

The Identification and Development of Sunflower Germplasm with Resistance to *Alternaria* Blight

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Certification

I certify that the substance of this thesis has not already been submitted for any degree and is not being currently submitted for any other degree.

I certify that the assistance received in preparing this thesis and all other sources used, have been acknowledged in this thesis.



Abstract

The purpose of this study was to develop a system for identifying sunflower germplasm with resistance to *Alternaria* blight, which is caused by the necrotrophic fungus, *Alternaria helianthi*. Field and greenhouse screening procedures were studied, so that a complementary system could be developed. Components of resistance measured in the greenhouse were tested for their correlation with epidemic parameters obtained from field experiments.

The following procedures are recommended to screen sunflower lines for their resistance to *alternaria* blight under greenhouse conditions. The first or second pair of leaves of seedling plants at the V8 growth stage were inoculated using inoculum grown on sunflower leaf extract agar for 5-10 days. Approximately 30 spores were applied to each leaf. Inoculated plants were misted and subjected to a dew period of 48h inside a sealed plastic tent. A dew period temperature of 26/26°C night/day and a post-dew period temperature similar to the average temperature experienced under local growing conditions should be applied. All lesions were measured 7 days after inoculation and lesion size (area mm²) was calculated. The lesion size of lines being tested was expressed as a proportion of the mean lesion size of a susceptible standard included in each screening experiment. The susceptible line B89 was used as a standard line in all the screening experiments described in this study. Infection frequency of each line was expressed as a proportion of the infection frequency of the susceptible standard and was used in conjunction with mean lesion size to assess lines for resistance.

Bacteria found contaminating cultures of *A. helianthi* inhibited the germination of conidia, sporulation of cultures and the growth of germ-tubes and mycelium. Germ-tube swelling causing vesicle formation, excessive germ-tube branching and lysis of germ-tubes, were observed in bioassays using bacterial isolates obtained from healthy and

diseased sunflower leaves. Some bacteria appeared to be endoparasitic, persisting inside the lumina of conidia and causing erosion of the conidium wall which resulted in the destruction of conidial cells. The decrease in germination and infectivity of ageing conidia and the attenuation of ageing cultures of *A. helianthi* was attributed to the presence of antagonistic bacteria.

Sources of resistance to *A. helianthi* were not available at the time this research began. Therefore, locally developed inbred restorer lines (F_4) were accessed from a public breeding program and screened for resistance to *A. helianthi* in the field using a generated epidemic. Of the 37 lines evaluated, 32 had less disease than the susceptible line B89. Twelve lines had approximately half the amount of disease of B89 and 7 lines had less than one third of the disease found on B89. Variation for disease reaction within lines was high. Although no lines were immune, plants with very low levels of disease were observed in many of the lines. Single plant selections were selfed. Selections from eighteen lines ($P_1 - P_{18}$) were used in field and greenhouse experiments to evaluate methods of differentiating resistance. These lines were selected because they expressed disease reactions that ranged from highly resistant to susceptible.

Epidemic development was examined in a subset of ten lines ($P_1 - P_{10}$) using an artificially generated epidemic of *A. helianthi* that was replicated at two field sites. Experiments were designed to study epidemic development from a line source in plots surrounded by a buffer of forage sorghum that was included to reduce interplot interference. The epidemics that developed in each line were characterised by calculating parameters that described disease spread in either space or time or both space and time. Parameters were evaluated primarily for their usefulness in differentiating quantitative resistance (QR), however they were also examined to detect aspects of epidemic development which may help further in the characterisation of QR or be useful for future decisions of experimental design and disease assessment methods. Disease severity ratings (DSRs), area under the disease progress curves (audpcs) and volumes beneath the plot of disease progress in space and time (GVs) were good indicators of QR, while apparent infection rates (r),

disease gradients (b) and velocities of spread (v) were limited in their ability to differentiate QR. Three-dimensional surface plots of disease progress in both space and time allowed epidemic parameters to be viewed simultaneously. Inferences about the interrelationships between epidemic parameters could be drawn from these surface plots.

Allen (1981) proposed that anthesis was the critical point for disease assessment. In a breeding program, this would mean that large numbers of plants would need to have their flowers covered to prevent outcrossing prior to selection. This imposes constraints on time and labour. In this study, the DSRs taken prior to flowering were found to be well correlated with DSRs taken at flowering and post-flowering. Therefore, selection could be carried out prior to flowering and only resistant plants covered to allow controlled pollination. Thus, much time and effort was saved.

Disease assessment in a mature sunflower crop is an arduous task, particularly if the lowest leaves are used for assessment. If disease levels in the upper parts of plants could be used for disease assessment, then disease assessment could be made easier. However, the DSRs obtained for leaves in the middle and upper plant positions were poorly correlated with the DSRs of lower leaves and therefore could not be used for evaluating resistance.

Ten selected restorer lines (R-lines) were test-crossed with A89 (A-line) to produce F_1 hybrids that were evaluated in the field for resistance to *A. helianthi*. Two of the ten R-lines were selected for further evaluation based on the performance of these hybrids. Five commercial A-lines and the public line A89 were crossed with two restorer lines (R_1 and R_2), to produce twelve F_1 hybrids. These hybrids, their parental lines and three commercial hybrids were exposed to generated epidemics of *A. helianthi* at two field sites. Area under the disease progress curves (audpcs) were calculated for each line, from disease severity ratings (DSRs) taken from budding to late flowering. The commercial A-lines were as susceptible to *A. helianthi* as the susceptible line A89. R_1 and R_2 had high levels of resistance. Generally, the F_1 hybrids had much smaller audpcs than their

midparent estimates, indicating a high degree of dominance for genes controlling resistance in the resistant parents R_1 and R_2 . Overall, the F_1 hybrids had the same resistance to *A. helianthi* as the commercial hybrids.

Eighteen sunflower lines (P_1 – P_{18}) were inoculated with conidia of *Alternaria helianthi* under controlled conditions and components of QR, (spore production, incubation period, infection frequency and mean lesion size) were measured. The disease severity ratings (DSRs) of lines P_1 – P_{14} were measured in the field in 1994 and 1995, using a generated epidemic. The DSRs of the lines varied from highly susceptible to highly resistant. Spearman's ranking of the DSRs was highly correlated ($R = 0.9$) for both years. The rankings of lines by components of QR measured under controlled conditions were poorly correlated with the rankings of lines by DSRs. However, the linear regression of components with DSRs showed that mean lesion size was highly correlated ($R = 0.74$) and infection frequency was moderately correlated ($R = 0.58$) with the DSRs observed over the two years. Infection frequency was also well correlated ($R = 0.75$) with mean lesion size. Spore production and incubation period were poorly correlated with the DSRs for both years. An index based on infection frequency and mean lesion size gave a better correlation with the DSRs determined in 1995 than either component alone. However, in 1994 the index was not as well correlated with the DSRs as mean lesion size alone.

Mean lesion size and infection frequency were determined under controlled conditions, for twenty-three sunflower lines, comprising six parental lines and their F_1 hybrids and three commercial cultivars. The area under the disease progress curves (audpc) of the same lines were previously determined at two field sites (Chapter 6). Both Spearman's ranking and linear regression analysis showed that on average, mean lesion size was highly correlated and infection frequency was moderately correlated with the audpc. There was also a high correlation for the audpc between field sites.

It is recommended that mean lesion size, determined from seedling plants 7-9 days after inoculation could be used to select for resistance to *A.helianthi* in the greenhouse. Infection frequency could also be used as a predictor of resistance, but only in conjunction with mean lesion size. In the field, disease severity ratings (DSRs), area under the disease progress curves (audpcs) or volumes (GVs) below the surface plot of disease progress in space and time, can be used to evaluate resistance to *A. helianthi* .

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Table of Contents

THE IDENTIFICATION AND DEVELOPMENT OF SUNFLOWER GERMPLASM WITH RESISTANCE TO ALTERNARIA BLIGHT.....	I
CERTIFICATION.....	II
ABSTRACT.....	III
ACKNOWLEDGEMENTS	VIII
TABLE OF CONTENTS	IX
CHAPTER 1.....	1
GENERAL INTRODUCTION	1
1.1 <i>Sunflower Production in Australia</i>	1
1.2 <i>The Host : Helianthus</i>	4
1.2.1 <i>Origins and Taxonomy</i>	4
1.2.2 <i>Disease and Disease Resistance</i>	5
1.3 <i>The Pathogen</i>	7
1.3.1 <i>Origins and Distribution</i>	7
1.3.2 <i>Taxonomy and Morphology</i>	8
1.3.3 <i>Biology</i>	9
(i) <i>Disease symptoms</i>	9
(ii) <i>The Infection Process</i>	11
(iii) <i>Toxin Production</i>	12
(iv) <i>Dispersal of A. helianthi</i>	14
(v) <i>Survival of A. helianthi</i>	15
1.4 <i>Resistance to A. helianthi in Helianthus</i>	16
1.5 <i>Economic Importance and Control</i>	18
1.6 <i>Objectives of this Study</i>	19
CHAPTER 2.....	22
GENERAL MATERIALS AND METHODS	22
2.1 <i>Collection of Isolates of A. helianthi</i>	22
2.2 <i>Culture and Storage of Isolates of A. helianthi</i>	22
2.3 <i>Growth of Sunflower Plants</i>	23
2.4 <i>Production and Preparation of Inoculum</i>	23
2.4.1 <i>Conditions for Culturing A. helianthi</i>	23
2.4.2 <i>Preparation of Inoculum</i>	24
(i) <i>Single spore inoculum</i>	24
(ii) <i>Spore suspension</i>	24
2.5 <i>Inoculation Procedures</i>	25
2.5.1 <i>Single spore inoculum</i>	25
2.5.2 <i>Spray inoculation</i>	25
2.5.3 <i>Incubation of Inoculated Plants</i>	25
2.6 <i>Disease Assessment Methods</i>	26
2.7 <i>Statistical Analyses</i>	28

CHAPTER 3.....	29
DEVELOPMENT OF A GREENHOUSE ASSAY TO SCREEN SUNFLOWER FOR RESISTANCE TO <i>ALTERNARIA HELIANTHI</i>	29
<i>Summary</i>	29
3.1 <i>Introduction</i>	29
3.2 <i>Materials and Methods</i>	34
3.2.1 Statistical Analyses of Data.....	34
3.2.2 Experiments to Standardise the Production of Inoculum.....	35
(i) Determining the effect of culture media on mycelial growth, sporulation and conidial infectivity.....	35
(ii) Determining the germination and infectivity of conidia obtained from sporulation bands of different age.....	36
(iii) Determining the effect of spore morphology and germination characteristics on infectivity of conidia.....	37
(iv) Determining the effect of successive subculturing on the infectivity of conidia.....	38
(v) Examination of bacteria contaminating cultures of <i>A. helianthi</i>	39
(vi) Determining the variation in pathogenicity among isolates.....	40
3.2.3 Experiments to Establish Optimal Host and Environmental Conditions for Infection.....	40
(i) Determining the effect of leaf position on lesion size.....	40
(ii) Determining the effect of the method used to maintain leaf wetness on lesion size.....	41
(iii) Determining the effect of dew period temperature regimes and duration of dew period on infection.....	41
(iv) Determining the effect of post-dew period temperature regimes on lesion size.....	42
(v) Determining the effect of plant density on infection.....	42
(vi) Determining the effect of inoculum dose on infection of susceptible and resistant lines.....	42
3.3 <i>Results</i>	42
3.3.1 Experiments to Standardise the Production of Inoculum.....	43
(i) Effect of culture media on mycelial growth, sporulation and conidial infectivity.....	43
(ii) Germination and infectivity of conidia obtained from sporulation bands of different age.....	44
(iii) Effect of spore morphology and germination characteristics on infectivity of conidia.....	45
(iv) Effect of successive subculturing on infectivity of conidia.....	46
(v) Inhibition of <i>A. helianthi</i> caused by bacteria isolated from sunflower leaves and <i>A. helianthi</i> cultures.....	46
(vi) Variation in pathogenicity among isolates.....	50
3.3.2 Experiments to Establish Host and Environmental Conditions.....	50
(i) Effect of leaf position on lesion size.....	50
(ii) Effect of the method used to maintain leaf wetness on lesion size.....	51
(iii) Effect of dew period temperature regimes and duration of dew period on infection.....	51
(iv) Effect of post dew period temperature on lesion size.....	54
(v) Effect of plant density on infection.....	54
(vi) Effect of inoculum dose on infection of susceptible and resistant lines.....	54
3.4 <i>Discussion</i>	55
CHAPTER 4.....	64
INITIAL SELECTION OF RESISTANT GERmplasm.....	64
<i>Summary</i>	64
4.1 <i>Introduction</i>	64
4.2 <i>Materials and Methods</i>	65
4.3 <i>Results</i>	67
4.4 <i>Discussion</i>	69
CHAPTER 5.....	72
SPATIAL AND TEMPORAL DEVELOPMENT OF <i>ALTERNARIA</i> BLIGHT EPIDEMICS IN SELECTED SUNFLOWER LINES.....	72
<i>Summary</i>	72
5.1 <i>Introduction</i>	72
5.3 <i>Materials and Methods</i>	78
5.3.1 Field trial sites and trial design.....	78
5.3.2 Inoculation of plants and assessment of disease.....	81
5.3.3 Data Analysis.....	83

5.4 Results.....	83
5.4.1 Rainfall and temperature data.....	83
5.4.2 Plant phenologies throughout the rating period.....	85
5.4.3 Disease progress in time.....	85
(i) Disease Severity.....	85
(ii) Disease progress curves.....	87
(iii) Apparent infection rate.....	90
(iv) Area under the disease progress curve (audpc).....	92
5.4.4 Disease progress in space.....	93
(i) Disease gradients.....	93
5.4.5 Disease progress in space and time.....	94
(i) Surface response maps.....	94
(ii) Velocity of disease spread and grid volumes.....	98
5.4.6 Correlations between epidemic parameters.....	99
5.4.7 Determining the relationship between DSRs for different leaf positions.....	102
5.5 Discussion.....	103
CHAPTER 6.....	112
EVALUATION OF RESISTANT RESTORER LINES IN HYBRID COMBINATIONS.....	112
Summary.....	112
6.1 Introduction.....	112
6.2 Materials and Methods.....	116
6.2.1 Preliminary selection of R-lines.....	116
6.2.2 Hybrid production and field trial design.....	117
6.2.3 Analysis of data.....	119
6.3 Results.....	119
6.3.1 Audpcs of parental lines and F ₁ hybrids.....	119
6.3.2 Differences between F ₁ hybrids and midparent audpcs.....	121
6.3.3 Combined analysis of Variance for Sites 1 and 2.....	122
6.3.4 Thousand grain weights and oil contents of hybrids.....	122
6.4 Discussion.....	123
CHAPTER 7.....	126
CORRELATION BETWEEN GREENHOUSE AND FIELD RATINGS OF RESISTANCE TO A. HELIANTHI.....	126
Summary.....	126
7.1 Introduction.....	126
7.2 Materials and Methods.....	128
7.2.1 Growth, inoculation and incubation of plants.....	128
7.2.2 Genotypes.....	128
7.2.3 Design of Greenhouse Experiments.....	130
(i) Experiments involving lines P ₁ -P ₁₈	130
(ii) Experiments involving R-lines, A-lines and their F ₁ hybrids.....	130
7.2.4 Measuring Components of Quantitative Resistance.....	131
7.2.5 Field Screening of Sunflower Lines.....	133
(i) Experiments involving lines P ₁ -P ₁₈	133
(ii) Experiments involving R-lines, A-lines and their F ₁ hybrids.....	133
7.2.6 Statistical Analysis.....	133
(i) Experiments involving lines P ₁ -P ₁₈	133
(ii) Experiments involving R-lines, A-lines and their F ₁ hybrids.....	134
7.3 Results.....	134
7.3.1 Uniformity of experimental conditions.....	134
7.3.2 Components of resistance and field severity of alternaria blight.....	135
(i) Lines P ₁ -P ₁₈	135
(ii) R-lines, A-lines and their F ₁ hybrids.....	137
7.3.3 Correlations between components of resistance measured in the greenhouse and resistance measured in the field.....	139
(i) Lines P ₁ -P ₁₈	139

(ii) R-lines, A-lines and their F ₁ hybrids.....	140
6.4 Discussion.....	141
CHAPTER 8.....	148
GENERAL DISCUSSION.....	148
<i>Future Research</i>	158
REFERENCES	160
APPENDIX I.....	180
RECIPES OF MEDIA USED IN THIS STUDY.....	180
APPENDIX II.....	183
A TECHNIQUE FOR ESTIMATING THE NUMBER OF MICROORGANISMS IN A SAMPLE.....	183
APPENDIX III	185
A PICTORIAL KEY FOR ASSESSING THE PROPORTION OF LEAF AREA INFECTED WITH <i>A. HELLANTHI</i>	185
APPENDIX IV	187
PUBLICATIONS ARISING FROM THE RESEARCH REPORTED IN THIS THESIS.....	187