

# Chapter 8

## **General Discussion**

The overall aim of the work reported in this thesis, was to develop a reliable system for screening sunflower for resistance to *A. helianthi*. A substantial part of achieving this involved the development of a standard screening procedure that could be used in the greenhouse. This greenhouse assay was intended to supplement field screening, by confirming resistance reactions, increasing the speed of selection and reducing the number of lines that had to be screened in the field. The greenhouse assay was then used to measure components of resistance in a number of lines that ranged in their susceptibility to *A. helianthi*. In conjunction with this, epidemic parameters for the same lines were examined in the field and analysed to determine their ability to differentiate levels of QR. Components of QR measured in the greenhouse were then correlated with parameters of resistance measured in the field, to determine which components and epidemic parameters could be used for selection purposes. Finally, inbred restorer lines that were selected using both field and greenhouse experiments, were evaluated in hybrid combinations using the greenhouse assay and field experiments.

In developing a system for selecting for resistance to *A. helianthi*, consideration was given to the basic concepts that characterise quantitative traits. In many host-pathogen systems, it is more difficult to screen and select for quantitative resistance (QR) than it is for qualitative resistance (Parlevliet, 1986). The main reason for this is that QR is generally controlled by many genes, whose small, similar and supplementary effects on the expression of the phenotype give rise to continuous variation (Mather and Jinks, 1977).

Breeding for QR requires that the many genes that contribute to resistance are accumulated in a single genotype. The segregation of a large number of genes whose individual effect on the phenotype may not be distinguishable, make this task extremely difficult. In addition, other factors such as environment, nutrition and age of the host, inoculum load and any factor that affects these, add to the amount of phenotypic variation expressed in a population of plants. The variation caused by these non-genetic factors is therefore, non-heritable. In a breeding program, these factors mask genetic effects and reduce the reliability of selection, such that each cycle of selection will have a component of 'genetic drag' due to the presence of undesirable genotypes (Falconer, 1989). Progress in this system will be proportional to the level of 'drag' and the heritability of the characters being selected. Since heritability is a genetic fixture, screening procedures must focus on reducing the level of 'drag' by improving the accuracy of selection. The extent to which this can be done depends largely on the host-pathogen system and the genetic basis of resistance.

In developing the greenhouse assay (Chapter 3), procedures and techniques were used that would help reduce and control non-genetic variation. It must be accepted, that variation arising from experimental procedures or environmental conditions cannot be eliminated and at best, may only be reduced and controlled to a relatively consistent level. Experiments were conducted to establish optimum environmental conditions, such as the temperature used for inoculation and incubation, the duration of the dew period used for inoculation and incubation and methods of maintaining leaf wetness during the post-inoculation dew period. Inoculation procedures were strictly controlled to ensure that inoculum quality was standardised and that plants were inoculated with a known spore concentration. Inoculum was directed at leaves of a specific age on host plants at a particular growth stage. Experimental designs aimed at minimising variation were recommended and methods for assessing resistance were established.

Among researchers who have screened sunflower for resistance to *A. helianthi* in the greenhouse (Morris and Yang, 1983; Lipps and Herr, 1986; Block, 1990), few gave any

consideration to minimising the non-heritable portion of variation. Since the expression of resistance to *A. helianthi* is quantitative, it must follow that it can only be measured by using quantitative procedures, yet few researchers, if any, have applied quantitative methods when screening sunflower for resistance to *A. helianthi*. Such procedures require that the factors contributing to the disease phenotype are equal for all plants or lines being evaluated. Clearly, equal application of these factors cannot be attained, but steps can be taken to minimise deviations. The work described in Chapter 3 has gone some way towards meeting these requirements. A basic greenhouse assay was recommended (section 3.4) and used in further experiments to measure components of QR.

Selection for QR is usually conducted in the field. This is because the correlations between greenhouse and field reactions are often poor and inconsistent (Simmonds, 1991). The reason for this may be partly due to the complexity of some host-pathogen systems, but may also be due to the use of inadequate greenhouse screening procedures (Rotem, 1988a). Verification of the greenhouse assay was dependent on 'feedback' from field data. Therefore, field and greenhouse screening should ideally, have proceeded together, but seasonal restrictions and the failure of disease development hindered the rate at which field experiments could proceed. The severe five-year drought that was experienced throughout eastern Australia while this work was being conducted, constrained the development of field epidemics of *A. helianthi*. In some field experiments, it was only luck and perseverance that resulted in disease development at all (see Chapter 5). Hence, development of the greenhouse assay was forced to proceed somewhat independently of field screening at first, as germplasm had not been sufficiently characterised in the field.

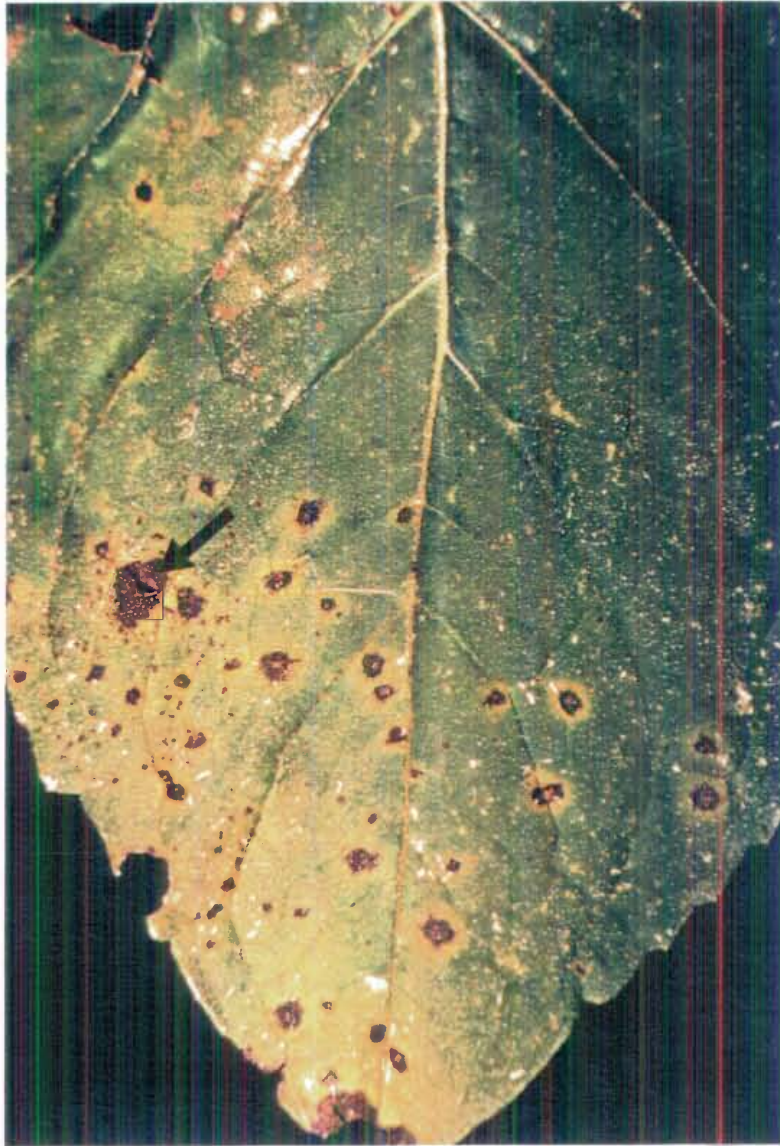
Screening for QR in the field must contend with a number of problems that generate variation which is not easily controlled. Interplot interference, influences of plant habit on micro-environment, method and timing of disease assessment, differences in maturity between various lines, disease pressure, type of epidemic and orientation of plants or plant parts to prevailing winds are all factors that generate variation in experimental plots.

Experimental procedures can be adjusted to account for some of the effects of these factors and various analytical methods can be employed that minimise their impact on the selection process, but overall, control of this type of variation is limited.

In most field experiments, designs that specifically minimise the impact of interplot interference were not used. The reason for this is that the designs that lessen interference between plots require a great deal of space. This places logistical demands on management of the site and limits the number of lines that can be included in a single experiment. The use of flanking spreader rows of the susceptible line B89 (Chapters 4, 7) attempted to provide uniform disease levels and while this may have lessened interference, it might not have prevented it entirely.

The experimental design that was described in Chapter 5 did however, attempt to reduce the amount of interference between plots. Observations of the epidemics that developed in each plot suggested that the level of interference might not be large, because allo-infection of adjacent rows appeared to be quite low despite high levels of infection at the disease focus. Auto-infection appeared to contribute most to rapid epidemic development and infection patterns on leaves tended to support this contention. These patterns indicated that under optimal weather conditions, many new infections occur as local lesions, which develop when spores from a sporulating lesion are washed across the leaf surface during periods of high moisture. Lesions tend to concentrate around an existing 'parent' lesion and towards the tips of leaves where moisture levels are high due to leaf orientation (Figure 8.1). Under optimal weather conditions, lesions expand, coalesce and give rise to successive cycles of local infection. Blighting is probably caused by infections resulting from extremely high numbers of spores concentrated in a small area around lesions. It is therefore possible that only a small proportion of spores from any given lesion contribute to allo-infection, but a much larger proportion are involved in auto-infection.





*Figure 8.1. Patterns of local infection appear as new infections surrounding a mature lesion of *A. helianthi* (arrowed). Lesions tend to concentrate towards the tip of the leaf where moisture levels are high.*

Some preliminary spore-trapping experiments (not reported in this study) indicated that spore dispersal during the early epidemic phase and during periods of wet weather were extremely low. Also, attempts to induce sporulation on attached leaves in the laboratory (Chapter 7) and in the field (not reported) indicated that sporulation is not simply a function of temperature and leaf wetness, but may also require other host or pathogen related signals. Sporulation occurs easily on detached tissue, such as sunflower residues (Jeffrey *et al.*, 1984) and senesced leaves, particularly those that have fallen from plants

and lie on moist soil. It may be that air-borne spore dispersal and allo-infection are greatest at the late stages of the epidemic when large amounts of dead tissue contribute to the available inoculum load. Interference would be greatest under these conditions but, epidemics of this magnitude are not always experienced in experimental field plots. In this study, only one epidemic (Site1, Chapter 5) approached these proportions.

The timing and method of disease assessment are two factors over which there can be some control. Since susceptibility of sunflower to *A. helianthi* increases at anthesis, using this as the critical point for disease assessment (Allen, 1981) would seem to be logical. However, if plants are not assessed for resistance until flowering or post-flowering, then cross pollination would occur unless all plants were bagged prior to flowering. This imposes high demands on available resources, particularly where large plant populations are used. In studies conducted in Chapter 5, good correlations were found between disease severity ratings (DSRs) taken prior to flowering and those taken at and after flowering. If this were a general condition which applied also to other sources of germplasm and other epidemic patterns, then selection for resistance to *A. helianthi* could be carried out before flowering and only selected plants would have to be bagged for controlled pollination.

Estimation of disease severity using pictorial keys that contain a limited set of infection types is a common method of disease assessment. The pictorial key devised by Allen (1983c) contained few classes between 5% and 25 % leaf area infected. The key was modified so that more classes were represented in this range (Appendix III), however, it must be acknowledged that the key presented a poor guide for matching infection patterns. This is understandable when one considers the infinite number of patterns that lesions can form following successive cycles of infection. No key could realistically account for even a small percentage of these patterns. There is therefore considerable opportunity for inaccurate assessment of disease severity, particularly at very low levels of disease where the relative bias and imprecision is highest (Parker *et al.*, 1995). Disease in this range (< 25%) tends to be overestimated (Forbes and Jerger, 1987).

Providing that any bias is consistent, this factor would not pose a problem, but differences are likely to occur between researchers and even between years for the same researcher. The relatively high correlation obtained for estimates of DSR between years and sites in the experiments described in Chapters 5, 6 and 7 indicate that at least, disease estimations were consistent. However in Chapter 5, the flat disease gradients that were observed at very low levels of disease may have been due to the failure to accurately estimate very low levels of infection. Similarly, flat disease gradients were observed at low levels of disease caused by *Peronospora manshurica* (Naum.) Syd.ex Gaum. (Lim 1978) in soybean and *S. nodorum* in wheat (Jerger *et al.*, 1983), but no explanations were given for these observations. It is possible that they were due to inaccurate disease estimates. The use of relative rather than actual disease severity ratings may help overcome the problem of variation in disease assessment. Preliminary work using digital imaging to assess disease due to *A. helianthi* (Tucker, *et al.*, 1994) shows promise, particularly for greenhouse assessments. This system has the potential to measure disease quickly, accurately and consistently. Automation and portability of the imaging system will be of great benefit for field assessments.

A further problem encountered in disease assessment is that of distinguishing between necrosis due to disease and necrosis due to nutritional/physiological disorders and senescence. Certain genotypes are predisposed to physiological disorders resulting in tissue necrosis and necrotic lesions can occur on plant tissue as a result of nutrient deficiencies or natural senescence. The line ARpop// Rx677 (P<sub>17</sub>) developed necrotic lesions on leaves, as a result of a physiological disorder (Figure 2.1). Necrotic lesions surrounded by chlorotic halos can occur on leaves due to phosphorous deficiency (Figure 2.2).

Disease assessment can also be biased if differences in susceptibility among sunflower lines is caused by differences in maturity. Cultivars that exhibit early maturity relative to other cultivars are often highly susceptible (Wolfe and Gessler, 1992). For example, no 'early' cultivars of potato with QR to late blight have been observed (Parlevliet, 1992). It



is likely that the rapid increase in disease severity for the line Rpop ( $P_{18}$ ) late in the epidemic (Tables 5.2 and 5.7), was due to early maturity. Similarly, the line 10008-3-3-5 ( $P_9$ ) was late to mature, which may account for its high level of resistance. The problem of different maturities is difficult to resolve in field experiments. One solution might be to only test lines of similar maturity together, but this may create some logistical problems. Moreover, differences in maturity between lines may not be sufficiently known during the early generations of a breeding program.

The epidemics examined in this study (Chapter 5) were probably typical of *A. helianthi* epidemics experienced in Australia. They were characterised by a long lag phase followed by a rapid increase in disease. This pattern may reflect the relationship between age-induced susceptibility and weather patterns in Australia. The increase in disease during the early growth stages of the crop is dependent on successive periods of rainfall. The intensity of an epidemic resulting from an extended rainfall event at anthesis depends on the length of the wet period and the level of disease that developed prior to anthesis. In Australia, severe epidemics of *A. helianthi* occur infrequently, perhaps once in every five years. In India however, *A. helianthi* epidemics occur more frequently due to the regular periods of rainfall experienced during the monsoon season (Borkar and Patil, 1992). Epidemics can develop early in the life of a crop, causing seedling death and/or severe defoliation throughout the life of the crop, particularly at anthesis. Whether the lines selected under Australian conditions would maintain their resistance when subjected to the kinds of conditions experienced in India is unknown. Experimental evidence suggests that there is an infection threshold above which resistance fails to be effective (Chapter 3). It may be that the levels of resistance required to withstand the kinds of environmental conditions experienced in India are unattainable by conventional breeding methods. Application of the methods described in this thesis, to conditions experienced in India, might enable more efficient selection of resistant germplasm.

Other factors that can bias field assessments include plant density or plant architecture which can modify the micro-climate close to the infection court (Burdon, 1982; Carson,



1986). Plant densities higher than those normally used for the commercial production of sunflower in Australia were used in all field experiments. It was hoped that this would increase the chances of epidemic development by creating a highly favourable micro-environment for disease development. However, equal plant densities does not mean equal micro-environmental effects, because of differences in plant architecture (leaf number, size and orientation; plant stature) between lines. For example, lines 10020.11.1.18 (P<sub>1</sub>) and Rx 677 (P<sub>17</sub>) exhibited 'open' plant habits and had good levels of resistance, but it is difficult to separate resistance due to physical attributes that diminish micro-environmental effects and resistance due to post-infection defence mechanisms. Greenhouse screening using seedling plants fails to differentiate resistance due to these factors. For example, based on mean lesion size, the line Rx677 was rated as susceptible to *A. helianthi* in greenhouse screenings (Tables 7.3 and 7.4, Chapter 7) but was resistant in the field.

One of the major difficulties in evaluating QR is that the phenotypic expression of resistance is often affected by interactions between genotype and the environment. In order to take account of the average effect of this interaction, lines must be evaluated in different environments (locations) over time. In this study, it was expected that the impact of environment on the expression of QR could be determined from the degree of correlation for disease reaction, between lines tested at different locations and /or times. This was based on the assumption that environment and growing conditions at the two sites were inherently different. Using DSRs and/or audpcs, Spearman's' rank correlations gave generally good coefficients of correlation for lines tested at different sites in the same year (Chapters 5 and 6) and lines tested at the same site in different years (Chapter 7). This suggests that the evaluation of resistance was consistent and reliable under the epidemic conditions experienced at the respective locations and in different years.

Epidemic parameters that were well correlated with disease severity ratings (DSRs) were considered to be the best indicators of resistance in the field (Chapter 5). The area under the disease progress curve (audpc) and the volume (GV) under the three-dimensional surface

plot of disease progress in space and time, were well correlated with DSRs. The lack of correlation between DSR and apparent infection rates ( $r$ ), disease gradients ( $b$ ) and velocities of spread ( $v$ ) may indicate that these parameters are inadequate for differentiating QR among sunflower lines, but are useful for studying epidemic patterns in individual lines. Three-dimensional surface plots of disease progress in space and time provided a rapid way of visualising epidemic parameters, DSR,  $r$ , and  $b$  together. Sunflower lines could be easily compared using the surface plots because the relationships between epidemic parameters were easily evaluated.

There was good correlation between mean lesion size (MLS) measured in the greenhouse and DSRs, audpcs and GVs measured in the field. MLS is a direct measure of the rate at which *A. helianthi* colonises tissue. It correlates well with measures of resistance in the field because disease severity ratings (DSRs) are a function of infection frequency and lesion size. Infection frequency was not as well correlated with DSR and therefore is not a reliable indicator of resistance. Nonetheless, it could be used in conjunction with MLS in a two-stage screening procedure where seedlings are initially selected according to their infection frequencies, then examined more closely using MLS. Other components of QR, incubation period and spore production were poorly correlated with DSRs. These components are more sensitive to environmental conditions and experimental techniques and consequently have high coefficients of variation (Rotem, 1992).

The cytoplasmic male sterile (*cms*) system used to produce sunflower hybrids further complicates the process of breeding for QR, because commercial hybrids are produced by crossing two or more inbred parents. The resistance phenotype of the resulting F<sub>1</sub> hybrid can be predicted, more or less, from the midparental pattern of inheritance. This pattern suggests that the F<sub>1</sub> will have a phenotypic value equal to the mean of the parents. However, deviations from the midparent value, (towards greater resistance or susceptibility) can occur, because we do not know how the genes affecting the character combine to produce their effects. Studies could be conducted to determine heritabilities and combining abilities, but often, these merely confirm the adage, 'breed from the best'.

Furthermore, 'It does not pay a breeder to examine a genetical situation in detail, if he has to wait a long time for the answers' (Gilbert, 1989). The testing of  $F_1$  hybrids is therefore, the most important phase of a breeding program for commercial sunflower breeders in Australia and is the final test of the value of inbred lines.  $F_1$  phenotypic values that are less than the midparent value indicate a level of dominance. The  $F_1$  hybrids made from resistant restorer lines and susceptible female lines (Chapter 6) were more resistant than suggested by their midparent values, indicating a high level of dominance among the gene(s) controlling resistance. More of the lines selected and developed in this study need to be tested in this way.

In this study, a system for identifying sunflower for resistance to *A. helianthi* was established. This system could potentially improve the accuracy and speed of selection of resistant germplasm. However, it remains constrained in some ways by the many variables that affect QR and which, when acting collectively and at different intensities, force selection errors. It was hoped that the procedures developed in this study would help reduce these errors, but it is acknowledged that they will not be eliminated. Nevertheless, the procedures developed here form the basic framework from which further research can proceed. For example, resistant germplasm identified using this system can be used to improve existing techniques or help to develop new techniques, such as those described below.

### **Future Research**

- (i) Further refine the greenhouse screening procedure by developing techniques for mass inoculation using large numbers of plants at a younger growth stage.
  
- (ii) Investigate alternative methods for identifying resistant germplasm. For example, a study of host defence and the mechanisms of resistance could be used to develop assays using defence-related compounds as markers for selection. Similarly, assays could be developed pending an investigation of the relationship between sensitivity to phytotoxins



produced by *A. helianthi* and resistance to infection. Likewise, sensitivity to ethylene could be investigated as a method of identifying resistant germplasm

(iii) Resistance to *A. helianthi* is known to occur among various species of *Helianthus* as well as related genera, *Tithonia* and *Viguiera*. Interspecific and intergeneric hybridisation provides a difficult, but feasible breeding option to improve levels of resistance in *H. annuus*.

(iv) It is likely that the levels of resistance attained through conventional breeding methods will be inadequate under some epidemic conditions. It may be possible to increase resistance by transforming resistant plants with genes that encode for specific antifungal proteins (AFPs). Novel AFPs have been identified and shown to have bioactivity against *A. helianthi* (Kong *et al.*, 1996).

(v) The genetics of resistance could be studied using germplasm identified with this screening technique. Heritability, combining ability estimates and the nature of gene action may be useful for deciding further breeding strategies.

(vi) Digital image analysis could be used to provide faster, more accurate estimates of disease in both the greenhouse and the field.

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# Appendix I

## ***Recipes of media used in this study***

### **1. Potato-Dextrose Agar (PDA)**

Potato	200 g
Dextrose	20 g
Agar	17 g
Distilled Water	1000 mL

Add peeled and diced potato to 500 mL of distilled water; add agar to 500 mL of distilled water. Place both in a steamer for 1 hour. After steaming, strain potatoes with cheesecloth and add the liquid obtained to the agar. Add dextrose and bring volume to 1 litre. Autoclave at 120°C/138KPa for 20 minutes.

### **2. Potato-Carrot Agar (PCA)**

Potato	20 g
Carrot	20 g
Dextrose	17 g
Tap Water	1000 mL

Procedure is the same as that used to make PDA.

### **3. Sunflower Leaf Extract Agar (SLEA)**

Fresh Sunflower Leaves	100 g
Distilled Water	1000 mL
Agar	17 g

Place leaves in water and steam for 1 hour in a steamer. Pour off the liquid and add agar. Return to steamer until agar has melted. Autoclave as prescribed for PDA.

**4. Malt-Extract Agar (MEA)**

Malt Extract	20 g
Agar	17 g
Distilled Water	1000 mL

Place malt extract in water and steam until dissolved. Add agar and steam until melted. Autoclave as prescribed for PDA.

**5. Oatmeal Agar (OMA)**

Oatmeal	50 g
Agar	17 g
Distilled Water	1000 mL

Add oatmeal to water and steam for 1 hour. Strain through cheesecloth. Add agar and steam until dissolved. Autoclave as prescribed for PDA.

**6. Cornmeal Agar (CMA)**

Cornmeal Agar (Difco)	17 g
CaCO <sub>3</sub>	4 g
Distilled Water	1000 mL

Add cornmeal agar to water and steam until dissolved. Add CaCO<sub>3</sub> and stir until dissolved. Autoclave as prescribed for PDA.

**7. V-8 Juice Agar (V-8)**

Campbell's V-8 Juice	200 mL
Agar	17 g
Distilled Water	800 mL
CaCO <sub>3</sub>	

Add agar to water. Steam both V-8 juice and water/agar for 20 minutes or until the agar is dissolved. Add V-8 juice to water/agar and adjust the pH 6.0 with CaCO<sub>3</sub>. Autoclave as prescribed for PDA.

**8. Synthetic Media (SM) (after Islam and Maric, 1978)**

Mg SO <sub>4</sub> . 7 H <sub>2</sub> O	3 g
NH <sub>4</sub> Cl	3 g
KH <sub>2</sub> PO <sub>4</sub>	3 g
Fe Cl <sub>3</sub> . 6 H <sub>2</sub> O	0.24 mg
Zn Cl <sub>2</sub>	0.15 mg
H <sub>3</sub> BO <sub>3</sub>	0.06 mg
Cu Cl <sub>2</sub> . H <sub>2</sub> O	0.05 mg
Mn Cl <sub>2</sub> . 2 H <sub>2</sub> O	0.04 mg
Na Mo O <sub>4</sub> . 2 H <sub>2</sub> O	0.03 mg
Thiamine	0.1 g
Dextrose	20.0 g
Agar	17 g
Distilled Water	1000 mL

Add all ingredients to 1000 mL of water and place in a steamer until dissolved.  
Autoclave as prescribed for PDA.

## Appendix II

### ***A technique for estimating the number of microorganisms in a sample***

Most of us have at some time, been faced with the problem of estimating the the total population of some microorganism from a representative sample of the population. Such samples might contain bacteria, spores or sclerotia per unit volume of soil, or the number of spores produced per unit area of diseased tissue etc. Whatever they might be, population samples are often made into a suspension and counts of the organism are performed on subsamples or aliquots drawn from the main sample. An estimate of the total sample is thus derived. Obviously, as the number of microorganisms per sample increases, and as the size of the subsamples increase as a proportion of the total sample volume, the accuracy of the estimate also increases.

Sampling in this way is usually very time consuming and is often undertaken without knowing either the level of accuracy that is required or even expected of the technique that is employed. The following is a simple method which allows the operator to set the sampling requirements needed to attain a certain level of accuracy, thereby saving time and effort.

#### **Accuracy of an estimated total**

The following assumes that the organism is uniformly distributed throughout the sample. This assumption can be checked after the aliquots have been counted, and is referred to later.

**Example:** An aliquot representing  $p\%$  of the total sample contains  $r$  spores. Then an estimate of the total number  $N$  is:

$$N = 100 \times (r/p)$$

Then the standard deviation (SD) is:

$$SD(N) = 10/p \sqrt{r(100-p)}$$

and the percent SD is:

$$\% \text{ SD (N)} = 10 \sqrt{(100-p) / r}$$

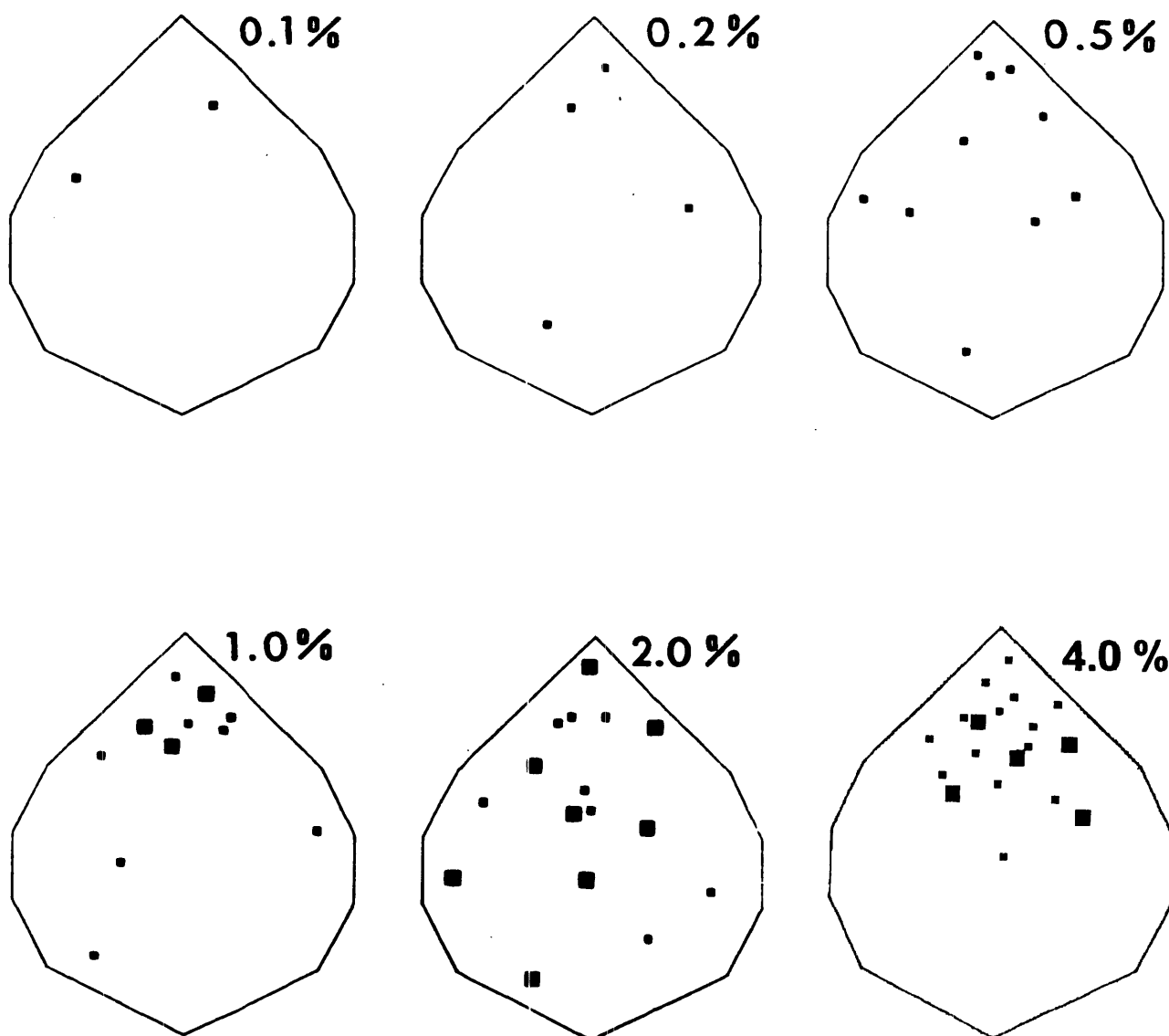
The criterion for accuracy is the % SD.

As an example, if 10 spores were found in a 1% sample,  $N = 1000$  and the SD is 320 or 32%. The true number will, 95 % of the time, lie within 2 SD of the estimate. ie.  $1000 \pm 640$ .

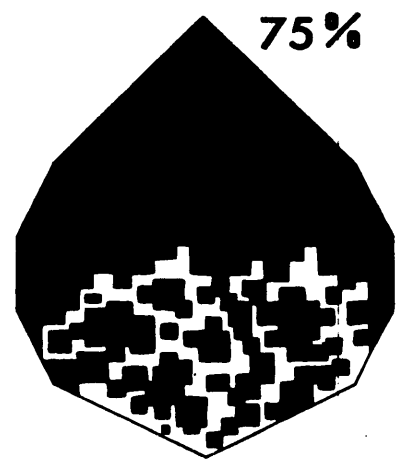
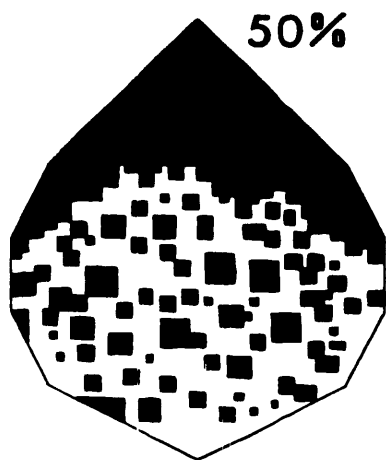
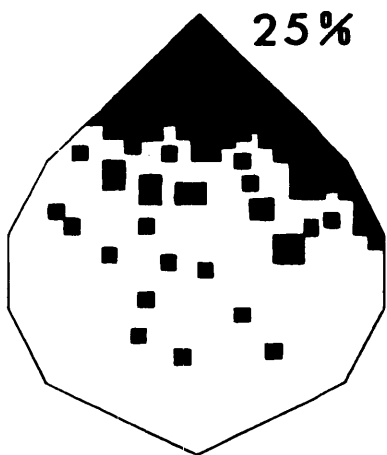
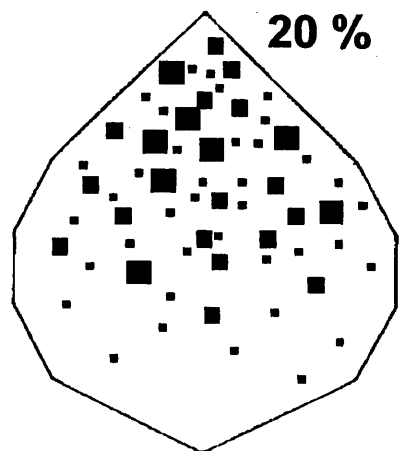
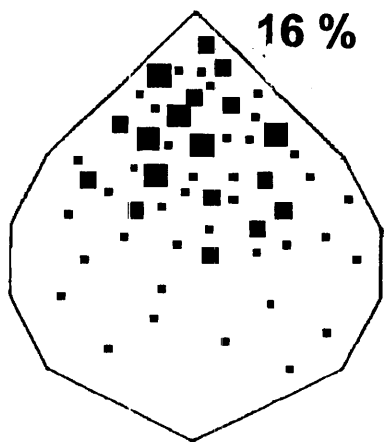
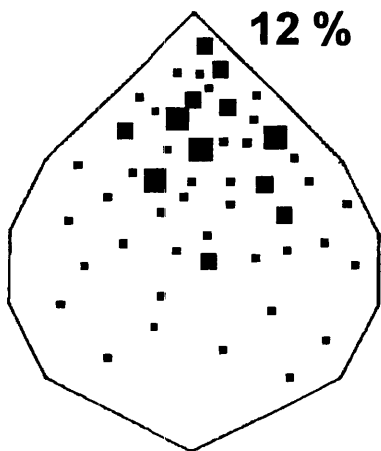
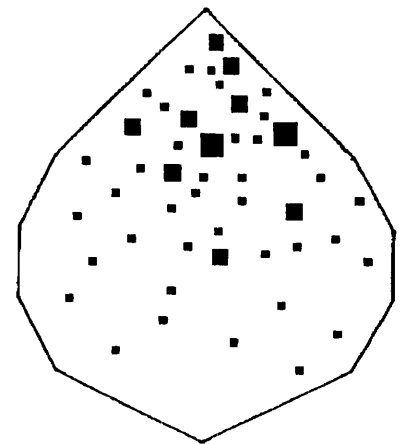
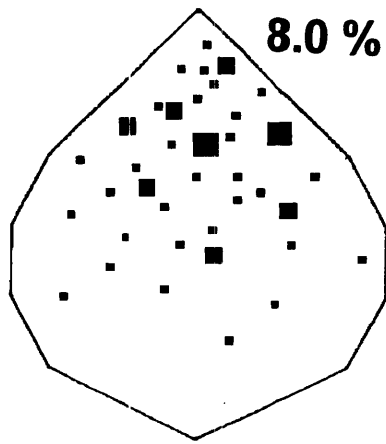
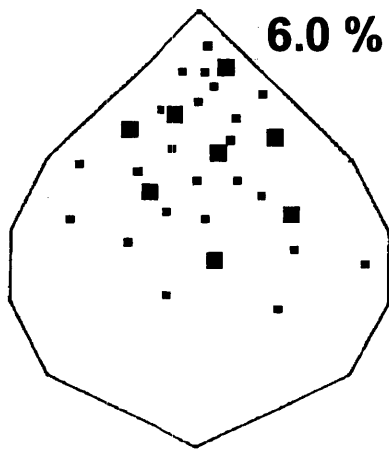
Thus, counting of aliquots should continue until a certain specified % SD is reached.

# Appendix III

***A pictorial key for assessing the proportion of leaf area infected with *A. helianthi* .***







## Appendix IV

### ***Publications arising from the research reported in this thesis.***

**Kong G A, Kochman J K, Brown J F. 1995.** A greenhouse assay for screening sunflower for resistance to *Alternaria helianthi*. *Annals of Applied Biology* **127**: 463-478.

**Kong, G A, Kochman, J K and Brown, J F. 1997.** Phylloplane bacteria antagonistic to the sunflower pathogen, *Alternaria helianthi*. *Australasian Plant Pathology* **26**: 85-87.

**Kong, G A, Kochman, J K and Brown, J F. 1997.** Components of quantitative resistance to *A. helianthi* in sunflower. *Annals of Applied Biology* **128**: In Press