IMPROVE YOUR BREEDING DECISIONS WITH MATESEL

The decision of which bull to mate with which cow impacts the rate of genetic improvement, inbreeding levels and overall profitability of a herd. MateSel is software which use pedigree, $Index and EBV information to create suggested mating lists based on nominated candidate sires and dams to increase the genetic merit of the progeny while containing inbreeding in the herd.

AWA licences MateSel software and can provide this service to members whose herd is registered with the Australian Wagyu Association on a fee-for-service basis.

WHAT IS MATESEL?

MateSel is short for Mate Selection and is software developed by Professor Brian Kinghorn at the University of New England. It is used in breeding programs of many species around the world including fish, prawns, poultry, pigs, sheep and is finding increased application in cattle, including Wagyu. It considers the simultaneous choice of available parents to select for breeding and then use the breeding objectives specified by the breeder to generate a suggested mating list as well as backup matings.

THE BASICS OF A BREEDING PROGRAM

In its most simplistic form, the key objective of a well-structured breeding program is to balance the relative emphasis on genetic gain and inbreeding of current and future generations. There are several methods described in scientific literature which achieve this objective. Most commonly, it is done by including a negative weighting on animal relatedness whilst optimising animal contributions to genetic gain. The limitation of using such a simplified method is that it can't accommodate the complexity of many modern breeding programs.

MATESEL HANDLES THE COMPLEXITY

In addition to increasing genetic gain and containing inbreeding, progressive breeding programs are required to address many other issues including linkage between herds, management of genetic conditions, multi-stage selection, various types of costs, and various logistical constraints.

MateSel can accommodate these complexities by allowing the user to nominate the number of matings, available parents lists, available number of paddocks, number of straws of semen available for AI sires, IDs of natural service sires available for backup matings and the levels of use of embryo transplanting.

Through use of the MateSel program, far greater numbers of iterations and more production and breeding factors can be used in designing a breeding program using all available data, rather than what you can manage just with your spreadsheeting capabilities.

Comprehensive use of MateSel involves decision making at various stages of the life cycle, including selection/culling at various juvenile and adult stages, selections for main round matings and selection of sires for backup matings.

MateSel can accommodate all animals in the population, across different groups, including embryos in-utero, calves at foot, first calf heifers and pregnant females, as well as candidates for active matings. This helps to accommodate overlapping generations, and to account for matings already made as reflected by calves and pregnancies in the analysis – sires that have already been used extensively will be somewhat inhibited from further use.

STEP BY STEP   BREEDING WITH MATESEL

MateSel creates a list of optimal matings for a group of candidate animals based on information and trait parameters set by the breeder. The breeder still makes the decisions about what they want to achieve in their breeding program. MateSel delivers the optimal outcome for the breeder based on the parameters they chose. To do a MateSel analysis the breeder needs to:

1. **Indicate the breeding objective** (eg. select a targeted $Index)

2. **Nominate the breeding strategy** being targeted i.e. "Low Inbreeding", "Balanced Genetic Gain and Inbreeding" or "High Genetic Gain".

3. **Indicate EBVs or genetic conditions** which are of special interest to increase, decrease or maintain in the matings.

4. **Supply a list of candidate sires** for the breeding program. This can be a specific list of sires within your herd or a broad list of potential animals that may be available for the breeding program. It is good practice to include all semen sires listed in the AWA's web semen catalogues, this can show you the potential of what is available compared with the potential of what you have.

5. **Supply a list of candidate females** available for mating based on cows in the herd, age groups, last calving and registration status.

6. **Specify mating groups** to suit the joining program including such things as heifer versus mature cow matings, and natural versus AI matings.

7. **Set maximum usages** for sires and min. cow mob sizes for natural matings.

Once the MateSel analysis is completed based on the breeder specified parameters, a MateSel report and suggested mating allocation list is generated and supplied to the member.

The member will also be able to see the available herd progress at different levels of management for inbreeding or genetic gain.

The outcome of the MateSel analysis is aimed at achieving a balance across a range of objectives, including direction, magnitude and pattern of genetic change for different traits over time, avoidance of genetic defects, avoidance of progeny inbreeding, use of reproductive boosting (i.e. embryo transplanting), and a range of logistical constraints (i.e. number of available mating paddocks) on what is practical to implement.

WHAT IS COANCESTRY AND WHY IS IT THE BEST INDICATOR OF CURRENT AND FUTURE INBREEDING?

MateSel manages relatedness by focussing on coancestry (true relatedness) rather than inbreeding. This is an important distinction and the following example should help to explain the reason: You may choose to use a bull that has moderate inbreeding, but if that bull is totally unrelated to your whole herd and you use that bull over all your cows, you will have zero inbreeding in the resultant progeny.

However; because you used the same bull over all your cows, all the progeny will now be at least 50% related. This will dramatically reduce your options of bulls for use in the future.

Coancestry is therefore a very important indicator of relatedness in the herd and is the only practical way to effectively manage long term inbreeding in the herd.

The MateSel interface consists of the several components to help visualise and manage aspects of the analysis.

The Frontier of genetic improvement is the black line displayed on the graph in Figure 1 and shows the most extreme selection response possible when all emphasis is shared by just the two major objectives i.e. genetic merit (expressed as Progeny Index – Y axis) and future inbreeding (expressed as Parental Coancestry or relatedness – X axis). The frontier line shows the balance between the $Index outcome at different coancestry levels given the $Index values and pedigree information of the nominated available parents.

The blue crosshair in Figure 1 gives a visual indication of how well the MateSel solution for this test herd can optimise genetic gain by balancing the available genetic merit, inbreeding and individual trait thresholds for the currently nominated parents.

The red trail on the graph shows the pathway the analysis followed while optimising the matings before settling on the current "best" solution (the blue crosshair).

In most cases the most favourable direction is to have the crosshair pointing towards the top left, that is, the spot between Zone A and Zone B.

Zone A represents potential solutions where very little increase in future inbreeding results in a relatively large increase in progeny genetic merit. Zone B represents potential solutions where a large increase in future inbreeding results in relatively little further increase in progeny genetic merit.
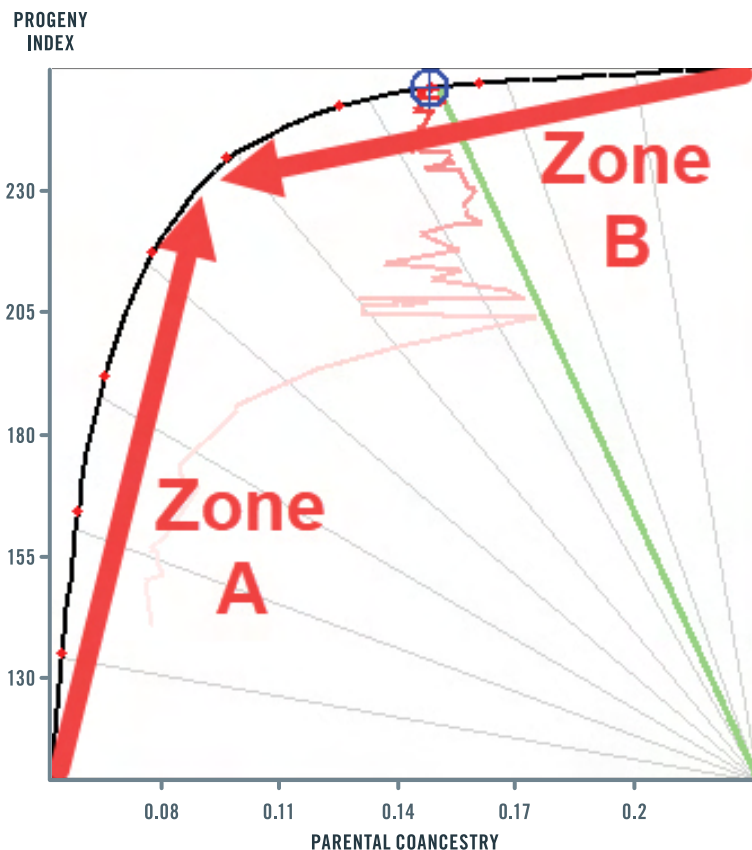

FIGURE 1

The frontier shows the highest selection response possible if different levels of genetic merit (Progeny Index) and future inbreeding (Parental Coancestry) drive the breeding objective.

TRAIT MANAGEMENT

The Trait Management feature of MateSel, shown in Figure 2, can be used to direct the analysis to put emphasis on individual traits (eg, genetic conditions or performance traits).

Within MateSel, breeders can select a range of options to increase or decrease the mean genetic merit for traits or manage the genetic variation within a herd. Figure 2 shows an example of genetic progress that can be made by placing weighting on individual traits. The Black tab on each bar graph shows the average genetic merit of the parents in the herd. The Red tab on each bar graph shows the achieved progeny values from the optimised mating solution.

In the example MateSel run shown in Figure 2, the scenario for the herd was to increase the Self-replacing $Index as the primary driver (blue cross hairs shown earlier in Figure 1), with minimum limit set on Carcase Weight (middle bar graph in Figure 2) and no increase in genetic conditions. Figure 2 shows the progeny outcomes of the optimised breeding program design for the member.

FIGURE 2

Individual trait management can be done by implementing Trait Management strategies.

The black tab on each bar graph is the average mid-parent value for the herd, the red tab is the optimised progeny outcome for the herd.
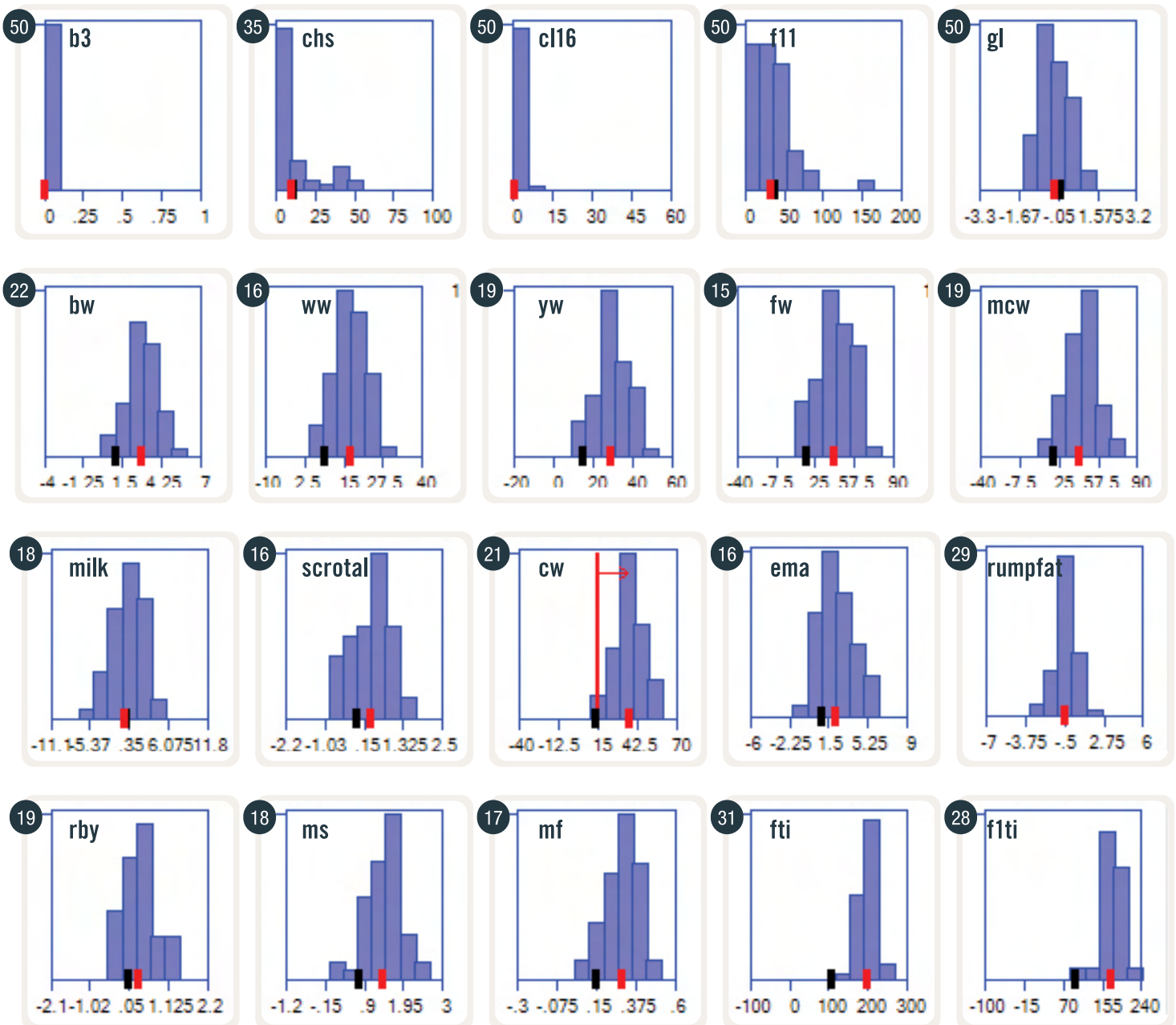
In Figure 3, an example strategy has been implemented to set a minimum Carcase Weight EBV value of 15 kg on the mating outcomes. Once the strategy is implemented the analysis ensured none of the matings will have a Carcase Weight EBV outcome of less than 15kgs.

Figure 3. The minimum Carcase Weight EBV value has been set at 15 and therefore the analysis only nominates matings where the progeny will be expected to have EBVs higher than 15kgs.

This herd example demonstrates the enormous power available to members to design their breeding programs controlling as many as 20 variables, in addition to optimising a primary $Index and inbreeding outcome. This is far greater control than can be achieved through manual planning and spreadsheet methods and there is no limit to the scale of breeding program that MateSel can be used for. It can be used by small herds and herds with over 10,000 matings.

SUMMARY BENEFITS OF USING MATESEL

» It allows you to specify your desired breeding direction (eg. by nominating the $Index that reflect your production system and controlling inbreeding across the whole herd).

» It maximises the rate of genetic gain in your herd while managing inbreeding.

» It objectively uses all pedigree and genetic evaluation trait information (EBVs) to improve your mating decisions.

» It saves significant time previously spent compiling mating lists.

» It can help you to make informed decisions about semen purchases (which bulls and number of straws), which backup bulls to use, selection or culling of cows/heifers and optimising backup mating group formation.

» The breeder controls the breeding objective whilst the program delivers the optimum outcome to meet the breeding objective.

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FIGURE 3

The minimum Carcase Weight EBVs value has been set at 15 and therefore the analysis only nominates matings where the progeny will be expected to have EBVs higher than 15kgs.
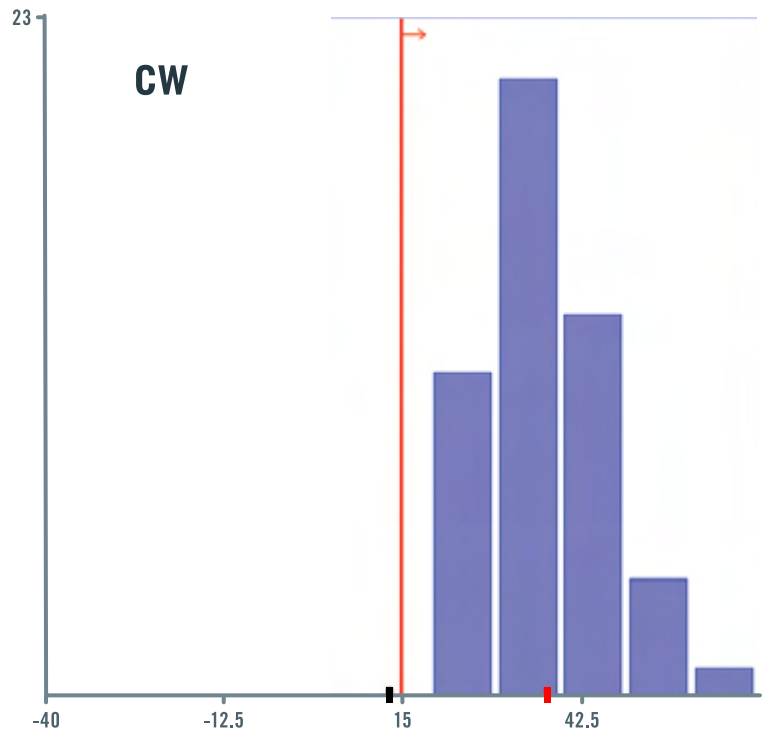
CAN I ACCESS THE MATESEL SERVICE?

As MateSel optimises the genetic merit of the mating based on nominated $Index, EBV and pedigree information, MateSel can only be utilised by a herd that is currently an Australian Wagyu Association member and has EBVs and $Index values for registered animals of interest.

MateSel is licensed to AWA and AWA provides MateSel analysis as a cost recovery service to its members. As the results of MateSel are directly of benefit to the individual breeder, licence costs and the time it takes to optimise MateSel to the member's breeding objectives are charged to the individual member.