

Travel Fund Report

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12th International Verticillium Symposium (IVS)

6 – 9 October, 2016

Ljubljana, Slovenia



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Emma Cascant Lopez

NIAB-EMR, East Malling, Kent

The International Verticillium Symposium (IVS) is held every 3-4 years and this year the 12th IVS took place from 6-9th October 2016 in Ljubljana, Slovenia. This conference brought together researchers and agribusiness from around the world with the common goal of gaining on the scientific progress achieved during the previous 3 years in understanding Verticillium life-cycles, fungus epidemiology, disease control and management, taxonomy, genetics and genomics, host-Verticillium interactions and resistance.

Verticillium spp are economically important soil-borne plant pathogens responsible of Verticillium wilt disease. They affect over 300 plant species including relevant UK crops such as potatoes, hops and strawberries. They infect the plants via the root system causing chlorosis, wilting of the foliage and subsequent death. The disease causes significant losses in yield, largely due to the withdrawal of broad-spectrum chemical fumigants. Furthermore, the dormant survival structure, known as microsclerotia, can survive up to 14 years in the soil, making effective control difficult. Therefore, the characterization of the fungal biology and pathogenicity and the breeding of resistant cultivars are important for an efficient disease control and management.

IVS gathered for four days with approximately 100 people from 22 different countries attending. The main Verticillium species addressed were *Verticillium dahliae*, *Verticillium nonalfalfae* and *Verticillium longisporum*. More than 20 different hosts were tackled, including; cotton, hops, olive trees, oilseed rape, tomatoes and potatoes. Strawberry plants were mentioned for the first time in the history of the IVS by the author of this report representing NIAB-EMR. Predominantly, researchers around the world would have dedicated much effort towards the search for resistance of different cultivars and deciphering the genetic basis of pathogenicity. It was an extensive symposium, bringing together the wisdom of veteran specialists in the field of Verticillium and the strong influence of genetic and genomic studies that had substantially increased from previous editions.

The different sessions involved keynote lectures and selected abstract talks. In addition, there were two poster sessions. The conference started with an interesting talk about retrospective prospects of Verticillium wilt in Slovenia, and how lethal pathotypes arised approximately 50 years after the appearance of mild pathotypes in England, Slovenia and Germany throughout history. Hops are a very important crop in Slovenia and England and both suffer from severe damage caused by *V. nonalfalfae*. To supress and prevent the disease, research activities have focused on resistant breeding

programmes and the identification of QTLs for *Verticillium* resistance in hops. They also emphasised the importance of plant waste burning methods after harvesting, crop rotation in affected fields and the positive effect of solarisation in warm regions as a control method. Another relevant talk discussed the *Verticillium dahliae* management through soil disinfection. The idea was to reset the microbial population to increase beneficial microbes, and attack at the most vulnerable stage of the disease (the end of the cycle where microsclerotia is incorporated into the soil), where the soil-borne pathogen is concentrated and has not spread around the field. Therefore they performed crop rotation, replacing the sensitive host eggplant with broccoli or lettuce. Furthermore they included organic soil amendments such as broccoli residue and crab meal (which have demonstrated disease suppressive effects in previous research). They observed a significant reduction of microsclerotia particles in the soil at the end of each season.

The session on taxonomy and genetics focused on *V. longisporum*, which is an interspecific hybrid and the only non-haploid species in *Verticillium* genus, and *V. dahliae*, which is one of the parental strain of *V. longisporum*. At present, the evolutionary mechanism responsible of segregation within lineage of *V. longisporum* A1/D1 (responsible of the disease), may originate from the same hybridization event followed by subsequent divergence or may represent two separate hybridization events. In *V. dahliae*, studies by means of vegetative compatibility groups (VCGs) showed evidence of recombination events distributed throughout the genome and widespread among clonal lineages, suggesting that clonal lineages arose by sexual reproduction. Genomic data also showed that transposons are the major driving force for adaptive genome evolution and that lineage-specific (LS) regions are enriched in active transposons. Furthermore, virulence genes reside in these transposon-rich genomic regions. Studies conducted in *V. nonalfalfae* revealed a lethal specific (LthS) genomic region common to aggressive strains and absent in mild strains. Interestingly, conserved blocks of genes were found between *V. nonalfalfae* LthS regions and a LS region of *V. dahliae*, suggesting inter-species gene transfer.

Moving to the virulence and host-pathogen interactions session, description of new putative effector genes were mentioned. VdSCP7 is a novel nuclear effector described in *V. dahliae* with the ability to modulate immunity of cotton plants. NLP (NEP1 like) proteins from *V. dahliae* showed effector properties, and its overexpression in different fungal pathotypes increased virulence in different hosts. An interesting study carried on the model plant *Arabidopsis* identified two disease phenotypes, 'wilting' and 'chlorosis'.

The 'chlorosis' phenotype was accompanied by *de novo* xylem formation in plants infected by *V. longisporum*, resulting in enhanced plant water storage capacity and drought tolerance. A highly relevant study to my project was looking at the velvet superfamily. This protein superfamily formed by VeA, LaeA and SteA, regulate secondary metabolism and induces differentiation of fungal development and regulates reproduction and pathogenicity. Moving onto the epidemiology and disease management session, an study showed that the application of fungicides during the potato growing season lead to a significant reduction in *V. dahliae* disease parameters and an increase of plant parameters. The fungicides tested were thiophanate methyl and azoxystrobin and were applied by foliar spray or by chemigation through drip irrigation. Researches in Spain raised awareness about the dispersal of *V. dahliae* by symptomless planting stock and reported the positive effect of mycorrhizae in olive trees. One German researcher suggested that *V. longisporum* could be retrieved from oilseed rape seeds of inoculated plants and the amount of the fungus recovered was dependent to the susceptibility of the plant. Highlighting the need for careful selection of seeds. During the host resistance session, investigators in China showed that the expression levels of lignin synthesis-related genes are induced more quickly in resistant cultivars of cotton. Specially, the gene GbERF1 which was found to contribute substantially to resistance to *V. dahliae*. Resistant olive rootstocks were evaluated for effectiveness in the south of Spain, but results showed that high disease pressure could overcome the resistance conferred by the rootstock to the grafted variety over the time. *Pseudomonas fluorescens* PICF7 was found to be an endophyte of olive roots exerting effective *Verticillium* disease biocontrol. A very interesting talk showed that the biocontrol agent, *Paenibacillus polymyza* Sb3-1, was able to reduce the growth of *V. longisporum* EVL43 significantly in the *in vitro* and *in planta* experiments. To finish, Belgian scientists described that the isolate *Verticillium isaacii* Vt305 has a biocontrol effect on *V. longisporum* wilt in cauliflower. To date, none of these biocontrol agents have been trialled on a commercial scale.

I am very grateful to GCRI trust that enabled me to attend the IVS 2016 conference. This was particularly important for me since it was my first international conference and also because it was very relevant for my current research and provided me the opportunity to meet and network with key researchers in the area of *Verticillium* wilt and to discuss novel strategies that will allow me to enhance and complement the research I am undertaking for my PhD.

