



15th World Congress on Parasitic Plants

June 30 – July 5 2019, Amsterdam, The Netherlands





Sponsors 15th World Congress on Parasitic Plants, 30 June – 5 July 2019, Amsterdam, the Netherlands



University of Amsterdam





RESEARCH PROGRAM ON Grain Legumes and Dryland Cereals



The Federation of European Societies of Plant Biology



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SCHEDULE OF ORAL PRESENTATIONS

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16.00 20.00	SUNDAY, JUNE 30	
16.00 - 20.00	Registration open	
18.00 - 21.00	Welcome mixer with snacks sponsored by Trends in Plant Science Cell Press	
MONDAY, JULY 1		
09.00 - 09.20	Welcome by Julie Scholes and Harro Bouwmeester	
09.20 – 12.40	Host plant resistance Session chair: Steve Runo	
09.20 - 09.55	The parasite <i>Cuscuta australis</i> with a streamlined genome mediates inter-plant systemic signals <i>Jianqiang Wu</i>	
09.55 – 10.30	Cuscuta microRNAs target host mRNAs involved in defence and vascular function Michael Axtell	
10.30 - 11.00	Coffee break	
11.00 – 11.25 11.25 – 11.50	Interspecific long-distance movement of <i>Cuscuta</i> small RNAs control biological processes in host-parasitic plant complex <i>Koh Aoki</i> A peptide motif of a parasitic plant cell wall protein is recognized by the receptor protein CuRe1 and induces defence	
11.50 – 12.15	in tomato Markus Albert Molecular basis for tomato resistance to the parasitic plant Cuscuta	
	Neelima Sinha	
12.15 – 12.40	Characterization of resistance to sunflower broomrape (<i>Orobanche cumana W.</i>) in sunflower (<i>Helianthus annuus L.</i>) <i>Dana Sisou</i>	
12.40 – 12.50	International consortium on sunflower broomrape resistance Stephane Munos & Begoña Pérez-Vich	
12.50 – 14.15	Lunch	
14.15 – 18.00	Ecology, phylogeny and evolution Session chair: Claude DePamphilis	
14.15 – 14.50	Eco-evolutionary causes and consequences of parasitism in plants	
14.50 – 15.25	Susan Wicke Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant Balanophora Claude dePamphilis	
15.25 - 15.50	A neglected alliance in battles against parasitic plants: AM and rhizobial symbioses alleviate damage to a legume host by root hemiparasitic <i>Pedicularis</i> species <i>Airong Li</i>	
15.50 - 16.20	Coffee break	
16.20 - 16.45	When the same is not the same Peter Toth	
16.45 – 17.10	Genetic diversity of <i>Orobanche cumana</i> (sunflower broomrape) populations at the world level revealed by SSR markers Luyang Hu	
17.10 - 17.35	Facultative parasitism: an evolutionary precursor of complete parasitism or an effective strategy in its own right? Lammert Bastiaans	
17.35 – 18.00	Fitness of reciprocal F1 hybrids between <i>Rhinanthus minor</i> and <i>R. major Renate Wesselingh</i>	
18.00 - 19.30	Poster viewing with drinks	
19.30 - 21.00	Dinner	
21.00 -	Bar conference centre open	
TUESDAY, JULY 2		
09.00 - 12.45	Genes and genomes	
09.00 - 09.35	Session chair: <i>Jim Westwood</i> Cuscuta campestris: A plant genome under the influence of a parasitic lifestyle	
09.35 – 10.10	Kirsten Krause Genetic basis for host and parasitic plant communication	





Satoko Yoshida

10.10 - 10.35	Exploring the evolutionary origin of haustorium development in root parasitic plants Daniel Steele
10.35 – 11.05	Coffee break
11.05 – 11.30	Where the action is: gene expression at the parasite-host interface
11.30 – 11.55	Elizabeth Kelly Convergent horizontal gene transfer and crosstalk of mobile nucleic acids in parasitic plants Claude dePamphilis
11.55 – 12.20	The identification of candidate pathogenicity-related genes from the genome of <i>Striga hermonthica James Bradley</i>
12.20 – 12.45	Lack of evidence for horizontally transferred genes in mitochondria of <i>Cuscuta</i> species <i>Benjamin Anderson</i>
12.45 - 14.15	Lunch
14.15 – 18.10	Molecules and Biochemistry Session chair: David Nelson
14.15 – 14.50	CHEMICALS that control Striga germination
14.50 – 15.25	Tadao Asami Signalling pathways in Striga hermonthica germination Shelley Lumba
15.25 - 15.50	Complementary hormone-based approaches for Striga Control Salim Al-Babili
15.50 - 16.20	coffee break
16.20 – 16.55	Unravel strigolactone signaling and controlling parasitic plant behaviors in Striga
16.55 – 17.20	Yuichiro Tsuchiya Structural and biochemical characterization of strigolactone parasitic receptors, understanding their functionality and how to inhibit them
17.20 - 17.45	Amir Arellano Saab Identification and characterization of α-galactosidase capable of hydrolyzing planteose in <i>Orobanche minor</i> as a target for control of root parasitic weeds Atsushi Okazawa
17.45 – 18.10	Cannalactone: a new non-canonical strigolactone exuded by <i>Cannabis sativa</i> roots with a pivotal role in host specialization within French broomrape (<i>Phelipanche ramosa</i>) populations Jean- <i>Bernard Pouvreau</i>
18.10 - 19.30	Poster viewing with drinks
19.30 - 21.00	Dinner
21.00 -	Bar conference centre open
09.00 – 12.45	Control and Management Session chair: Maurizio Vurro
	WENDNESDAY, JULY 3
09.00 – 09.35	Striga research on finger millet: protocols, GWAS and RNA sequencing
00.25 10.10	Damaris Odeny
09.35 - 10.10	Damaris Odeny Parasitic weed management - opportunities and challenges Hanan Fizenbara
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THURSDAY JULY 4		
09.00 – 12.45	Parasitic plant biology Session chair: Airong Li	
09.00 - 09.35	Understanding the arms race: host resistance and parasite virulence in the <i>Striga</i> -cereal interaction <i>Julie Scholes</i>	
09.35 - 10.10	Native parasitic plants: a solution of plant invasions worldwide? Jakub Tesitel	
10.10 – 10.35	Transcriptomics to farmer field: a system biology approach for commercializing root parasitic <i>Santalum album</i> (Sandalwood) Pradeepa Bandaranayake	
10.35 - 11.05	Coffee break	
11.05 – 11.30	Reproductive biology and pollination of <i>Cynomorium songaricum</i> (Cynomoriaceae) <i>Guilin Chen</i>	
11.30 – 11.55	Triphysaria controls vegetative self-recognition by restricting release of HIFs in roots Yaxin Wang	
11.55 – 12.20	Analysis of genetic variation in pre and post attachment resistance mechanisms in maize inbred lines to the parasitic weed <i>Striga hermonthica</i> ; implications for control <i>Mamadou Cissoko</i>	
12.20 – 12.45	Impact of the soil microbiome on <i>Striga</i> -sorghum interaction Desalegn Etalo	
12.45 - 14.15	Lunch	
14.15 – 18.00	Parasitic plant-host interaction Session chair: John Yoder	
14.15 – 14.50	War and peace – the molecular dynamics of compatible and incompatible <i>Striga</i> -host plant associations <i>Mike Timko</i>	
14.50 – 15.25	What model plants can tell us about parasitic plants Thomas Spallek	
15.25 - 15.50	Message received: Evidence for translation of mobile mRNAs in <i>Cuscuta</i> -host interactions <i>James Westwood</i>	
15.50 - 16.20	Coffee break	
16.20 – 16.45	The roles and functions of lignin in parasitic plant-host interaction Songkui Cui	
16.45 – 17.10	A receptor and pathways discovered in the lignin-based resistance to <i>Cuscuta campestris</i> in Heinz hybrid tomato cultivars Min-Yao Jhu	
17.10 - 17.35	Cytokinins act as signaling molecules within the rhizosphere to trigger haustorium formation in the holoparasitic plant <i>Phelipanche ramosa</i> Estelle Billard	
17.35 – 18.00	Striking vegetative developmental convergence in endoparasitic angiosperms Luiza Teixeira-Costa	
18.00 - 19.30	Poster viewing with drinks	
19.30 - 21.00	Dinner	
21.00 -	Bar conference centre open	
	Departure participants	





[P24] Validation of broomrape resistance QTLs in sunflower line HA-267

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Broomrape (Orobanche cumana) is a parasitic weed that causes substantial yield losses in sunflower. While chemical options for suppressing sunflower broomrape are available, breeding for resistance has both economic and environmental advantages. In a previous study, we reported on the mapping of polygenic broomrape resistance in the HA-267xOD-DI-82 mapping population. We identified 2 major quantitative trait loci (QTL), or 7.1 and or12.1, as well as numerous small effect QTLs that were dispersed across the genome. While these results provided valuable insights into the complexity of resistance to broomrape, QTL validation is an important and often overlooked step for breeding. The aim of this study is to assess the effects of these QTLs in an unrelated genetic background and to identify QTLs that are stable and thus have the highest breeding value. To achieve this goal, resistant line HA-267 was crossed with a susceptible parental line HA-26-PR, and a mapping population consisting of 189 individuals was developed. Following phenotyping, we used selective bulked segregant analyses coupled with genotyping-by-sequencing (GBS) to re-map QTLs conferring resistance to broomrape population LP12BSR. A total of 7 QTLs were identified. The results confirmed that the effects of QTLs or 7.1 and or 12.1 was large and consistent. Importantly, an additional QTL located on sunflower chromosome 3 (or3.1), which was previously proven to control resistance to broomrape race E, appeared to have a larger effect in the new HA-267xHA-26-PR cross compared to the previous one (HA-267xOD-DI-82). These validated and stable QTLs will be prioritized in breeding, and associated molecular markers will facilitate marker-assisted selection.