

	Nifty	Lusty	Curly	Admiral
EBVs	+20 kg	-20 kg	+40 kg	0 kg

Table 2. The resulting EBVs of the sires, assuming dams are of equal genetic merit for 400 Day Weight.

The example shown in Table 2 assumes that Admiral has an EBV of zero, that reasonable numbers of progeny were measured and that the dams are of equal genetic merit for 400 day weight (same average EBVs). Adjustments are made if the dams are known to have different average EBVs for the trait being measured.

In addition, if the progeny numbers are not large, the sire EBVs will be less than double the progeny differences, as BREEDPLAN makes “conservative predictions”. The “scaling factor” depends on the number of progeny of the home sire and the link sire and the heritability of the trait in question.

Please contact staff at BREEDPLAN should you have any further queries regarding genetic linkage.