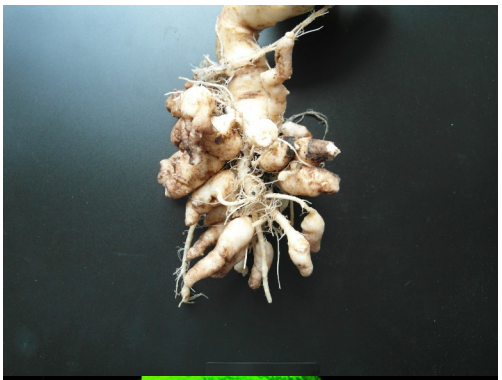
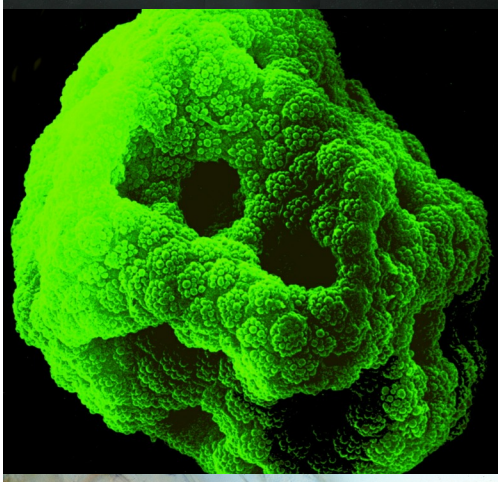
10TH INTERNATIONAL CONGRESS OF PLANT PATHOLOGY 2013 (ICPP 2013), BEIJING, CHINA

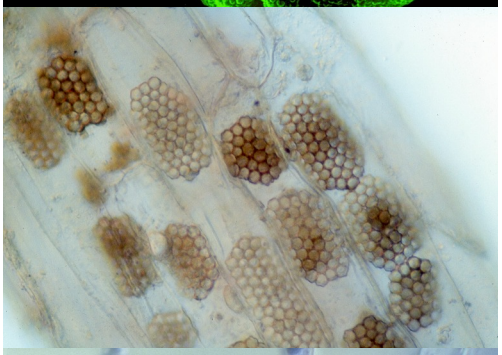
Management of

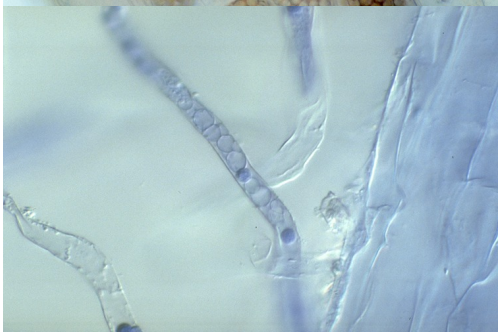
Plasmodiophorid Plant Pathogens

to Ensure Food Security









International Workshop

August 24 - 25, 2013

International Convention Centre

Beijing

Photographs front cover (from top):

- Clubbed roots of Broccoli (*Plasmodiophora brasicae*)
- Sporeball of *Spongospora subterranea*
- Sugar beet roots containing resting sporeballs of *Polymyxa betae*
- Brocolli root hair with an empty zoosporangia of *Plasmodiophora brassicae*

Photographs courtesy of Ueli Merz, Plant Pathology, ETH Zurich, Switzerland

PROGRAMME

Saturday, August 24, 2013

Afternoon Registration and Welcome Reception

Sunday, August 25, 2013

Morning Session: Chairman Ueli Merz

9 - 9.10 Welcome address and housekeeping details

9.10 - 9.45 **Occurrence, biology and epidemiology of *Spongospora subterranea*** (1)

U. Merz, Plant Pathology, ETH Zurich, Switzerland

9.45 - 10.20 **Clubroot in the Canadian Canola (*Brassica napus)* crop: An update on the epidemic** (2)

S. Strelkov and H.S. Wang, Dept of Agric., Food and Nutritional Science, Univ. Alberta, Edmonton, Alberta, Canada

10.20 - 10.45 **Quantification of *Plasmodiophora brassicae* in the cruciferous crop field by using quantitative real-time PCR** (3)

S. Guo and L.Q. Zhang, China Agricultural University, Beijing 100193, China

10.45 - 11.15 Tea break

11.15 - 11.40 **Characterization of Chinese cabbage clubroot by Fourier transform infrared spectra** (4)

B. Li, C.L. Shan, H. Qiu, M.Y. Ge, L. Wang and G.L. Xie, Zhejiang University, Hangzhou 310029, China

11.40 - 12.05 **The genome of the club root pathogen *Plasmodiophora brassicae*** (5)

A. Schwelm, J. Fogelqvist and C. Dixelius, Swedish Univ. Agricul. Sci. & Linnean Center for Plant Biology, 75007 Uppsala, Sweden

12.05 - 13.45 LUNCH, with Postersession

Efficacy of Vapam to control clubroot (*Plasmodiophora brassicae*) in canola

Sheau-fang Hwang, Crop Divers. Centre North, Alberta, Canada

Afternoon session: Chairman Yong Pyo Lim

13.45 - 14.10 **Use of genetics and genomics approaches to fine map the clubroot resistance "CRb" locus in *Brassica rapa*** (6)

Su Bin Im, Nirala Ramchiary, Su Ryun Choi, and Yong Pyo Lim, Chungnam National University, Daejeon, 305-764, Korea

14.10 - 14.45 **Clubroot Disease Control and Genome Sequencing of *Bacillus substilis* XF-1** (7)

S. Guo[1], Z. Mao[1], Y. Wu[1], K. Hao[1], P. He[2] and Y.-Q. He[1], [1] Yunnan Agricultural University, Kunming 650201, China, [2] Huazhong Agricultural University, Wuhan 430070, China

14.45 - 15.10 **Effects of the biocontral agent *Bacillus subtilis* xf-1 on microbial community diversity in the chinese cabbage rhizosphere** (8)

W. Wang and Y. Zhang, State Key Laboratory of Bioreactor Engineering, East China University of Sci. & Tech., Shanghai 200237, China

15.10 - 15.35 **Characterization of antibiotic substances from secondary metabolite of *Lysobacter* spp. strain** (9)

G.-H Ji, L.-H Zhou, L.-F. Wei, L.-H Zhang and Y.-Q He, Yunnan Agriculture University, Yunnan 650201, China

15.35 - 16.10 Tea break

16.10 - 16.35 **Water-mediated dissemination and chemical control of cabbage clubroot disease** (10)

X. Yu[1], Y. Wu[2], Z. Mao[2] and Y. Q. He[1, 2], [1] College of Plant Protection, Yunnan Agricultural University, Kunming 650201, China, [2] College of Agronomy and Biotechnology, Yunnan Agricultural University, Kunming 650201, China

16.35 - 17.10 **Integrated control of *Spongospora subterranea*** (11)

U. Merz, Plant Pathology, ETH Zurich, Switzerland

17.10 - 17.45 **New knowledge for sustainable management of powdery scab of potato: *Spongospora* research in New Zealand** (12)

R.E. Falloon, S.J. Baldwin, S.R. Bulman, A.J. Conner[1], R.A. Genet, M.L. Hernandez Maldonado, J.M.E Jacobs, M.F. Paget and F.A. Shah, Plant and Food Ldt, Christchurch, New Zealand, [1] AgResearch Ldt, Palmerston North, New Zealand

17.45 - 18.00 **Closing remark**

18.00 **End**

Oral presentations

PAPER 1

Occurrence, biology and epidemiology of *Spongospora subterranea* f.sp. *subterranea*, the cause of powdery scab of potato

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Powdery scab of potato, caused by the zoosporic pathogen *Spongospora subterranea* f. sp. *subterranean* (*Sss*), is an important disease in commercial potato production worldwide. Infected seed lots may be rejected or extra grading is needed. Similarly, supermarket quality standards for ware potatoes may require additional grading and infected potatoes for processing produce more waste and less profit. *Sss* is also vectoring a plant pathogenic virus, *Potato mop-top virus*, which causes internal symptoms on tubers, a quality problem especially for processing. Furthermore, root infection (galling) can reduce yield. *Sss* is an obligate, non-culturable zoosporic parasite, making research difficult. It has a wide host range but the resting spore stage has only been observed on solanaceous plants. The pathogen survives as resting spores (sporosori) in the soil for many years. The nature of both zoospore release stimulus and host recognition is unknown but all the Plasmodiophorids have a unique mechanical penetration method. It is also unknown which factor(s) determine if a plasmodium either develops into a zoosporangium or a gall after infection of a root. It is commonly assumed that powdery scab prefers cool and wet conditions and heavy soils. Soil water is essential for the spread of the zoospores thus stopping irrigation around tuber initiation (susceptible stage) can prevent infection. A wet-dry-wet soil moisture pattern seems to favor the disease which might explain that powdery scab occurs also in hot and dry regions were irrigation is applied and sandy soils seem to be the worst.

PAPER 2

Clubroot in the Canadian Canola (*Brassica napus*) Crop: An update on the epidemic

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Clubroot, caused by the obligate parasite *Plasmodiophora brassicae*, is a major disease of the Brassicaceae family. However, until a decade ago, clubroot had not been reported in Canadian canola (*Brassica napus*), a crop that contributes more than $15 billion annually to Canada's economy. The identification of clubroot was a major cause for concern and stimulated significant research into this disease. Initially, the outbreak was confined to central Alberta, where 12 clubroot infested fields were identified in 2003. Continued surveying has shown that clubroot is spreading, and as of 2012 there were at least 1,064 fields with confirmed infestations. While most of these fields are located in central Alberta, isolated cases of clubroot have also been identified in southern Alberta and the neighboring province of Saskatchewan. *P. brassicae* inoculum has also been detected in a few fields in Manitoba. Most of the spread has resulted from the movement of infested soil on farm and other machinery, although other mechanisms of dissemination have also been implicated. Pathotype 3 of *P. brassicae*, as classified on the differentials of Williams, appears to be predominant on canola. Clubroot management strategies have focused largely on exclusion and sanitation, as well the cropping of clubroot-resistant canola cultivars, a number of which have been released since 2009. Genetic resistance will have to be well-managed, however, as the virulence of pathogen populations can shift as a consequence of the selection pressure imposed by the cropping of resistant cultivars.

PAPER 3

Quantification of *Plasmodiophora brassicae* in the cruciferous crop field by using quantitative real-time PCR

S. Guo and L.Q. Zhang
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Clubroot, caused by the obligate endoparasite *Plasmodiophora brassicae*, is recognized as a serious soilborne disease on cruciferous crops in China. A soil DNA-based real-time polymerase chain reaction (Q-PCR) method was developed for the direct detection and quantification of *P. brassicae* in soil samples. Total genomic DNA was extracted from 50-g soil samples, purified according to an optimized protocol, and used as the PCR template. Species-specific primers (Rennie et. al, 2011) were employed to amplify a 90bp fragment of *P. brassicae* ribosomal DNA. The standard curve of the soil-derived resting spores was generated by PCR-amplifying soil DNA samples containing different amounts of plasmid-carried *P. brassicae* target sequence, then regression analysis showed that the standard curve was linear over at least six orders of magnitude ($R^2 > 0.99$). Less to only five copies of the target DNA sequence could be detected with a high amplification efficiency (>94%). The protocol was verified in the detection of artificially infested soil samples containing different concentrations of *P. brassicae* resting spores, and used to investigate the distribution and population of *P. brassicae* in the fields for the clubroot risk prediction.

PAPER 4

Characterization of chinese cabbage clubroot by fourier transform infrared spectra

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Fourier-transform infrared (FTIR) spectroscopy technique has been used to detect and identify a variety of plant pathogen. In this study, roots and leaves from health and *Plasmodiophora brassicae* infested Chinese cabbage were characterized and compared based on FTIR spectroscopy. Our results showed that there were 11 and 12 peaks in FTIR spectra of roots from health and *P. brassicae* infested Chinese cabbage, respectively, while there were 5 and 6 peaks in the leaves from health and *P. brassicae* infested Chinese cabbage, respectively. Interestingly, there was a difference in FTIR spectra of roots and leaves from between health and *P. brassicae* infested Chinese cabbage. In particular, FTIR spectra revealed that 3 peaks at 3013.23, 2851.24 and 1331.61 were specific to roots of *P. brassicae* infested Chinese cabbage, while 2 peaks at 1257.55 and 1051.98 were specific to leaves of *P. brassicae* infested Chinese cabbage compared to the corresponding that of healthy Chinese cabbage. Overall, this study clearly indicated that FTIR spectra may give a new strategy for rapid identification of Chinese cabbage clubroot.

PAPER 5

The genome of the club root pathogen *Plasmodiophora brassicae*

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Plasmodiophora brassicae is the casual agent of the club root disease of the *Brassicaceae*, one of the most damaging diseases within this plant family. Despite its agricultural importance, the biology of *P. brassicae* remains poorly understood. Due to its obligate biotrophic nature, *P. brassicae* remains impossible to grow in axenic culture and the typical experimental systems for working with *P. brassicae* are comparatively unsophisticated. Molecular studies are especially challenging with only approximately 100 known genes. We recently succeeded obtaining the whole genome sequence from a *P. brassicae* single spore isolate. Our current assembly draft shows a total length of the genome sequence of 24 Mb, slightly larger as the previously estimation of the genome size of 18–20.3 Mb. Transcriptome data were obtained from clubs of infected Chinese cabbage and some life stage specific states from which around 10,000 genes were predicted. The sequence of our *P. brassicae* single spore isolate will be substantial as a reference to determine differences of *P. brassicae* races. Furthermore the exploitation of the life stage specific transcripts will shed light in the understanding of the life cycle at a molecular basis, which will in the long run help to understand and control club root disease. Further details on genome and transcriptome are presented.

PAPER 6

Use of genetics and genomics approaches to fine map the clubroot resistance "*CRb*" locus in *Brassica rapa*

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Clubroot disease, caused by the obligate plant pathogen *Plasmodiophora brassicae* Wor, is one of the most economically important affecting Brassica crops worldwide including oilseed *Brassica napus*, vegetable *Brassicas* such as *B. rapa* and *B. oleracea*. The genetics basis of clubroot resistance (CR) has been well studied and mapping of resistance loci have been reported in these species. We earlier reported mapping of clubroot resistance "*CRb*" locus in A3 chromosome of *B. rapa* (Chinese cabbage) using $F_{2/3}$ mapping populations derived from resistance and susceptible parental cross and tightly linked sequence characterized amplified region (SCAR) markers were developed by converting amplified fragment length polymorphism (AFLP) markers. In this study, fine mapping of *CRb* locus was done using 1500 F_2 lines. Combination of genetic mapping using SNP and other gene other gene specific markers, comparative mapping with *Arabidopsis thaliana* to identify potential resistance genes, and whole genome re-sequencing of resistance and susceptible parental lines were used to identify candidate gene causing resistance and susceptible phenotypes. We identified several candidate genes around the *CRb* region and parental nucleotide polymorphism were used to design SNP primers and validated by mapping. Of the 20 genes found to be putative candidate genes, one gene was found co-segregating with resistance phenotype. We developed few SNP markers (CRb-SNPs) based on parental differences observed in that gene which could be applied for marker assisted breeding of clubroot resistance phenotype in *B. rapa*, and believed that this gene is responsible for causing clubroot resistance. TIR-NBS-LRR domain was detected as a disease resistant candidate gene which showed consequential expression in the real-time PCR analysis that confers significant phenotypic relationship. The functional validation though transformation is underway.

PAPER 7

Clubroot disease control and genome sequencing of *Bacillus substilis* XF-1

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Bacillus subtilis XF-1 was isolated from *Plasmodiophora brassicae*-infected soil. It has been commercialized and can control clubroot disease of cruciferous crops with high efficiency, which is distributed worldwide and controlled difficultly, and suppressing many fungal pathogens of plants. The genome sequencing of *Bacillus subtilis* XF-1 was performed with a strategy involving Solexa paired-end sequencing technology. A library containing 500-bp inserts was constructed. Sequencing was performed with the paired-end strategy of 72,75-bp reads to produce 400 Mb of filtered sequences, representing a 100-fold coverage with an Illumina Solexa GA IIx (Beijing Genomics Institute at Shenzhen, China), and the reads were assembled into 148 contigs and 20 scaffolds using the SOAP denovo alignment tool (http://soap.genomics.org.cn/index.html#intro2). Both the gaps within and between the scaffolds were filled through sequencing of PCR products by primer walking through the use of an ABI3730 capillary sequencer. The complete genome sequence of strain XF-1 consisted of a circular 4,061,186-bp chromosome with a G□C value of 43.8%.The chromosome consisted of 3,853 genes (CDS), 9 rRNA operons, and 95 tRNAs. Genome annotation was performed at the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP), and the GenBank NR database and the KEGG and COG databases were employed for BLASTP identification. And its complete sequence of *Bacillus subtilis* XF-1 has been deposited in NCBI (Accession number CP004019). Five gene clusters, covering 3.5% of the whole genome, were involved in nonribosomal synthesis of lipopeptides, such as surfactin and fengycin; the polyketides bacillaene; and the dipeptide bacilysin. The complete gene cluster for synthesis and modification of TasA protein, a type of broad spectrum antibacterial protein, was detected in XF-1 and did mirror perfectly published gene *TasA*(corresponded with *Bacillus subtilis subsp. subtilis str.*168, Accession No:NP_390342.1). Chitosanase gene(*csn*) of XF-l, had an 83l bp coding sequence with 99% of similarity with those of *B. subtilis* 168. The *sacA* gene was detected in XF-1, shared 97% homology to the gene cluster of *B. subtilis* 168, which might improve the efficiency in use of sucrose.

Acknowledgement: This study was funded by the Ministry of Agriculture, China and the Department of Science and Technologies, Yunnan Province, China under the funds, Special Fund for Agro-scientific Research in the Public Interest (201003029) and the Natural Science Foundation of Yunnan Province (2008CC024), respectively.

PAPER 8

Effects of the biocontral agent *bacillus subtilis* xf-1 on microbial community diversity in the chinanese cabbage rhizosphere

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Microbes and microbial community play important roles in soil ecosystem. *Bacillus subtilis* XF-1 had strong inhibitory on the resting spore activety of *Plasmodipophora brassicae*. However, its potential effect on soil microbial community was still unknown. The objective of this study was to investigate the influence of biocontrol agent *Bacillus subtilis* XF-1 on microecosystem in the rhizosphere of Chinese cabbage, and to provide biosafety evaluation for the application of the bioagent. The TRFs obtained by T-RFLP was analyzed by PCA (Principal Component Analysis) with SPSS. There were a few differences between the control group(C1-7,every week) and the treatment group (X1-7, every week). Three weeks after applying XF-1, the difference between C3 and X3 was the most significant. And from the forth week, the influence of XF-1 became less and less obvious.The influence of biocontrol strain XF-1 to microbial diversity was obtained by the method T-RFLP analysis, and the effect of XF-1 on the rhizosphere soil bacterial communities and fungal communities was similar. The results showed that there were little influence to the soil microbial community at the beginning of its inoculation, and the effects of the third and the fourth week was the most apparent. Then, the impact of *B. subtilis* XF-1 on soil microbial community alleviated slowly weekly. At last, there was little difference between the control and treatment. The biocontrol agent XF-1 did not significantly affected the diversity of microbial communities in Chinese cabbage rhizosphere.

PAPER 9

Characterization of antibiotic substances from secondary metabolite of *Lysobacter spp.* strain

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Several *Lysobacter* spp. strains with antagonistic activities against *Xanthomonas oryzae* and *Plasmodiophora brassicae* were isolated from the rhizosphere of konjac and other plants. antibiotic compounds were obtained from the ethyl acetate, and further purified by sephadex LH-20 column chromatography, reverse C-18 Silica gel and high performance liquid chromatography (HPLC).The purified compounds was identified as 6-Methoxy-1-phenazinol-10-oxide, Phenazine, 1-Phenazinecarboxylic acid and 1-Hydroxy-6-methoxyphenazine (strain 13-1) by nuclear magneticresonance (NMR), ESI-Massspectrum and 1,6-Dimetho- xyphenazine (YFY02) by Gas chromatography-Mass Spetrometer(GC-MS) analysis; four kinds of Phenazine analogs strongly inhibited multiple Xoo strains growth. and reduced rice bacterial blight were above 60% in field experiments; YFY02 fermentation liquid and their cell-free culture filtrate both reduced the clubroot severity on Chinese cabbage by 62.41 74.6%.

PAPER 10

Water-mediated dissemination and chemical control of cabbage clubroot disease

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By planting a susceptible Chinese vegetable in the seed ling bed irrigated with Plasmodiophora brassicae Woronin contaminated water from floatation culturing system (FCS) and inoculated with the resting spores of the pathogen,the pathogenicity was analyzed in water and soil, the spread distance of the pathogen and clubroot disease severity in the soil with different water contents and irrigated with different resting spores water was investigated, and chemicals were screened in the FCS for the disease control. The results showed that FCS inoculated with the pathogen favored the disease spread, And disease severity was positively related to the inoculum number. Disease incidences were 9.51%,19.88%, 44.31%, 63.65% and 76.00% in FCS and 5.33%, 15.00%, 20.67%,43.33% and 45.00% in traditional soil culturing system when 103,104,105,106,107spores/g were inoculated onto Chinese cabbage respectively. Chinese cabbage became diseased when it was seeded in the culture substrate with 38%-115% water content, but the culture substrate with 77% water content best benefited the disease. When the plants growing in the substrate were 5cm and 10cm far from the pathogen, the disease incidence were 20.43% and 10.23% respectively. The active ingredient of 375.0mg/L chlorothalonil WP, 250.0mg/L carbendazim WP, 25.0mg/L cyazofamid SC, 125.0mg/L fluazinam SC and 262.5mg/L BAS651F were applied to the FCS, they could control 96.65%, 94.19%, 87.93%, 80.18% and 88.02% of the disease, respectively, but fluazinam SC and BAS651F inhabited the plant growth when their concentrations were used in this experiment.

Acknowledgement: This study was funded by the Ministry of Agriculture, China under the project, Special Fund for Agro-scientific Research in the Public Interest (201003029).

PAPER 11

Integrated control of *Spongospora subterranea* f.sp. *subterranea*, the cause of powdery scab of potato

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The soilborne pathogen *Spongospora subterranea* f.sp. *subterranean* (*Sss*) produces many resting spores which can remain dormant for long periods being highly resistant to environmental stresses and spread the disease mainly on seed potatoes but also via contaminated soil. Despite many years of research, no efficient and economically sound control method is available for powdery scab. A disease management strategy which integrates several components is the best long term approach to powdery scab control. 'Plant clean seed into clean soil' is a simple advice but yet very difficult to be fully applied. Planting clean seed prevents spread of the disease especially over long distances. This requires implementation of effective and internationally standardized certification rules. Visual inspection has to be optimized to avoid misidentification of scab symptoms, supported by immunotest, ELISA and molecular markers. A potential way of short distance dissemination is the spread of effluent of animals fed with diseased potatoes. Bioassay, immunology and molecular marker are all able to detect and quantify the pathogen in the soil, with different sensitivity. Unfortunately, none of them allow to clearly identify a healthy soil and, except for the bioassay, they detect also non-virulent inoculum. Host resistance breeding will be a key component. Numerous field screenings showed substantial differences in susceptibility to tuber infection but root infection should also be assessed. Powdery scab resistance is not yet a high priority trait in modern breeding. Recently, it was shown that the *Sss* populations worldwide possess a low genetic diversity, with the exception of South America, allowing future selection for resistance which is likely to be durable.

New knowledge for sustainable management of powdery scab of potato: *Spongospora* research in New Zealand

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Spongospora subterranea continues to cause problems for potato production in New Zealand, in seed tuber, processing and fresh market crops. Current research projects aim to develop effective, non-pesticide management for *Spongospora* diseases of potato (root infection, root galling and tuber powdery scab).

Potato breeding for powdery scab resistance Field trials to screen breeding lines for resistance to powdery scab have been a key component of the New Zealand potato cultivar development programme since 1991. Empirical breeding values (EBVs) are calculated from analysis of field disease assessments, taking account of pedigree relationships between breeding lines. Selection based on EBVs assists improvement of resistance levels in breeding populations, and development of new cultivars resistant to powdery scab.

Genetics of host resistance A bi-parental potato mapping population segregating for resistance to powdery scab, along with breeding lines and cultivars with known resistance phenotypes, are being used to identify genetic markers for resistance. The markers will be correlated with phenotypes (degree of susceptibility) determined in greenhouse and field trials, to assist rapid identification of germplasm with useful powdery scab resistance.

qPCR for *Spongospora* detection Quantitative PCR has been shown to be a sensitive tool for detection of early *Spongospora* infection of potato roots. The pathogen develops similarly in roots of cultivars with markedly different susceptibilities to tuber powdery scab, and qPCR has potential to differentiate host resistance to root infection.

Induced resistance to *Spongospora* Multiple applications of the defence elicitor ?-aminobutyric acid (BABA) reduced Spongospora root infection in a very susceptible cultivar. The chemical also up-regulated genes (e.g. chitinase, PR1-b) known to be involved with host defence.

Weeds confirmed as *Spongospora* hosts Nightshade weeds (*Solanum nigrum, S. physalifolium)*, commonly found in cropping fields, have been confirmed as hosts for the pathogen. Effective elimination of these weeds in crop rotations will diminish soil inoculum, and reduce incidence of powdery scab when potatoes are planted.

***Spongospora* root infection** The zoosporangium stage of the *Spongospora* life cycle (infection and multiplication in root epidermis cells), disrupts water and nutrient uptake by potato plants. These effects occur at low soil inoculum levels, and similarly in cultivars that are either resistant or susceptible to tuber powdery scab.

Soil nutrients and *Spongospora* infection Glasshouse experiments have assessed effects of different soil nutrients (as single factors) on potato root infection by the pathogen. Sulphur, boron and ammonium nitrogen markedly reduced infection, and silicon mitigated harmful effects of root infection on plant growth. Iron, sulphate sulphur, manganese, zinc, nitrate nitrogen and differing soil pH had minimal or no effects.

***Spongospora* effects on crop yields** A recent intensive crop monitoring project has shown that potato yields were reduced in crops where soilborne diseases were most severe. Yields were least where *Spongospora* root galling, *Rhizoctonia* stem canker and soil compaction were detected, and greatest where these factors were absent or rare. Field crops with severe *Spongospora* root galling are common, and the root stages of the pathogen cycle are increasingly recognised as limiting to tuber yields.

Poster

Efficacy of Vapam to control clubroot (*Plasmodiophora brassicae*) in canola

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Clubroot, caused by *Plasmodiophora brassicae*, is a serious threat to canola (*Brassica napus*) production across large regions of the Canadian prairies. Experiments were conducted under controlled environmental conditions to assess the effect of sodium N-methyldithiocarbamate (a soil fumigant, trade name Vapam) on primary and secondary infection, final clubroot severity, and on the growth parameters of a susceptible canola cultivar. Each of the application rates of Vapam (0.4, 0.8, 1.6 mL L^{-1} soil) produced a 12–16 fold reduction in primary infection, secondary infection, and clubroot severity. After the initial crop was harvested (and all clubbed roots removed), canola was reseeded in the same pots. The residual effect of Vapam at 0.8 and 1.6 mL L^{-1} reduced infection and clubroot severity, and improved plant growth relative to the nontreated control. Application of Vapam at soil moisture levels in the range of 10–30% (water:soil, v:v) reduced clubroot severity and improved plant growth, compared to application of water at lower volumes. We conclude that application of Vapam substantially reduced clubroot severity and may be useful for clubroot management in Brassica vegetables, and reduction/eradication of localized infestations of clubroot in commercial canola fields.