Session VII
Epidemiology
Highlights of 15 years of research on ascochyta blight on pea in France: Epidemiology and impact of the disease on yield and yield components.

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Ascochyta blight is a serious disease affecting field peas and since the early '90s, we have conducted studies on the pathosystem Pisum sativum/Mycosphaerella pinodes. The plant, the pathogen and the environment were considered as essential to understand the epidemic development of the disease and the impact of the disease on plant functioning and yield.

**Epidemiology** Schoeny *et al.* (2007) developed a model to predict ascochyta blight onset in field peas based on calculations of weather-dependent daily infection values. Moreover, Moussart *et al.* (1998) had shown the role of seed infection in disease transmission. We have established the epidemiological conditions for disease epidemiology development (Roger *et al.*, 1999a; 1999b; Roger and Tivoli, 1996; Tivoli and Banniza, 2007). Disease severity on pods and stems was substantially reduced in a pea-cereal intercrop treatment compared to the pure pea crop treatment when the epidemic was moderate to severe (Schoeny *et al.*, 2009). Disease development depends on characteristics of the cultivars (Onfroy *et al.*, 1999, 2007). Moreover, Le May *et al.* (2009a, 2009b) compared the reaction of several winter and spring pea types. Schoeny *et al.* (2008) had investigated the effect of canopy architecture on splash dispersal of the asexual spores of the fungus in controlled conditions, using a rainfall simulator. All this knowledge in epidemiology was used in several programs of genetics for ascochyta blight resistance on pea (Prioul *et al.*, 2003; Tivoli *et al.*, 2006a; Onfroy *et al.*, 2007) or on the model plant Medicago truncatula (Tivoli *et al.*, 2006b; Moussart *et al.*, 2007).

**Overall effects of ascochyta blight on yield and yield components** The effect of the disease on yield and yield components was investigated by Tivoli *et al.* (1996). Moreover, disease affected the photosynthetic activity (Garry *et al.*, 1998a) and the remobilisation of carbon and nitrogen (Garry *et al.*, 1996; Garry *et al.*, 1998b; Béasse *et al.*, 1999); the number of seeds per stem and mean seed weight were significantly decreased.

**Effect of plant growth stage and plant organs infected on yield** The impact of the disease on yield is not fixed and depends on growth stage at the onset of disease (Garry *et al.*, 1996) and the location of the disease on the plant (Béasse *et al.*, 1999, 2000). Using and building upon a disease-coupled crop growth model published by Béasse *et al.* (2000), Le May *et al.* (2005) developed an improved model to predict the impact of ascochyta blight in pea on yield components by incorporating a combination of disease progression in the canopy (number of nodes affected by the disease) and the structure of the canopy (leaf area index profile).

The approach which takes account of disease severity, plant growth stage, the risks of epidemic development, and the impact of the disease on yield losses, should lead to a better characterization of cultivars in terms of the role of their architecture in the development of disease epidemics.

References


O36
SPATIAL DISTRIBUTION OF *DIDYMELLA PINODES* PETRAK AND *ASCOCHYTA PINODELLA* L.K. JONES ON AUSTRIAN WINTER PEA PLANTS.

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Introduction
Although little empirical evidence exists it has been reported that the distribution of Ascochyta blight disease symptoms on pea plants can often be used to discern between *D. pinodes* and *A. pinodella* (Bretag et al. 2006; Kraft and Pfleger 2001). The purpose of this study was twofold i) to develop and demonstrate a rapid PCR based assay to assist in the identification of *Ascochyta* spp. of the Ascochyta complex of pea, and ii) investigate the spatial distribution of *D. pinodes* and *A. pinodella* on pea plants collected from the field.

Materials and Methods
A severe outbreak of Ascochyta blight on Austrian Winter peas (*Pisum sativum* L.) was detected in northern Idaho, USA. Whole plant samples were collected randomly from the field on May 26 2007. Spatial sampling of *Ascochyta* spp. isolates from disease lesions from ten plants was performed in order to characterize the position of each isolate collected from the plant. The plants were divided by branch, node, stipule and tendril. Plant parts were coded for reference and isolations were performed on symptomatic plant parts. Plant parts were surface sterilized and single spore isolates were derived following standard procedures. Isolates were identified with a rapid PCR assay designed on the intergenic spacer region of ribosomal RNA gene cluster (Chilvers and Peever, unpublished).

Results and Discussion
The molecular assay expedited the identification of 151 isolates from 10 plants. 61 isolates (40%) were identified as *A. pinodella* and 90 isolates (60%) as *D. pinodes*. Accuracy of the molecular assay was confirmed by identifying a subset of isolates by cultural and conidial morphology after Onfroy et al. (1999). All plants were infected with both species of Ascochyta. *A. pinodella* and *D. pinodes* were found to be randomly distributed over the diseased plant parts.

References
**O37**

RESPONSE OF FIELD PEA VARIETIES TO THE FUNGAL COMPONENTS OF THE ASCOCHYTA COMPLEX.

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**Introduction**

Ascochyta blight of field pea (*Pisum sativum*) is caused by a complex of four fungal species: *Ascochyta pisi*, *Mycosphaerella pinodes*, *Phoma medicaginis* var. *pinodella* and *Phomakoolunga* sp. nov. (Davidson et al., 2009). To date, studies on resistance to the ascochyta blight complex in pea have described it as a partial resistance that is difficult to evaluate in the field. A controlled environment screening method is, therefore, a practical solution. A method using drop spore suspensions on detached leaves has been used previously to identify partial field pea resistance sources and to study the epidemiological components of resistance in field pea (Onfroy et al., 2007).

Within this current study a detached leaf assay was used to assess how field pea varieties respond to the fungal species found in the Australian ascochyta blight complex. This information will then be used to identify varieties to be used as controls for future screening of Australian field pea breeding material for resistance to each component of the ascochyta blight complex.

**Materials and Methods**

A set of thirty one field pea varieties with putative resistance to ascochyta blight, and of various origins, was used to identify potential controls to the individual fungal components of the ascochyta complex. Six different isolates were used; three single isolates (*Mycosphaerella pinodes*, *Phoma medicaginis* var. *pinodella* and *Phomakoolunga* sp. nov.) and three ascochyta blight complexes collected from Australian field pea crops. Plants were grown in a glasshouse until the 5 to 6 leaf stage, with 4 replicates of each variety. Using a method developed from Onfroy et al. (2007), detached pea leaves on 0.5% water agar were inoculated with a 10 μl droplet of a $5 \times 10^4$ spores/ml spore suspension. The detached leaves were assessed each day after inoculation using a 0-3 scale as described by Onfroy et al. (2007). Once lesions began extending beyond the borders of the droplet the lesion diameter was measured daily until the lesions grew beyond the leaf edges and onto the agar.

**Results and Discussion**

Significant interactions between the varieties and fungal isolates were observed for both disease appearance and disease extension. This work has identified field pea varieties that will act as useful controls for the screening of breeding lines against ascochyta blight. However, different standard control varieties will be required for each separate fungal species due to the different response of varieties to the fungal species. Because of the small space required this method will allow for screening of a large number of field pea varieties or fungal isolates. Whilst acting as a methodology for screening breeding material, it can also give an insight into the components of resistance of field pea to specific species of the ascochyta blight complex.

**References**


O38
OPTIMIZING ASCOCHYTA BLIGHT MANAGEMENT IN CHICKPEA ON THE CANADIAN PRAIRIES.
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Introduction
Despite improvements in disease resistance in chickpea (Cicer arietinum) cultivars adapted to our semi-arid climate and short growing season, ascochyta blight (Didymella rabiei, anamorph Ascochyta rabiei) continues to be a serious issue. Fungicides are an important tool in an integrated management strategy, and our research has focused on optimizing fungicide use. Western Canadian producers tend to use lower than recommended carrier volumes, due to water supply issues and time constraints. In response to this situation, studies were conducted to examine the effect of carrier volume on fungicide efficacy in the field, and on spray deposition and penetration in the laboratory. The potential for spray quality to influence fungicide coverage, and in turn, fungicide efficacy, was also investigated in field and laboratory trials. Fungicide application timing and product sequences have been studied previously, and ongoing field research is being conducted in this area using cultivars with improved resistance.

Materials and Methods
Field studies on the effect of carrier volume on ascochyta blight were conducted using three carrier volumes: 100, 200 and 300 L ha⁻¹. The impact of spray quality on ascochyta blight was also investigated in field trials using three nozzle types. Spray retention and canopy penetration were studied in two concurrent indoor trials, one comparing the three carrier volumes and the other comparing the three nozzle types. Simulated chickpea canopies of cvs. Myles and Sanford were sprayed with fluorescent tracer dye using an indoor track sprayer. Various fungicide product sequences and application timings have been assessed in two ongoing field trials to determine the impact of these factors on ascochyta blight management using improved cultivars (cvs. CDC Frontier, CDC Luna, and CDC Vanguard).

Results and Discussion
Under low to moderate disease pressure, increasing carrier volume for fungicide applications was not critical for ascochyta blight control. When disease pressure was high (>49%), however, higher carrier volumes significantly reduced ascochyta blight development in seven out of nine trials. The use of higher carrier volumes increased the penetration of spray into the fern-type canopy of cv. Myles in laboratory studies, but had a less pronounced effect on penetration of the unifoliate canopy of cv. Sanford. Nozzle type had no effect on disease development or yield in all seven site-years, and had no effect on spray coverage or spray penetration. Results of application timing trials are preliminary, but seem to support prior work in which the importance of early application(s) were demonstrated. Preliminary results of fungicide sequencing trials suggest that sequences of a pyraclostrobin/boscalid mix and prothioconazole or chlorothalonil provide effective control.

References
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EFFECT OF GROWTH STAGES OF CHICKPEA ON THE GENETIC RESISTANCE OF ASCOCHYTA BLIGHT

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Introduction
Ascochyta blight (AB, Ascochyta rabiei (Pass.) Lab.) is one of the most important foliar disease of chickpea (Cicer arietinum L.), globally (Pande et al. 2005). Chickpea is attacked by AB at any growth stage in cool and humid weather depending on the inoculum availability. However, the disease epidemics are most prominent during the flowering and podding growth stages. Higher susceptibility of chickpea to AB at reproductive growth stage may be due to senescing of the plant tissue and to favorable environmental conditions. The main objective of this study was to determine the effect of growth stages of chickpea on the genetic resistance of AB and use this information in resistance breeding program.

Materials and Methods
Following staggered intervals, two susceptible (ICC 4991 and ICCV 10) and two moderately resistant (ICCV 05562 and ICCV 04512) chickpea cultivars to AB were sown in pots in the green house. Plants in seedling (GS1), post-seedling (GS2), vegetative (GS3), flowering (GS4) and podding (GS5) growth stages were spray inoculated with A. rabiei conidial suspension (5 x 10^3 conidia/ml). The experiment was arranged in a randomized complete block design with four replications in controlled environment facility at ICRISAT, Patancheru, India. Four pots (five-seedlings/pot) constitute a replication. Data on incubation period (IP) in days after inoculation and disease severity on 1-9 rating scale was recorded.

Results and Discussion
Irrespective of crop cultivars the IP was shorter in GS1, GS4 and GS5 and significantly extended than IP of GS2 and GS3. This is attributed to the development gene expression, as resistance genes reported to be highly expressive during the vegetative growth stages than at maturity (Trapero-Casas and Kaiser 1992). However, symptom development was delayed by 2-3 days in moderately resistant cultivars. The AB severity 10 days after inoculation ranged between 7 and 9 in susceptible cultivars and 3 and 5 in moderately resistant cultivars. Further the correlation coefficient between GS1, GS4 and GS5 was highly significant (r = 0.95) indicating that, evaluation for resistance to AB can be done at GS 1 (10 days old seedling stage), and or GS4 (flowering stage) to GS5 (podding stage) growth stages of chickpea. This supports the evaluation for AB resistance using 10-day-old-seedlings in controlled environment at ICRISAT and adult plant field screening at hot-spot locations in Dhaulakuan and Ludhiana in India (Pande et al. 2009 unpublished).

References
O40
DEVELOPMENT OF SCREENING TECHNIQUES AND IDENTIFICATION OF NEW SOURCES OF RESISTANCE TO ASCOCHYTA BLIGHT DISEASE OF CHICKPEA.
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Introduction
Ascochyta blight (AB), caused by Ascochyta rabiei (Pass) Lab. (anamorph), is a devastating disease of chickpea (Cicer arietinum L.) in areas where cool and humid weather prevails during the cropping season. Fungicidal management of AB is unsustainable and hazardous to environment. Host plant resistance (HPR) is most effective either alone or as a major component of integrated AB management. The preliminary step for exploiting HPR is the development of reliable and repeatable techniques for large-scale screening of germplasm. A number of such techniques under field and green house conditions have been developed (Sharma et al. 1995; Bretag and Meredith 2002; Pande et al. 2005). The objective of this study was to develop better screening techniques and/or improve the existing techniques developed earlier, and examine correlation between these techniques. Sources of stable host resistance were also identified.

Materials and Methods
Components of resistance screening techniques using detached - leaf (cut-twig) and whole plants (10-day-old seedlings) were standardized and a controlled environment facility (CEF) developed to facilitate reliable large scale screening for AB resistance. Similarly, components of field screening (FS) were standardized at Dhaulakuan and Ludhiana in India, where environmental conditions were found to be more favorable for AB development. A large number of breeding (F2 to F7) lines were screened. Correlation coefficient between disease severity rating in CEF and FS was calculated. Stable sources of AB resistance in breeding lines with good agronomic background were identified.

Results and Discussion
The results of the CEF using cut-twig (detached-leaf) were found to be highly correlated with the 10-day-old seedlings (r = 0.94) and FS (r = 0.88). Similarly results between 10-day-old seedlings and FS were also highly correlated (r = 0.89). The detached-leaf method is quick and reliable, and thus useful in screening segregating breeding lines and wild Cicer species. The remaining plants can then be used to screen for other target traits and seed production. Using these techniques high levels of stable resistance in new breeding lines were identified.

References