**International Allium Conference, Madison Concourse Hotel, Madison, Wisconsin, USA, 24th – 27th July 2019.**

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**Headlines**

* CRISPR genome editing is being developed as a technique for onion improvement and could be a vitally important technique for the sustainability of future crop production
* An onion genome sequence should be available in the future. This has been particularly challenging due to the huge genome size, but with advances in long-read sequencing, it seems likely that any plant species could be sequenced in the future.
* Fusarium disease continues to be a problem for onion and many other crops. Control is challenging and host resistance is key. Saponins (mainly produced by shallots) play an important role in resistance to *Fusarium*.
* Based on extensive field trials in the USA, arbuscular mycorrhizal fungi had no growth promoting effects on onion.
* Floral morphology and sugar content play an important role in seed production as they directly influence the number of honeybee visits. Therefore it may be possible to select for more productive lines based on floral morphology.
* Less thrip damage occurs on onion plants with a glossy (not waxy) or semi-glossy phenotype.

**Background**

This conference was held in Madison, Wisconsin, in a location that was close to the University of Wisconsin. It was held as a joint meeting of the American National Onion Association, the American National Allium Research Conference and the International Allium Research Symposium. This made the event particularly valuable and meant it was attended by a wide range of people including growers, industry representatives and academics. There were attendees many different countries and the conference included a visit to Gumz Farms and Seminis Seeds. Whilst this event focussed on Allium crops, many of the topics discussed have relevance across a range of crops.

**Travel Findings**

On the first day of the conference, Brian Kvitko from the University of Georgia presented some interesting work on bacterial rots of onion caused by *Pantoea* species, particularly *P. ananatis*. This pathogen becomes systemic, may move in the vascular tissue and can reach very high concentrations, especially in dead tissue. Using whole genome sequencing, they identified 57 plasmid genes potentially involved in infection and 2 virulence factors. It is proposed that the acquisition of genes that confer tolerance to allicin, a pungent antimicrobial compound found in Alliums, has led to the emergence of highly pathogen strains on *Pantoea* and other bacterial pathogens. There was also an interesting talk from Patrick Krysan from the University of Wisconsin. In collaboration with Warwick University, they are developing a protocol for CRISPR/Cas9 gene editing in onion, something which will be of great value to future research. Genome editing is currently being pursued in a range of crops and allows for precise editing of any known gene to provide a desired phenotype such as disease resistance. In this project, building on foundational work in the model plant *Arabidopsis thaliana*, they are particularly interested in developing haploid-inducer lines for onion, something which would greatly accelerate the production of doubled haploid lines for hybrid seed production and could potentially be applied to other crops. Oori Weisshaus from NRgene presented some preliminary data from garlic genome sequence and set out some proposals for sequencing the onion genome. This has been challenging due to size of the onion genome and the presence of repetitive regions. However, with the advent and evolution of long-read sequencing technologies, an onion genome sequencing project is now feasible and Oori plans to set up a consortium to achieve this goal.

On the second day, Brian Thomas (University of Warwick) gave a fitting tribute to the works of Jim Brewster, a prominent Allium scientist who sadly passed away in 2015. Jim is particularly well known for his book ‘Onions and other vegetable Alliums’ which brings together many years of Allium research in a single text. Brian also presented data on the role of several different *FLOWERING LOCUS* T (*FT*) genes in flowering or bulbing in onion. FT genes are well known for controlling flowering in other crops and it appears that these genes play a key role in other daylength controlled processes such as onion bulbing. Irwin Goldman (University of Wisconsin) gave an interesting presentation on speeding up onion breeding and through a greater understanding of dormancy and vernalisation they can now go from seed to seed in 12 months. The optimum conditions for vernalisation were found to be 10°C for 14 weeks although this is cultivar dependent. A 2-4 hour treatment of bulbs with hydrogen peroxide also helped break dormancy. Lindsey du Toit (Washington State University) spoke about the results of many field trials on the possibility of utilising arbuscular mycorrhizal fungi (AMF) to improve onion yield. Past research in controlled environment / glasshouse conditions have shown a strong growth-promoting effect of AMF. Whilst more colonisation and AMF diversity was observed in organic vs conventional soil, no significant growth enhancements were observed with any AMF product tested. For several liquid AMF formulations, no colonisation was observed at all. Whilst these results are disappointing, it is very important information for onion growers. Whilst the utility of AMF inoculants cannot be dismissed, under the production practices (direct-seeding) in the Columbia Basin, they offered no advantages.

*Fusarium oxysporum* causes disease on a wide range of horticultural crops throughout the world (e.g. onion, lettuce, daffodil, tomato, cucumber). Control is challenging and host resistance is key. At this conference, I presented work on identifying resistance to *Fusarium oxysporum* f. sp. *cepae* (FOC), causing onion basal rot, and the identification of molecular markers linked to resistance. Day 3 began with a keynote presentation from Masayoshi Shigyo (Yamaguchi University) who has worked on onion breeding / genetics for many years. Much of his work has been done on *A. fistulosum* – *A. cepa* monosomic addition lines which have used for obtaining genomic information in *A. cepa*. He revealed that his group have generated genome sequence data which has been combined with data from a commercially funded (SEQUON) project in the Netherlands to reduce the number of contigs from 6 million to 90,000, providing a significant step towards a high quality onion genome sequence. He also discussed his work on FOC resistance and the role of saponins, particularly alliospiroside a and b. High levels of these compounds are strongly associated with disease resistance. Olga Scholten (Wageningen University) discussed her work on surveying *Fusarium* populations on onions in the Netherlands and is using PCR primers from previous research I carried out to characterise isolates. Recent advances in our understanding of pathogenicity in *Fusarium oxysporum* has allowed for the identification of pathogenic isolates through molecular tests, thus removing the need for expensive and time-consuming pathogenicity testing. Our group has also developed a quantitative molecular diagnostic assay for FOC, something which will be greatly useful for future testing of plant and soil samples for disease. Mike Havey (University of Wisconsin) gave an update on many years of work on the role of leaf waxes In resistance to thrips. Less thrip damage occurs on plants with a glossy (not waxy) phenotype. However, onions need waxes to protect them from other pathogens so he has been working on a ‘semi-glossy’ phenotype which does not have less wax, just a different compliment of waxes. He has found that you can select for the right compliment of waxes that still gives a resistant phenotype.

Finally, on day 4, the keynote speaker was Claudio Galmarini (Instituto Nacional de Tecnología Agropecuaria, Argentina) who discussed the role of honeybees in seed production. He found that open-pollinated lines have more honeybee visits than male sterile lines, due to more sugars being present. This leads to greater seed production. He also reported an influence of floral morphology on seed production and it should therefore be possible to select more productive male sterile lines using floral morphological characters. The conference also included visits to Gumz Farms and Seminis Seeds, allowing all attendees to see the scale of onion breeding and production in the USA. It was particularly interesting to observe onion production on the very high organic ‘muck’ soils in Wisconsin, an area that is very highly productive.



Onion production on high organic matter ‘muck’ soils (left) and onion seed production in cages at Seminis Seeds (right) where either blow flies or bees are used as pollinators.

**Personal Statement**

This trip allowed me to learn about the latest techniques and problems associated with crop production. As a researcher who works very closely with the UK Horticultural industry, I hope to use this knowledge to directly benefit UK horticulture. Having worked on Fusarium diseases for nearly 10 years, it was of great benefit for me to discuss the issues with fellow researchers such as Chris Cramer (New Mexico State University), Masoyoshi Shigyo (Yamaguchi University) and Lindsey du Toit (Washington State University) who have vast experience in this area. I was also able to make numerous contacts for future collaborative projects. In the future, I will be part of the onion genome sequencing consortium, a resource which will eventually have a great benefit for horticultural research. This trip also gave me the opportunity to present my research on an international stage, benefiting my own development and showcasing UK horticultural research.

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**Acknowledgements**

I am grateful to the GCRI Trust as well as the Vegetable Research Trust for funding my trip. I would also like to thank Professor Mike Havey (University of Wisconsin) for inviting me to speak and supporting our work for many years.