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Abstracts

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Alphabetized by first author's last name

LOCUS HETEROZYGOSITY AND CYTOPLASM SOURCE AFFECT THE REACTION OF WHEAT TO THE TOXIN PRODUCED BY *PYRENOPHORA TRITICI-REPENTIS*. W. W. Bockus and M. A. Davis, Dept. of Plant Pathology, Kansas State University, Manhattan, 66506-5502.

Tan spot is a severe disease of wheat caused by *Pyrenophora tritici-repentis*. The fungus produces a cultivar-specific toxin that is useful in breeding for resistance. Susceptibility to the toxin is conditioned by a single, dominant gene. To study cytoplasmic effects, reciprocal crosses between 'TAM 105' (susceptible) and 'Red Chief' (resistant) were made in a greenhouse. Parent, F₁, and F₂ plants were evaluated over time for their reaction to the toxin with severity (0-3 scale) regressed against time. Regression lines of F₁ and F₂ plants of both reciprocals had significantly ($P < 0.0001$) lower slopes than those of TAM 105. Additionally, when Red Chief was used as a female (cytoplasmic donor), estimates of the Y intercept for F₁'s and F₂'s were lower ($P < 0.0001$) than those when it was used as a male. F₁ plants showed about a 1-day delay in their reaction to the toxin compared with homozygous susceptible plants. There was also a slight but significant cytoplasmic effect.

IDENTIFICATION OF RAPD MARKERS LINKED WITH DISEASE RESISTANCE GENES IN BARLEY. I. G. Borovkova¹, B. J. Steffenson¹, J. B. Rasmussen¹, Y. Jin¹, B. G. Rossnagel², and K. Kao³. ¹Dept. of Plant Pathology, North Dakota State Univ., Fargo, ND 58105; ²Crop Dev. Centre; Univ. of Saskatchewan, and ³Plant Biotech. Institute, Saskatoon, SASK.

A doubled haploid population of barley produced from anther culture and segregating for resistance to pathotype MCJ of *Puccinia hordeij* and pathotypes QCC and MCC of *P. graminis* f. sp. *tritici* was subjected to bulked segregant analysis to identify RAPD markers linked with the respective resistance genes. From over 180 10-mer primers (Operon) tested, one marker was found linked within 9.6 cM and two others within 28 cM of a gene (*Rph3?*) conferring resistance to pathotype MCJ of *P. hordeij*. One RAPD marker was found linked within 30 cM of *rpg4*, a gene conferring resistance to pathotype QCC, and four markers were linked within 21 cM of *Rpg1*, a gene conferring resistance to pathotype MCC. These data provide further evidence for the utility of bulked segregant analysis in identifying RAPD markers that are linked with disease resistance genes.

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ELECTROPHORETIC KARYOTYPES OF FIVE *STEMPHYLIUM* SPECIES PATHOGENIC TO ALFALFA. C. Chaisrisook¹, D. Z. Skinner², and D. L. Stuteville¹. ¹Dept. of Plant Pathology, ²USDA-ARS and Dept. of Agronomy, Kansas State University, Manhattan, KS 66506

Molecular karyotypes of *Stemphylium alfalfae*, *S. botryosum*, *S. herbarum*, *S. globuliferum*, and *S. vesicarium* were revealed by contour-clamped homogeneous electric field electrophoresis. Chromosomal DNAs were resolved from protoplasts released from mycelial fragments suspended in a mixture of cellulase, chitinase, and lyticase (40:1:1 mg/ml). Protoplasts were embedded in 1% low gelling temperature agarose plugs, sliced and placed in wells in 0.65% agarose in 0.5X TBE buffer. A 45-min switching interval at 1 V/cm for 5 d at 15 C was followed by a 35-min switching interval at 1 V/cm for 2 d. Four chromosomes of about 1.7, 2.4, 3.4, and 4.5 Mb, based on comparisons with yeast chromosomal DNA size standards from *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*, were common to all five species. This inferred a close genetic relationship among the five *Stemphylium* species.

FUSARIUM ROOT ROT OF DRY BEANS IN THE RED RIVER VALLEY OF NORTH DAKOTA. DeDene, D. D. and Venette, J. R. Department of Plant Pathology, North Dakota State University, Fargo, ND 58105

From July 30 to August 13, 1992, 10 randomly selected bean plants from each of 30 fields in the Red River Valley of North Dakota were rated for Fusarium root rot severity. Individual plant severity ratings, based on the CIAT scale, ranged from 1 (=none) to 7 (=50% of hypocotyl with lesions). Mean severity for all 30 fields was 4.1 (≈15% of hypocotyl with lesions). Disease severity was greater in the southern part of the valley. Five different species of *Fusarium* were isolated: *F. solani* (28% of the isolates), *F. oxysporum* (24%), *F. aquinatum* (11%), *F. equiseti* (8%), and *F. graminearum* (1%).

REACTION OF WHEAT GENOTYPES TO TAN SPOT IN THE 1993 SOUTHERN AND NORTHERN REGIONAL PERFORMANCE NURSERIES (SRPN AND NRPN). C.K. Evans, R.M. Hunger, and W.C. Siegerist, Plant Pathology Department, Oklahoma State University, Stillwater, OK 74078.

Following inoculation with conidia of *Pyrenophora tritici-repentis* in the greenhouse, the reaction of genotypes to tan spot in the 1993 SRPN and NRPN was determined. The largest lesion in the middle half of the first leaf was measured with calipers on four plants per entry. The reactions of entries 'MT8719' (NRPN), 'KS831374-142' (SRPN), and 'KS92P059E' (SRPN) were comparable to the resistant check 'Red Chief'. The procedure used, which resulted in quantitative data, did not consistently identify intermediate levels of tan spot resistance but did consistently identify wheat genotypes highly resistant to tan spot.

MOLECULAR GENETICS OF PLASMIDS FROM *CLAVIBACTER* SPECIES. J.A. Fahrlander, L.Y. Chuang, and A.E. Olsson, Biochemistry Dept., North Dakota State Univ., Fargo, ND 58105.

The number and sizes of plasmids resident in several strains of organisms in the plant pathogenic genus *Clavibacter* were determined. Hybridization studies revealed that the plasmids from *C. rathayi* and *C. tritici* form one group of related plasmids and those from 4 subspecies of *C. michiganensis* form another. The regions of plasmid pCS1 from *C. m. sepedonicus* that exhibit homology with related plasmids have been mapped. A conserved region of 0.7 kb was found both in plasmids from this group and the bacterial chromosome. Sequencing studies indicate that the conserved region codes for an unidentified open reading frame. The region of pCS1 that contains the replicon was located by hybridization, and constructs containing this region are able to replicate in suitable strains of *C. m. sepedonicus*. The minimal replicon exists within a 3.3-kb sequence, but genetic elements present in a 1.5-kb flanking region are required to improve construct stability.

Evidence for a new resistance gene in barley effective against *Puccinia graminis* f. sp. *tritici* (Pgt) race QCC. Stephen L. Fox and Donald E. Harder. Agriculture Canada, 195 Dafoe Rd. Winnipeg, MB, R3T 2M9.

Race QCC of Pgt has become recently prevalent in North America. It shows an adaptation to barley and has virulence to Rpg1. Effective resistance genes in barley to this race have not been identified in the field. In the cross Hiproly 15/Peatland 9, the presence of Rpg1, segregating in the F₂ generation, was identified with race MCC. When F₁ families derived from each F₂ plant were replicated three times, randomized and inoculated with race QCC in the field, Rpg1 conferred no resistance to race QCC. However, a second gene in Peatland 9, independent of Rpg1, was shown to provide a moderate level of resistance. The presence of this second gene was supported by evaluation of F₁ families of crosses involving the barley cultivars Husky and Diamond which are related to Peatland.

EFFECTS OF A FUNGICIDE ON A BEAN RUST EPIDEMIC. P. L. Gross and J. R. Venette. Department of Plant Pathology, North Dakota State University, Fargo, ND 58105

In 1992, chlorothalonil at a rate of 1.7 kg_{ai}/ha⁴ was applied 0, 1, 2, 3, 4, or 5 times to dry edible beans (pinto 'UI 111') grown in replicated field plots. Spreader rows between plots were inoculated with rust (*Uromyces appendiculatus* var. *appendiculatus*) spores. Ten leaves from each replicate were rated for rust severity on five different dates through the growing season. Ratings of each leaf were converted to pustules cm², and means were fit to curves. Sigmoid curves best fit the data with R² values of 0.99-0.95. Evaluation of the curves showed early application of chlorothalonil delayed epidemics by 6 days. A single application of fungicide reduced AUDPC by 49.6%. Two applications reduced AUDPC by 60.3%, and three applications reduced the area by 65.6%. Compared to three applications, more applications did not significantly reduce AUDPC. Yields were well described by a sigmoid curve (R²=0.90). Compared to three applications, more applications did not significantly increase yield.

CHARACTERIZATION OF *XANTHOMONAS MALTOPHILIA* ISOLATED FROM ENVIRONMENTAL AND CLINICAL SAMPLES. S. E. Hinz and C. A. Wozniak, Dept. of Plant Path., N. Dak. State Univ., and USDA-ARS, Northern Crop Sci. Lab., Fargo, ND 58105

Xanthomonas maltophilia (Xm) was established as a taxon following analysis of rDNA homologies between the genera *Xanthomonas* and *Pseudomonas*. Members of the genus *Xanthomonas* are typically plant pathogens and contain brominated aryl-polyene pigments. We have identified over 500 bacteria that fall under the designated species Xm from larvae of the sugarbeet root maggot (SBRM) and the sugarbeet rhizosphere. Isolates have been evaluated for their ability to produce disease symptoms or hypersensitive reactions on *Beta vulgaris* and *Nicotiana tabacum*. To date, no pathogenic or hypersensitive reactions have been attributable to Xm isolates from the sugarbeet rhizosphere, endogenous flora of the SBRM, or those of clinical origin. SDS-PAGE analysis of membrane proteins indicated substantial differences among isolates from SBRM and nosocomial origins. Further analyses of Xm will include plasmid characterization, RAPD profiles, fatty acid content, antibiotic resistance, and general biochemical characterization.

YIELD LOSSES IN MAIZE INBREDS INOCULATED WITH BARLEY YELLOW DWARF VIRUSES. R. L. Hnyre, C. J. D'Arcy, W. L. Pedersen, and A. D. Hewings. Department of Plant Pathology and USDA ARS, University of Illinois 1102 S. Goodwin Ave., Urbana, IL 61801.

Ten dent maize inbreds inoculated with several strains of barley yellow dwarf viruses (BYDVs) showed different levels of sensitivity. In 1992, ear weight was measured on ten ears from four replicates of inbreds B73 and Mo17. These inbreds were chosen because B73 had the highest number of inoculated plants testing positive in ELISA (susceptible), Mo17 had the lowest number of positives (resistant), and the two lines or their derivatives are used in many commercial hybrids. B73 had a significant decrease in ear weight, from an average of 1.5 kg for non-inoculated plots to 1.2 kg and 0.7 kg for plots inoculated with PAV-IL and RMV-IL, respectively. Mo17 showed no yield reduction when inoculated with either of these two BYDV strains and had an average ear weight of 1.0 kg. Incidence of virus was higher in B73 than Mo17. These results support the hypothesis that there is a difference in levels of resistance between inbreds and indicate that infection by BYDV can result in a significant yield loss.

IDENTIFICATION OF A NEW SORGHUM INFECTING SPECIES OF POTYVIRUS FROM SUGARCANE. S. G. Jensen and J. S. Hall, USDA-ARS Lincoln, NE and University of Nebraska, Lincoln, NE 68583

A potyvirus isolated from sugarcane from Pakistan infected sorghum carrying the Krish gene which imparts immunity to other sorghum infecting potyviruses. The virus appears as a long flexuous rod in the electron microscope. cDNA of the virus reacts with universal potyvirus primers in the polymerase chain reaction (PCR). The new virus has a wide host range, including sugarcane, sorghum, maize, millet, sudangrass, and johnsongrass but not oats. The host range distinguishes it from other species of sorghum infecting potyviruses, maize dwarf mosaic virus (MDMV), sugarcane mosaic virus (SCMV), johnsongrass mosaic virus (JgMV), or sorghum mosaic virus (SrMV). In reciprocal serological tests the Krish infecting virus and antiserum to it did not cross react with antisera or virions respectively, of the other four known species. There was no serological cross reaction with rymoviruses or their antisera. The coat protein is approximately 39 Kd in size and tryptic digests of the coat protein produced a pattern of peptides unlike that of any of the other poaceous potyvirus species. Also unlike the other potyviruses this Krish-infecting virus is unstable unless purified and held in alkaline conditions, pH 9.0. Other properties of the virus are being studied.

NATURAL OCCURRENCE OF BARLEY CROWN RUST ON FORAGE GRASSES IN NORTH DAKOTA AND ITS PATHOGENICITY ON GRAMINEOUS SPECIES. Y. Jin and B. J. Steffenson, Department of Plant Pathology, North Dakota State University, Fargo, ND 58105.

In 1992, crown rust of barley, caused by a variety of *Puccinia coronata*, was found on 11 grass species used for forage and soil conservation in North Dakota. Severe infection occurred in several nurseries of Canada wildryegrass, Russian wildryegrass, quackgrass, slender wheatgrass, and commercial seed production fields of western wheatgrass. Naturally infected grass species also included Basin and Virginia wildryegrasses, intermediate wheatgrass, and several other species in *Elymus* and *Leymus*. Greenhouse evaluations at the seedling stage indicated that the barley crown rust pathogen has a large host range, as 71 gramineous species were found to be susceptible. Susceptible species were mainly in the tribes Poaceae and Triticeae, including genera *Aegilops*, *Agropyron*, *Brachypodium*, *Bromus*, *Elymus*, *Elytrigia*, *Festuca*, *Hordeum*, *Leymus*, *Lolium*, *Pascopyrum*, *Phalaris*, *Psathyrostachys*, *Secale*, and *Triticum*.

IMPROVED PROCEDURES FOR SCORING REACTION OF WHEAT TO *PYRENOPHORA TRITICI-REPENTIS*. J. G. Jordahl and L. J. Francl, Plant Pathology Department, NDSU, Fargo, ND 58105.

Wheat genotypes susceptible or partially resistant to *Pyrenophora tritici-repentis*, the cause of tan spot, tend to show a more severe reaction in the distal portion of the leaf than the proximal end. We investigated the effect on infection of propagule type, inoculum dosage, and spatial interaction among lesions to improve our screening procedure. On susceptible plants exposed to a 24 hr wet period, hyphae were largely non-infectious and conidiophores were 3 to 12% as infective as conidia. We recommend, as a conservative approach, treating one conidium as equivalent to 25 conidiophores when counting inoculum containing both. Inoculum density influenced infection types that included coalescence as a criterion (i.e., susceptible classes) and conidiophores produced lower infection types than conidia at equivalent dosages. There was little evidence of interaction among lesions in the distal and proximal portions of the same leaf. Low and high extremes of infection type sometimes found near the collar and tip of the leaf, respectively, could be described by percentage disease severity. Only the middle portion of the leaf should be scored for infection type.

TRANSMISSION OF *ERWINIA STEWARTII* THROUGH SEED OF RESISTANT AND SUSCEPTIBLE MAIZE. A. Khan, S. M. Ries, and J. K. Pataky, Univ. of Illinois, Dept. of Plant Pathology, Urbana, IL 61801.

Twenty sweet corn hybrids and eight dent corn inbreds grown in field plots were inoculated repeatedly from 3 to 10 leaf stage with a rifampicin resistant isolate and wild type isolates of *Erwinia stewartii* (Smith) Dye. Seed from infected plants were harvested and assayed for the presence of *Erwinia stewartii*. Bacteria recovered from samples of 100 kernels taken randomly from each seed lot five months after harvest were tested for pathogenicity. An extract procedure was used to isolate *Erwinia stewartii* from seed samples. The extract was used to inoculate plants of Jubilee for a greenhouse assay of pathogenicity. Bacteria isolated from seed of the hybrids: 91-1574, 91-1209, 88-2757 and 89-3889 produced typical Stewart's wilt symptoms on 90%, 25%, 66% and 66% of the Jubilee plants inoculated, respectively. Symptoms were produced from extract collected from plants with the Stewart's wilt ratings above 4.5, while extract collected from plants with ratings below 4.5 did not produce symptoms.

GENE EXPRESSION IN THE *TRITICUM AESTIVUM* - *PUCCINIA RECONDITA* GENE-FOR-GENE SYSTEM. J.A. Kolmer and P.L. Dyck, Agriculture Canada, Winnipeg, Manitoba, Canada, R3T 2M9.

The progeny of a selfed single pustule isolate of *Puccinia recondita* segregated for virulence on 7 Thatcher wheat lines isogenic for leaf rust resistance genes. The Thatcher lines were crossed with Thatcher to produce F₁ plants that were heterozygous for resistance genes. Progeny rust isolates and host lines were inoculated in all nine genotype combinations. Most resistance genes were incompletely dominant when tested with rust isolates that were homozygous for avirulence, and were recessive when tested with heterozygous isolates. Most avirulence genes were incompletely dominant when tested with hosts that were homozygous for resistance, and were recessive when tested with hosts that were heterozygous. Results indicate that dominance or recessiveness of resistance and avirulence is highly dependent on the genotypes of the rust isolates and host lines.

AN ALTERNATIVE METHOD FOR THE ISOLATION OF THE NECROSIS TOXIN OF *PYRENOPHORA TRITICI-REPENTIS*. B.Z. Lin, S.W. Meinhardt, Dept. of Biochemistry, and L. J. Francl, Dept. of Plant Pathology, NDSU, Fargo ND, 58105.

An easily scaled up procedure for the isolation of the *P. tritici-repentis* necrosis toxin has been developed. The procedure involved the concentration of the crude extract 20 times by ultrafiltration, dialysis, and DEAE-trisacryl batch chromatography, three washes of 0.01 M sodium acetate pH 4.8, resulting in a colorless protein solution. Substitution of DEAE-cellulose resulted in decreased toxin yields. The sample was concentrated to half the volume applied to the DEAE-trisacryl and processed by FPLC gel filtration chromatography with a Pharmacia HR75 column. A final purification step involved chromatography on the HR75 column under low ionic strength conditions, 0.01 M sodium acetate. We have used this method as an alternative to the previously published procedures (Balance et al., *Physiol. Molec. Plant Path.*, 35, 203; Tomas et al., *Molec. Plant-Microbe Interact.* 3,221).

HIGH RESOLUTION MAPPING OF THE *Mi-a* POWDERY MILDEW LOCUS IN BARLEY. Mamatha Mahadevappa¹, Rich DeScenzo^{1,2} and Roger P. Wise^{1,2}, 1) Department of Plant Pathology and 2) USDA-ARS-Field Crops Research, Iowa State University, Ames, IA 50011.

In barley (*Hordeum vulgare* L.), the *Mi-a* locus conditions reaction to the powdery mildew fungus, *Erysiphe graminis* f. sp. *hordei*. Enrichment for genetic recombinants in the *Mi-a* region is possible by making use of the flanking marker genes, *Hor1* and *Hor2*, which encode storage proteins hordein C and B, respectively. Recombinants were identified from F₂ segregating families of crosses between Rupee (*Mi-a6*) and Franger (*Mi-a13*) isolines by analyzing the hordeins on SDS-PAGE. Of 1800 seeds screened, 270 had a recombinant gamete contributed by one parent, 10 had recombinant gametes contributed by both parents. Genetic distance between the *Hor1* and *Hor2* loci, based on recombination frequency is 8.05 map units. Mapping of the *Mi-a* alleles was done by inoculation with the A27, MK24-76 and CR3 isolates of *E. graminis*. RFLP analysis was done on 115 of the 270 single-parent recombinants to saturate the *Mi-a* region with DNA markers for mapping purposes.

COMPARATIVE ULTRASTRUCTURAL MORPHOLOGY OF *MELAMPSORA MEDUSAE* INFECTION PROCESS IN HOST AND NONHOST *POPULUS* LEAVES. P.A. Mason¹, R.W. Stack¹, and K. Iverson². ¹Dept. of Plant Pathology and ²Electron Microscopy Laboratory, North Dakota State University, Fargo, ND 58105.

Reactions to rust infections have been classified as 'host' or 'nonhost' depending on certain aspects of the infection process. To date, most studies of host and nonhost reaction have compared widely divergent plant species. Infection by *Melampsora medusae* on host and nonhost *Populus* species was examined by transmission electron microscopy. Hyphal ramification was extensive in all cases, but termination of the infection process had different outcomes. On *P. deltoides* (host) leaves, *M. medusae* exhibited multiple haustoria along with dark neck bands at 48 hr post inoculation, and formation of wall appositions at 144 hr. On leaves of *P. trichocarpa* (nonhost), colonization by *M. medusae* terminated shortly after formation of the first haustorium and by 96 hr post inoculation the haustoria were either encased within the cell or beginning to degenerate. These events are consistent with other reports of host and nonhost reactions in rusts.

CORRELATION OF VOMITOXIN LEVELS AND VISIBLE SCAB IN 1991 SPRING WHEAT. McMullen, M. P.,¹ H. Casper², and R. W. Stack¹. ¹ Plant Pathology Dept., ² Veterinary Science Dept., North Dakota State Univ. Fargo, ND 58105.

Fusarium head blight or scab was common during 1991 in spring wheats in eastern North Dakota and western Minnesota. Ninety-eight spring wheat samples from this region were analyzed for vomitoxin using gas chromatography/mass spectrometry and examined visually for percent scab infection. Vomitoxin levels and visible scab levels ranged from 0 to 56 ppm and 0 to 41%, respectively. Vomitoxin levels and percent visible scab were significantly correlated ($r = 0.739$, $p < 0.001$). The FDA guideline for vomitoxin in grain is 2 ppm. Vomitoxin levels exceeded 2 ppm in about 1 in 5 grain samples showing less than 2% visible scab and in about 1 in 3 samples when levels of visible scab were from 2-5%. All vomitoxin levels exceeded 2 ppm in samples with visible scab levels above 10%. Samples between 5 and 10% visible scab varied considerably in vomitoxin levels.

GENETIC ANALYSIS OF LEAF RUST RESISTANCE GENES IN *TRITICUM TAUSCHII*, THE D GENOME PROGENITOR OF WHEAT. D. E. Miller, W. J. Raupp, B. S. Gill, Department of Plant Pathology, Throckmorton Hall, Kansas State University, Manhattan KS, 66506-5502.

Triticum tauschii, the D genome diploid progenitor of wheat, is a good source of genes for resistance to the leaf rust fungus *Puccinia recondita* f. sp. *tritici*. Resistance genes previously transferred from *T. tauschii* include: *Lr* 21, 22, 32, 41, 42, and 43. Accessions of *T. tauschii* are currently being evaluated for additional leaf rust resistance genes. Initial screening of 64 resistant accessions with 6 pathogen races identified two basic types of seedling resistance. Type 1 accessions are environmentally stable, highly resistant to all 6 races, and phenotypically similar to *Lr* 21 and 41 donor accessions. Type 2 accessions are moderately resistant, sensitive to environmental conditions, and phenotypically similar to the *Lr* 32 donor accession. Of the 64 resistant accessions, 29 are type 1 and 35 are type 2. Eighteen accessions were crossed to *Lr* 21, 32, and 41 donor accessions in an allelism test. Segregation in the F₂ population of each cross will indicate whether the unknown gene and the identified resistance genes are independent. F₃ lines will be used to evaluate and confirm selected F₂ segregant and parental types. Preliminary F₂ data will be presented.

DETECTION OF BENZIMIDAZOLE-RESISTANT *FUSARIUM SAMBUCINUM* USING A MODIFICATION OF THE "BAG TEST." Phillip Nolte, University of Idaho, 1776 Science Ctr. Dr., Idaho Falls, ID 83402.

Benzimidazole resistance in the potato dry rot fungus, *Fusarium sambucinum*, is becoming widespread in potato-producing areas of the United States. Presence of a benzimidazole-resistant strain of this fungus in a seed lot can lead to unacceptable levels of both dry rot and soft rot seed piece decay in benzimidazole-treated cut seed. This resistance also appears capable of being transmitted to the progeny tubers, via the resistant inoculum left in the rhizosphere by the decaying seed piece. Transmission of resistance from one generation to the next has serious implications for both seed and commercial producers since the benzimidazole fungicide, thiabendazole, is the only post-harvest fungicide currently available for dry rot control. A modified form of the traditional "bag test" has been developed to identify seed lots that contain benzimidazole-resistant strains of *Fusarium sambucinum*.

COMPUTERIZED DISEASE ASSESSMENT TRAINING PROGRAMS: DO THEY WORK? F. W. Nutter, Jr. Dept. of Plant Pathology, Iowa State University, Ames, 50011

Experiments were conducted using Disease.Pro and Alfalfa.Pro to determine if computerized disease assessment training programs improve the accuracy and precision of visual disease assessments. Raters were asked to visually assess disease severities of 30 leaf images without knowing the actual severities (pretest). Pretests were evaluated by regression of actual severities (stimulus) on estimated severities (response). Slopes deviating from 1.0 or intercepts deviating from zero provided a measure of rater bias; R^2 values were used as a measure of accuracy. Following pretests, raters evaluated & received feed-back as to the actual severities of 30 additional leaf images, followed by post-tests without feedback. Intercepts, slopes and R^2 values of post-tests were compared to pretest results. Of those tested, 91% significantly improved their ability to assess disease.

QUANTIFICATION OF OOSPORES IN ROOTS OF SUGAR BEET CULTIVARS DIFFERING IN SUSCEPTIBILITY TO *APHANOMYCES COCHLIOIDES*. Bruce E. Paulsrud and Carol E. Windels, NWES, University of Minnesota, Crookston 56716.

Root regions (hypocotyl), root hair zone, zone of elongation, root tip) of three sugar beet cultivars (Maribo Ultramono [susceptible to *Aphanomyces*], ACH 17 [tolerant] and ACH 205 [tolerant]) were exposed to 700-1000 zoospores of two pathogenic isolates of *A. cochlioides* for 2 hr. The number of oospores per mm root length was quantified 1 wk later. In four trials, there were no significant differences in number of oospores that formed in Maribo Ultramono (mean = 99/mm), ACH 17 (69) and ACH 205 (59). The mean number of oospores across cultivars was significantly greater in hypocotyls (mean = 160/mm) and the root hair zone (77) than in the zone of elongation (26) and root tip (40). Both isolates of *A. cochlioides* differed in number of oospores produced (17 vs 134/mm root length). Oospores formed in all root regions of sugar beet seedlings but were most abundant in hypocotyls of the cultivar susceptible to *Aphanomyces*.

EVALUATION OF SLOW-RUSTING IN FLAX CULTIVARS. Khalid Y. Rashid, Research Station, Agriculture Canada, Morden, Manitoba, Canada, R0G 1J0

Eleven flax (*Linum usitatissimum*) cultivars of diverse origins and levels of susceptibility to the rust pathogen (*Melampsora lini*) were evaluated for their ability to retard rust development in small field plots during the period 1989-1991. A local rust isolate, race 371 was used to inoculate susceptible spreader rows. Slow-rusting evaluation was based on the area under the disease progress curve (AUDPC) and final rust severity. Significant differences were found among cultivars for the AUDPC and final rust severity values. Three cultivars exhibited slow-rusting and five moderate-rusting.

ISOLATION AND CHARACTERIZATION OF X-RAY-INDUCED AVIRULENCE MUTANTS OF THE FLAX RUST FUNGUS. Jack B. Rasmussen, Department of Plant Pathology, North Dakota State University, Fargo, ND 58105

An isolate of *Melampsora lini* race 1 characterized by Flor is heterozygous at *AvrP*, the avirulence locus expressing gene-for-gene specificity with the P resistance allele in flax (Phytopathology 45:680). Inoculations with wild-type race 1 urediniospores resulted in no lesions on 500 Koto flax (PP) seedlings, but in excess of 100 lesions per Bison flax (pp) seedling. Inoculation with race 1 urediniospores subjected to X-rays (30-50 krad) resulted in over 100 lesions per Bison seedling, and approximately one lesion per 10 Koto flax seedlings. Each lesion on Koto is a putative deletion mutant at *AvrP*. Putative mutants are being evaluated for experiments aimed at cloning *AvrP* by genomic subtraction.

INTERACTION OF CEREAL CYST NEMATODE AND COMMON ROOT ROT ON SPRING WHEAT AND BARLEY. R. W. Stack¹, F. Green², J. Lewis², and A. J. Dube². 1) North Dakota State Univ., Fargo ND 58105; and 2) South Australia Dept. of Agriculture, Field Crops Pathology Unit, Glen Osmond, SA 5064.

An interaction between cereal cyst nematode (CCN) and common root rot (CRR), caused by *Cochliobolus sativus*, was identified in field experiments in Australia. CRR was assessed using the subcrown internode index method. CRR severity in wheat and barley plants was significantly lower ($p < 0.001$) when CCN was present at high levels compared to plants at low CCN levels. Interaction between these two diseases has not been previously reported. CRR survey methods were developed for the spring cereal regions of North America where CCN is not a problem. Using these methods for CRR surveys in regions where CCN also occurs, as in South Australia, may produce underestimation of CRR losses if possible CCN infection of controls is not considered.

LACK OF EVIDENCE FOR METALAXYL TOLERANCE IN *PHYTOPHTHORA ERYTHROSEPTICA*, THE CAUSE OF PINK ROT OF POTATO. R. W. Stack, B. Salas, N. C. Gudmestad, & G. A. Secor. Dept. Plant Pathology, N. Dak. State Univ., Fargo 58105.

The systemic fungicide metalaxyl has been widely used for control of water mold pathogens. Metalaxyl tolerant strains of several fungi have appeared following extended use. Field application of metalaxyl is being used to control potato pink rot caused by *Phytophthora erythroseptica*. We tested 46 isolates of *Ph. erythroseptica* from Minnesota, Wisconsin, and Idaho. Some isolates came from regions where metalaxyl resistance in late blight is well established. All isolates of *Ph. erythroseptica* were sensitive to metalaxyl, having LD-90 values of 5-15 mg/l in culture. If metalaxyl resistant strains exist in the wild population they have not yet become the predominant type.

IMMUNOELECTROPHORETIC ANALYSIS OF BEAN POD MOTTLE COMOVIRUS. J. M. Theuri and O. P. Sehgal. University of Missouri, Columbia.

Electrophoretic forms of BPMV from *Phaseolus vulgaris*, *Chenopodium quinoa* and *Canavalia ensiformis* were analysed using rocket immunoelectrophoresis (RIE). Early and late-progeny virions from *C. ensiformis* migrated mainly towards the anode. Early-progeny virions from *P. vulgaris* and *C. quinoa*, however, migrated towards the anode, while late-progeny virions migrated towards the cathode. Apparently, the type of host influences BPMV conversion from anionic to cationic form. Cowpea mosaic comovirus (CPMV) propagated in *V. unguiculata* was exclusively anionic. Hydrophobic comparison of C-terminus sequences (15-20 residues) of small coat protein subunits of both viruses indicates a net negative charge on BPMV and a net positive charge on CPMV. Possibly, proteolytic cleavage of the C-terminus converts BPMV into the cationic form, while CPMV remains unaltered.

SOIL MICROBIOLOGY AND ROOT DISEASES. N. G. Vakili and J. L. Hatfield, USDA-Agricultural Research Service, National Soil Tilth Laboratory, 2150 Pammel Drive, Ames, IA 50011.

A field of clay loam soil with 12 years of continuous corn without insecticide or fungicide was used in 1990 for trials in no-till with different mulching treatments, which included crop residue (1.5 to 1.75 T/ha.), pressed peat moss, black plastic or bare soil as control. Plant residue slowed the cooling down in autumn and warming up of the soil in spring. Also, it caused a strong moderation in the fluctuations of diurnal maximum-minimum temperatures. Corn plants growing in crop residue for the second year had a greater number of green leaves at the dough stage than those growing for the first year. There was an increase in pathogenic fungi colonizing tissues of emerging seedlings and crowns of mature corn plants growing in residue. Application of residue caused reduction in grain yield as compared with plants grown in bare soil.

RESTRICTION FRAGMENT LENGTH POLYMORPHISMS OF PYRENOPHORA SPECIES PATHOGENIC ON BARLEY. H. Wu, B. J. Steffenson, L. You*, and A. E. Oleson*, Depts. of Plant Pathology and *Biochemistry, North Dakota State University, Fargo, ND 58105.

Twenty-five isolates of Pyrenophora teres f. teres, P. t. f. maculata, and P. graminea from different regions of the world were examined for genetic diversity by restriction fragment length polymorphism (RFLP) analysis. An anonymous 0.5-kb fragment (ND218) from the genomic DNA of a California isolate of P. t. f. teres was used as the probe. Every isolate tested, except two P. t. f. teres isolates from South Africa, exhibited a unique RFLP pattern indicating that Pyrenophora species and subspecies possess a high degree of diversity. No obvious correlation was detected between the RFLP pattern of isolates and their geographic origin or virulence phenotype on barley. The high degree of polymorphism revealed by ND218 will make it a useful tool for differentiating isolates of Pyrenophora pathogenic on barley and for population genetic studies.

OPTIMUM CONDITIONS FOR THE CHEMOTACTIC RESPONSE OF BACILLUS MEGATERIUM B153-2-2 TO SOYBEAN SEED AND ROOT EXUDATE. Xiangyang Zheng, Z. L. Liu and J. B. Sinclair, Dept. of Plant Pathology, Univ. of Illinois at Urbana-Champaign, Urbana, IL 61801-4709.

The chemotactic response (CR) of B. megaterium strain B153-2-2 to soybean seed exudate was evaluated by the exudate-in-capillary (1 μ l) method under conditions of: pH 5-9, bacterial concentration of 1×10^6 to 5×10^7 cfu/ml, exudate concentration of 0.01-15 mg/ml, and incubation for 5-90 min at 5-40 C. A chemotactic model was established as: pH 6-7, 4 mg/ml exudate, 5×10^6 cfu/ml bacterial concentration, and 45 min at 25-30 C. Under these conditions, a chemotactic ratio of 400:1 was reached at 1×10^6 cfu/ml B153-2-2 concentration; and 0.03 mg/ml exudate concentration initiated a significant CR. The early exponential growth stage resulted in a higher CR than later stages, especially in tryptone broth. The CR to seed exudate was greater than to root exudate for two cultivars. The CR of B153-2-2 to root and seed exudates may be the first step in the colonization of this bacterium on soybean roots and seeds.