

Project Summary

Improved subterranean clover seed production from multiple disease resistance

This project aimed to improve subterranean clover seed production by identifying and utilising multiple disease resistances. To achieve this the following steps were undertaken:

1. Assessment of subterranean clover diversity in relation to resistance to clover scorch (seedling and adult resistance to both race 1 and race 2), rust, Pythium and Phytophthora, studies that confirmed that a breeding solution for resistance to each disease was feasible.

2. Determination of the different genes or Quantitative Trait Loci (QTLs) required for resistance to each disease; this will enable future 'pyramiding' different resistance genes to increase resistance levels against these pathogens.

3. Identification of potential parents with disease resistance that now enable introduction of new resistance genes into subterranean clover crossing and breeding programs.

4. Discovery of molecular markers closely linked to genes or QTLs for some disease resistances, allowing marker-assisted selection of more disease resistant cultivars in the future.

The findings from this project have the potential to benefit all public and private breeding programs, with an interest in breeding subterranean clover across Australia.

Background

Diseases are a major cause of subterranean clover production losses in the seed (and livestock) industries. Soil-borne root rot pathogens can cause seedling losses exceeding 90%. This has a major impact on seed production stands and grazing paddocks, due to greater weed competition, weaker root systems and reduced biomass and seed production. Seed production stands are also particularly highly vulnerable to major seed yield losses by fungal foliar diseases as they are normally clover-dominant thick stands conducive to disease development. The most important diseases for seed producers include the soil-borne root rot diseases caused by Pythium and Phytophthora and the foliage diseases rust (Uromyces) and clover scorch (Kabatiella).

One approach to combating diseases is to breed resistant cultivars. However, prior to this project, little was known about the genetics and diversity for resistance to the four most important diseases of subterranean clover; viz. the soil-borne root rot diseases caused by Pythium and Phytophthora and the foliage diseases rust (Uromyces) and clover scorch (Kabatiella). This project has identified many new host resistances as well as molecular markers closely linked to genes and QTLs controlling resistance.



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Discoveries

The phenotyping component of this project was particularly successful. There was wide expression of host resistances across the subterranean clover 124-diversity panel (core collection genotypes and cultivars) against soilborne diseases Phytophthora and Pythium damping-off and root rots and against the foliar diseases rust, clover scorch and powdery mildew (the latter from opportunistic field screening). Significant numbers of potentially new high level resistances were highlighted in these studies. These resistances could be exploited via conventional breeding methodologies but, for Phytophthora root disease there is now the opportunity to exploit the QTLs identified for rapid integration of these resistances into new cultivars of subterranean clover. The wide range in expression of host resistance was ideal for identifying relevant QTLs associated with resistance against this particular pathogen.

Until now little was known about the genetics and diversity for resistance to these four most important diseases of subterranean clover. This project identified molecular markers closely linked to genes and QTLs controlling resistance against Phytophthora root disease. Subterranean clover breeding programs can use these findings to simultaneously select genotypes with genes for this along with other desirable traits, including multiple disease resistances when combined with conventional breeding methodologies. This AgriFutures™ Pasture Seeds Program project has exploited these technologies to research disease resistance traits against these diseases, being particularly successful for Phytophthora root disease. The project has established the methodologies such that resistance traits against other major diseases can now be exploited. As these diseases currently severely limit seed production, this project has undertaken critical research that prior to this project had not been conducted.

This project has identified many new host resistances to these major diseases of subterranean clover and multiple disease resistances which can now be applied in subterranean clover breeding programs. This has been achieved by the following.

1. The subterranean clover diversity for resistance to clover scorch (seedling and adult resistance to both race 1 and race 2), rust, Pythium and Phytophthora, and also powdery mildew, was successfully conducted and has confirmed that a breeding solution for resistance to each disease was feasible.

2. The number of different genes or Quantitative Trait Loci (QTLs) that determine resistance to Phytophthora root disease were successfully determined; this will enable future 'pyramiding' different resistance genes to increase resistance levels against this and other pathogens.

3. Potential parents with likely new disease resistances were identified, enabling introduction of new resistance genes into subterranean clover crossing and breeding programs.

4. The discovery of molecular markers closely linked to genes or QTLs for disease resistance against Phytophthora root disease, means these can now be used in breeding programs for marker-assisted selection of more disease resistant cultivars in the future; i.e., they can be used immediately for disease resistance against Phytophthora root disease and as a platform against other major soil-borne and foliar diseases.



Example of root rot susceptible plant



Example of rust resistant subclover (LHS) vs. rust susceptible clover (RHA)

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Outcomes

This study will provide evidence to assist breeding subterranean clover cultivars with new and multiple resistances to important foliage and root rot diseases in an efficient and timely manner. For Phytophthora damping off and root disease, it has also allowed identification of genes with small additive effects that provide a level of durable 'field' resistance, in addition to major genes. It is now possible to combine different, complementary genes for resistance to different races of Phytophthora, and application to each of the other diseases will soon follow, into the same genotype, along with genes for other desirable traits. The findings of this project also support breeding healthy seed production stands with reliable high seedling densities that require less fungicides and herbicides and produce higher seed yields. Longer-term these findings will support more sustainable legume-dominant grazing pastures that produce higher biomass and result in higher carrying capacities and animal production for the grazing-based animal industries across southern Australia.



Screening clover collection for Kabatiella resistance

Recommendations

The findings from this project have the potential to benefit all public and private breeding programs, with an interest in breeding subterranean clover across Australia, who will now have the freely available information on the new resistances, the genetic diversity and molecular makers.

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AgriFutures Australia Project No.: PRJ-009839
AgriFutures Australia Publication No.: 19-015

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