

isolates from multiple countries, which suggests international movement may have occurred more than once. The challenges to, and opportunities for, preventing future dispersal are discussed.

#### Identification of Resistance to Wet Bubble Disease and Genetic Diversity in Wild and Cultivated Strains of *Agaricus bisporus*

X. WANG, Y. Li, Y. FU, Jilin Agricultural University, CHANGCHUN, CHINA

Outbreaks of wet bubble disease (WBD) caused by *Mycogone perniciosa* are increasing across the world and seriously affecting the yield of *Agaricus bisporus*. However, highly WBD-resistant strains are rare. Here, we tested 28 *A. bisporus* strains for WBD resistance by inoculating *M. perniciosa* spore suspension on casing soil, and assessed genetic diversity of these strains using 17 new simple sequence repeat (SSR) markers developed in this study. We found that 10 wild strains originating from the Tibetan Plateau in China were highly WBD-resistant strains, and 13 cultivated strains from six countries were highly susceptible strains. A total of 88 alleles were detected in these 28 strains, and the observed number of alleles per locus ranged from 2 to 8. Cluster and genetic structure analysis results revealed the wild resources from China have a relatively high level of genetic diversity and occur at low level of gene flow and introgression with cultivated strains. Whole-genome resequencing got the same result and show that wild strains from the Tibetan Plateau and cultivated strains from Europe and America, maybe originated from two different ancestors, evolved parallelly in different ways because of geographic isolation, but there existed genetic exchanges. Moreover, the wild strains from China potentially have the consensus ancestral genotypes different from the cultivated strains and evolved independently. Therefore, the highly WBD-resistant wild strains from China and newly developed SSR markers could be used as novel sources for WBD-resistant breeding and quantitative trait locus (QTL) mapping of WBD-resistant gene of *A. bisporus*.

#### MLVA-based diversity analysis of *Xanthomonas axonopodis* pv. *manihotis* (*Xam*) populations in Mali

M. KANTE (1), L. Blondin (2), C. M. Flores M (3), L. Y. Rache Cardenal (4), I. Wonn (5), K. Dagno (6), S. Restrepo (4), A. J. Bernal (7), R. Koebnik (3), V. M. Verdier (8), O. Koita (9), C. Verniere (10), B. Szurek (3), (1) Université de Segou, IRD, LBMA, Segou, MALI; (2) CIRAD-UR Bioagresseurs, Montpellier, FRANCE; (3) IRD, Cirad, Université de Montpellier, IPME, Montpellier, FRANCE; (4) Universidad de los Andes, Bogota, COLOMBIA; (5) Institut de l'Environnement et de la Recherche Agricole (INERA), Bobo Dioulasso, BURKINA FASO; (6) Institut d'Economie Rurale (IER), Prog Sorgho/ Lab de Phytopathologie, CRR de Sotuba, Bamako, MALI; (7) Universidad de los Andes, Laboratorio de Interacciones Moleculares de Microorganismos Agr, Bogota, COLOMBIA; (8) IRD, Cirad, Univ Montpellier, IPME, Montpellier, FRANCE; (9) University of Sciences, Techniques and Technologies of Bamako (USTTB), LBMA, Bamako, MALI; (10) CIRAD, UMR BGPI, Montpellier, FRANCE

Cassava Bacterial Blight (CBB) caused by the bacterium *Xanthomonas axonopodis* pv. *manihotis* (*Xam*) occurs on several continents including West Africa where it has recently been reported in Burkina Faso and Ivory Coast, sometimes imposing severe yield losses. The genetic diversity of CBB in Mali, a country bordering both Burkina Faso and Ivory Coast, was investigated in 2015 in two cassava production regions (Bamako and Ségou). Forty strains were isolated from cassava leaves showing angular leaf spots symptoms typical of CBB. Colonies were identified as *Xam* after specific PCR diagnostic tests and pathogenicity assays. The Koch postulate was further validated. Subsequently, a multilocus variable number of tandem-repeat (VNTR) analysis (MLVA) scheme based on 14 microsatellites discriminated 18 haplotypes out of the 40 isolates. The two populations of Ségou and Bamako were genetically differentiated (RST = 0.262, P < 0.001). A greater diversity was observed in the population of the Bamako region compared to that of Ségou with an allelic richness of 2.96 and 2.07, respectively. A unique haplotype was shared by strains from Bamako and Ségou but strains from both regions are associated in different clonal complexes supporting epidemiological link between those two regions. New surveys carried out in 2016 in five production areas have made it possible to isolate 29 populations (corresponding to over 300 *Xam* strains), whose analysis of the genetic structure is in progress. The data collected will help to rationalize the use of cassava variety grown in Mali.

#### Virulence characterization of *Puccinia striiformis* f. sp. *tritici* collections from China, Italy, Mexico, and Ecuador

M. Wang PhD (1), A. Wan (2), M. Li (3), M. Maccaferri (4), P. Figueroa (5), C. W. Barnes (6), D. Campana (7), X. CHEN (8), (1) Washington State University, Pullman, WA, USA; (2) Washington State University, Pullman, WA, USA; (3) Institute of Agricultural Environment and Resources, Kunming, Yunnan, CHINA; (4) University of Bologna, Viale Fanin, ITALY; (5) Mexican National Institute for Agricultural Research, Obregon, MEXICO; (6) Instituto Nacional de Investigaciones Agropecuarias, Quito, Pichincha, ECUADOR; (7) INIAP Estación Experimental Santa Catalina, Quito, ECUADOR; (8) USDA ARS, Pullman, WA, USA

*Puccinia striiformis* f. sp. *tritici* (*Pst*) causing stripe rust is one of the most important pathogens on wheat worldwide. The fungus evolves into different virulent races to overcome resistance. In 2014-2017, 443 isolates were recovered from collections of China (141), Italy (133), Mexico (123), and Ecuador (46). These isolates were tested with 18 wheat *Yr* single-gene lines that are used to differentiate *Pst* races in the U.S. A total of 132 *Pst* races were detected, including 105 new races. The number of unique races in China, Mexico, Italy, and Ecuador were 54, 25, 24, and 18, respectively. None of the races were shared by more than two countries, but 4 races were shared by China and Italy, 3 by China and Mexico, and 4 by Ecuador and Mexico. The top three Mexican races, PSTv-37 (40.7%), PSTv-52 (17.1%), and PSTv-198 (9.8), were similar to those identified in the US in 2016. Overall, virulences to *Yr9*, *Yr43*, *YrExp2*, *Yr6*, *Yr7*, and *Yr44* were most frequent (81.0-90.3%); those to *YrTr1*, *Yr8*, *Yr76*, *Yr27*, *Yr17*, *YrSP*, and *Yr1* were moderate (17.8-59.6%); and those to *Yr10*, *Yr32*, and *Yr24* were low (0.5-1.1%). None of the races were virulent on *Yr5* and *Yr15*. Significant variations in frequency were detected for virulences to *Yr1* (10.6% in Mexico to 85.8% in China); *Yr17* (11.3% in China to 71.4% in Italy); *Yr27* (3.0% in Italy to 84.6% in Mexico); and *Yr76* (6.5% in Ecuador to 83.0% in China). The information is useful for understanding epidemiology and controlling stripe rust.

#### Population dynamics of the late blight pathogen in Canada for 2017

R. D. PETERS (1), K. I. Al-Mughrabi (2), F. Daayf (3), A. MacPhail (1), L. Kawchuk (4), (1) Agriculture and Agri-Food Canada, Charlottetown, PE, CANADA; (2) New Brunswick, Agriculture, Aquaculture & Fisheries, Wicklow, NB, CANADA; (3) University of Manitoba, Winnipeg, MB, CANADA; (4) Agriculture & Agri-food Canada, Lethbridge, AB, CANADA

Late blight was once again an important disease issue for both potato and tomato crops in Canada in 2017. Plant tissue samples infected with the late blight pathogen were received from several potato and tomato production regions in Canada. Using established protocols, *Phytophthora infestans* was isolated from these samples and assessed to determine genotype, mating type and metalaxyl-m sensitivity. Pathogen isolates collected from British Columbia potatoes were identified as the US-11 genotype, which is an A1 mating type and highly resistant to metalaxyl-m. Samples received from all other production regions, including Alberta, Manitoba, Ontario and New Brunswick yielded isolates of the US-23 genotype, which is an A1 mating type and sensitive to metalaxyl-m. Although isolates of US-23 were often sensitive to metalaxyl-m early in the season, increased resistance to this chemical pesticide was documented as the season progressed. Greenhouse/storage trials revealed that US-23 was less aggressive on potato foliage than US-8 or US-24, but equally aggressive as the other genotypes on potato tubers. The US-23 genotype has become the predominant genotype in most growing regions across Canada in recent years. However, every year there are fluctuations in the genotypes found, which underscores the importance of

Kante M., Blondin L., Flores C. M., Cardenal L. Y. R., Wonni I., Dagno K., Restrepo S., Bernal A. J., Koebnik Ralf, Verdier Valérie, Koita O., Icard-Vernière Christèle, Szurek Boris.  
(2018)

MLVA-based diversity analysis of *Xanthomonas axonopodis* pv. *manihotis* (Xam) populations in Mali

Phytopathology, 108 (10), 88-88. ISSN 0031-949X