location should be relatively simple. The Australian Grains Genebank (AGG) has been systematically introducing this collection (and others) over many years.

Powdery mildew resistance has similarly been a significant problem. Our experience was that the use of the *mlo* gene resulted in yield reductions of 5-10%. However varieties such as Fairview, Granger and RGT Planet maintain resistant or "R" ratings from using the *mlo* gene.

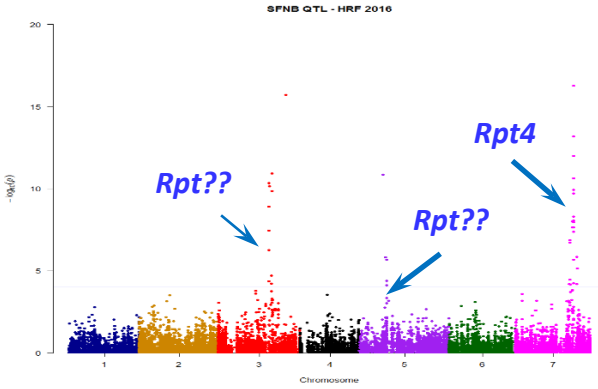

Figure 2a: Spot form of Net Blotch "Manhatten Plots" from NAM_LR (Fowler et al. 2017 unpubl.)

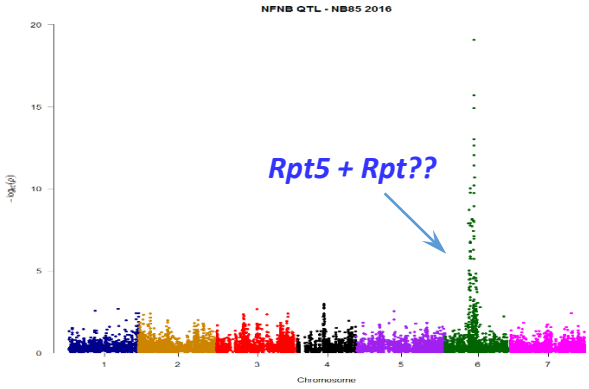

Figure 2b: Net form of Net Blotch "Manhatten Plots" from NAM_LR (Fowler et al. 2017 unpubl.)

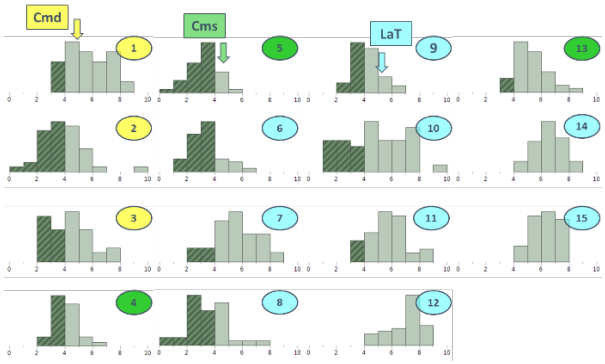

Figure 3a: NAM_DR : Spot Form Net Blotch (SFNB17) populations. 1- 15. Means for reference varieties: Commander (Cmd), Compass (Cms) and La Trobe (LaT) are given for their respective "first" populations. Populations are coded yellow Cmd, dark green Cms and light blue (LaT). Scale is 0-9 where 0 represents more resistance

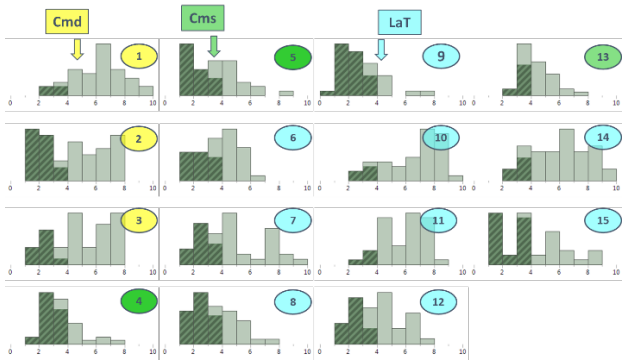

Figure 3b: NAM_DR : Net Form Net Blotch (NFNB17) populations. 1- 15. Means for reference varieties: Commander (Cmd), Compass (Cms) and La Trobe (LaT) are given for their respective "first" populations. Populations are coded yellow Cmd, dark green Cms and light blue (LaT). Scale is 0-9 where 0 represents more resistance

A simplified conceptual scheme is represented in the Figure 4. Disease resistance traits are represented by genes AA, BB, CC and DD. Our starting populations are from Nested Association Mapping (or NAM)

populations where specific lines have been crossed once to several “recurrent” parents. A second and third round of crossing to the “Recurrent” parent will effectively result in BC_2 populations. Populations are both crossed to “recurrent” parents and then selection progeny are intercrossed in pairs of populations e.g. combining AA and BB to give and AABB genotype (or A/a;B/b; homozygote or heterozygote selection). In a second population development CC will be combined with DD and CCDD (or C/c;D/d selected) selected. Finally AABB and CCDD are combined and ultimately AABBCCDD genotypes are selected. An additional round of inter-crossing may be desirable so the final population in Figure 4 is referred to as BC_2 IC_2 populations. Selected lines can be taken through several cycles of “Speed Breeding”

The improvement in the overall disease resistance of Australian barley varieties needs to proceed in two phases. The first is the R&D phase of unique gene/allele discovery including gene mapping. The second phase should be the pyramiding of genes into industry agreed “reference” varieties. The integration of a number of breeding and genetic biotechnologies is the preferred path for success. Male sterile facilitated recurrent selection (MSFRS) would be the preferred technology to effectively and efficiently accumulate the desirable disease resistance genes. The Figure 4 represents a simple scheme to illustrate the general approach. The male sterile (*msg6-rob-sex1*) gene block is back-crossed into the “reference” varieties. The *msg6* is used to facilitate the crossing, selection and inter-crossing of populations which have been selected (both genotypically and phenotypically) for different traits. The NAM populations NAM_LR and NAM_DR have used three reference varieties; Commander, Compass and La Trobe. All populations are therefore 50% reference varieties. Two further crosses to “*msg*-reference” varieties will result in in BC_2 populations. In the simple scheme, two rounds of crossing and inter-crossing would enable the accumulation of genes for four traits. A necessary extension to the simple scheme is to “self” selected F_2 derived lines and then progeny test these for yield, agronomic performance as well as grain quality and NIR predicted malting quality. So not only will selections being made for pyramided disease resistance genes, but the background reference variety germplasm will be selected for overall performance. As an extension to this approach, breeding companies would be encouraged to develop their own propriety “*msg* –reference” varieties or lines to enable the rapid crossing of “selected elite populations” into their own material. Again, the approach would be for the companies to utilise “speed breeding” of their own selected F_2 derived lines for variety development.

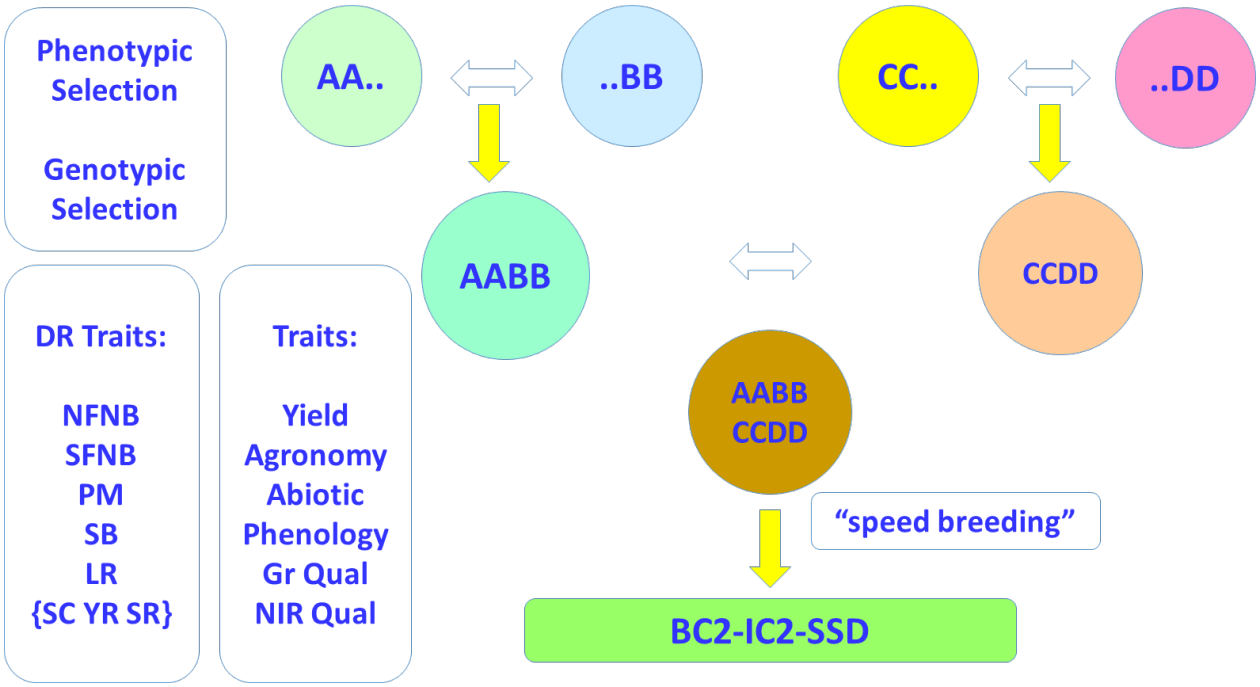

Figure 4: Male Sterile Facilitated Recurrent Selection (MSFRS) for Disease Resistance. A simplified schematic representation of the use of MSFRS, Genotypic and Phenotypic selection to Pyramid multiple genes for disease resistance into various "recurrent" parent backgrounds.

Conclusions:

Barley breeding and genetics has changed significantly over the past forty years or more. Australian malting varieties have improved to the point where they are competitive in the international market place. The longer term future of the barley industry will need to be competitive in relation to other crops. The industry needs to improve the overall barley disease resistance status both; to protect the yield, agronomic and quality improvements achieved but also to reduce the costs of managing multiple disease susceptibilities.

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