

**Abstracts from Oral Presentations**  
**North American Pulse Improvement Association (NAPIA)**  
**October 31 – November 2, 2007 Meeting**  
**Madison, Wisconsin, U.S.A.**

**Identification of QTLs controlling resistance  
to *Ascochyta* blight in chickpea**

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*Ascochyta* blight, caused by *Ascochyta rabiei*, is the most important disease of chickpea in western Canada and elsewhere. We are working to identify quantitative trait loci (QTL) conferring resistance to this disease in four divergent moderately resistant lines, such that the different QTLs could be combined into a single genotype to improve the level of resistance. Three QTLs were identified in the ICCV96029/CDC Frontier population and work is in progress with the three other populations ICCV 96029/Amit, ICCV 96029/ ICC 12512-1 and ICCV 96029/FLIP 97-133C.

**Development of field pea (*Pisum sativum* L.) varieties with  
improved protein content: Opportunities and challenges**

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Field tests revealed a significant difference in crude protein content among the germplasm lines of field pea, and two lines containing over 30% protein crude protein have been identified. The tests also showed the significant effect of growing locations on the protein content, but insignificant effect of location x genotype interaction. The opportunities and challenges for development of field pea varieties having high protein content will be discussed.

**Investigating the roles of melanin biosynthesis in  
pathogenesis of *Ascochyta rabiei* using albino mutants**

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*Ascochyta rabiei*, the causal agent of chickpea blight, produces melanin in culture and in infected plants. The possible role of melanin in pathogenicity of *A. rabiei* on chickpea was investigated using

spontaneous albino mutants of the pathogen. Unlike wild-type strains, the albino mutants were not pathogenic on chickpea. Specific melanin biosynthesis inhibitors, pyroquilon and tricyclazole, blocked melanin synthesis in culture by wild type strains, and reduced disease severity by the wild type when applied onto chickpea plants. Transcripts of scytalone dehydratase, an enzyme in the 1,8-dihydroxynaphthalene-melanin pathway, were detected in germinating spores using RT-PCR. The results suggest that melanin biosynthesis is a virulence factor of *A. rabiei* on chickpea.

### **Color retention in seed coats of green lentil**

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\*Presenter

The color of the seed coat is one of the main factors determining value of green lentils. We investigated the heritability of green seed coat color in lentil. A second set of experiments was designed to evaluate the effects of pre-harvest agronomic treatments on the color of green lentil seed coats.

### **Working with crop roots—an enjoyable challenge**

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Modelers and policy-makers often use an approximate approach to estimate root biomass or carbon values using root-shoot ratios. In cereal crops, various values of such estimate have been published in literature, but in pulse and oilseed crops there is lack of information on root biomass or carbon even in estimated value. This paper reports some of the results from experiments conducted at the Semiarid Prairie Agricultural Research Centre, Swift Current, SK, where root carbon and biomass of various crop species were determined by non-destructive methods. Also, discussions will be on the implementation details, costs, and challenges associated with working with roots and their analyses.

### **Highlights from GLIP, the European Grain Legumes Integrated Project**

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GLIP is a €24-M, 4-year European Project that involves 25 countries, 64 partners, in an effort to boost the production of grain legumes for animal feed and human consumption in Europe and beyond. The research program of GLIP encompasses economical, environmental, agricultural and nutritional issues of crop legumes, as well as the development of genetic resources and genomic tools in crop and model legumes.

As GLIP is approaching its term, I will highlight the main achievements of the project and select a few examples of interest for the genetic improvement of grain legumes. I will also bring an update on GL-TTP activities. GL-TTP, Grain Legumes Technology Transfer Platform, is a non-profit member-based organization that was primarily created to ensure the exploitation of the research results of GLIP. I will finally invite interested parties to join the latest GL-TTP initiatives for developing international resources for breeding, such as genotyping platforms for fingerprinting and diversity studies, at lower cost, by gathering resources from public and private institutions worldwide.

### **Evaluation of cold tolerance in pea (*Pisum sativum* L.) using a freezing chamber**

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Interest in fall-sown peas is increasing across the northern tier states of the U.S. Winter conditions in the Palouse region of the U.S. Pacific Northwest are sufficiently mild that adequate test conditions to identify breeding lines capable of surviving harsh Midwest winters is difficult. The USDA-ARS winter pea breeding program located in Pullman, WA, relies on cooperator nurseries located in the Midwest to evaluate resistance among advanced lines; however, evaluation in early generations is desired. A protocol using a controlled environment freezing chamber to evaluate tolerance to freezing temperatures has been developed. Results demonstrating the effect of acclimation period on survival and prospects for future applications will be presented.

### **Resistance to sclerotinia white mold in processed and dry pea cultivars and in the *Pisum* core collection**

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White mold, caused by *Sclerotinia sclerotiorum*, can be a major disease of irrigated and dryland peas. Management of white mold in peas is challenging because foliar fungicides are cost prohibiting to many pea growers, sclerotia survive for long periods of time limiting the effectiveness of crop rotations, and resistant pea lines are not available. Therefore, white mold resistance in processed and dry pea cultivars and in accessions from the *Pisum* Core Collection was characterized in the present study.

### **Characterization and genetic mapping of chickpea for drought tolerance**

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Drought is the most important stress throughout the chickpea growing areas and occasionally severe drought conditions lead to complete crop failure. The present study was thus envisaged to characterize a chickpea mapping population of a cross between drought tolerant and susceptible genotypes. A population consisting of 155 recombinant inbred lines (RILs) was studied under drought conditions in the

field in Syria for various morpho-physiological traits. STMP markers were used to tag quantitative trait loci (QTL) linked to important drought related traits.

### **The trend of chickpea breeding program in Canada**

Taran, B.<sup>1\*</sup>, Warkentin, T.,<sup>1</sup> Banniza, S.,<sup>1</sup> Vandenberg, A.,<sup>1</sup> <sup>1</sup>Crop Dev. Centre and <sup>2</sup>Dept. of Plant Sci. Kabeta, Y.,<sup>1</sup> Tullu, A.<sup>1</sup> and Bett, K.<sup>2</sup> Univ. of Saskatchewan, Saskatoon, SK, Canada  
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The chickpea breeding program at the Crop Development Centre is the only program developing cultivars for western Canada and germplasm to address the future challenges and opportunities for the industry. Major breeding objectives include high yield, ascochyta blight resistance and earliness on various seed size of kabuli and desi types. Breeding strategies to reach these objectives and the latest improved cultivars released through the Variety Release Program of the Saskatchewan Pulse Growers will be described.

### **Potential for biofortification of the human diet with lentils**

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We are exploring the potential for using genetic improvement for biofortification of lentils as a means of improving human nutrition. Genotype × environment analysis of the content of Zn, Fe, and Se in the seeds of lentil genotypes grown in various environments indicates that potential exists for genetic improvement of the concentration of these minerals in bioavailable form. Factors that may affect bioavailability such as cooking and processing have also been investigated.

### **Characterization of the genetic and biochemical basis of green cotyledon bleaching resistance in field pea**

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The objectives of the present study were to investigate the genetics and biochemical basis of green cotyledon bleaching resistance during both seed developmental and post harvest periods. A recombinant inbred line mapping population derived from a cross CDC Striker X Orb was evaluated in 2 locations for 2 years. The ongoing investigations of identifying QTLs using AFLP and SSR molecular markers will be discussed in this context. In addition, preliminary results of the gene expression study using Ps6kOLI1, *Pisum sativum*-16k microarray and the dynamics of the photosynthetic pigments of the cotyledons and seed coats at a series of seed developmental stages will also be discussed.

### Development of forage pea varieties

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In response to industry demand, a trial was established for the fifth consecutive year in western Canada in 2007 to evaluate pea varieties for forage potential. Varieties were assessed for biomass quantity and quality, as well as grain yield and other agronomic characteristics. CDC Tucker and CDC Leroy are new forage pea cultivars arising from this research, which have greater biomass yield and quality than the check cultivars Trapper and 40-10, combined with semileafless leaf type and good lodging resistance to facilitate harvest.

### Resistance to QoI fungicides in *Ascochyta rabiei* isolated from North Dakota

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*Ascochyta* blight, caused by *Ascochyta rabiei*, is the most damaging disease of chickpea in North Dakota. Chickpea producers in North Dakota rely on multiple applications of QoI (strobilurin) fungicides, such as azoxystrobin and pyraclostrobin, to manage this disease. Baseline sensitivity levels of *A. rabiei* isolates never exposed to QoI fungicides were established. Sensitivity to QoI fungicides of *A. rabiei* isolates collected from university research trials and producers' fields that were sprayed with QoI fungicides were determined and compared to baseline sensitivity levels. Based on these comparisons, isolates resistant to azoxystrobin and pyraclostrobin were identified.