



Global Council for Innovation in Rapeseed and Canola

“Building a World community for Innovation on Rapeseed and Canola”

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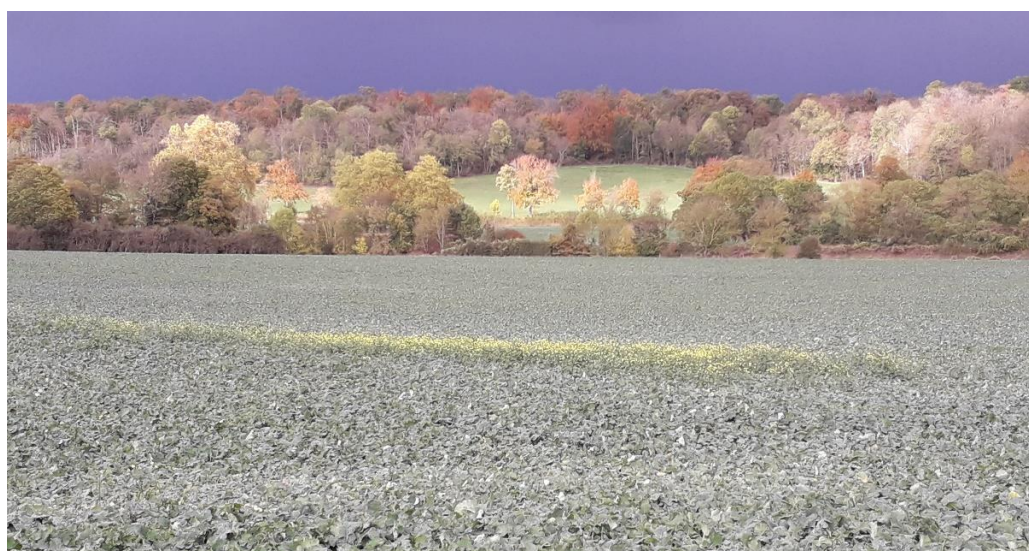


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Editorial

2019 has been a very rich year for the GCIRC, with key steps in its life, with a very successful world congress and important evolutions in its statutes. The end of the year was also very rich for rapeseed science, with a large amount of publications, as you will notice in this newsletter.

2020 will be a transition period until the General Assembly in 2021, meaning that continuous work is needed to develop, communicate and organize interactions through the GCIRC scientific committees and in thematic working groups.

Times are changing and a series of “hot topics” of different natures would deserve a specific thinking, like canola proteins, integrated insect’s management, clubroot control, pan genomics, emerging technologies, policy dialogue on future development, etc.... All these issues emerged those last years, linked to the evolutions of rapeseed crop environment on different dimensions going from policies and politics to new markets, social, technical or biological changes. Developing a prospective vision on these issues – and others, the list is open and subject to evolutions – would allow to specify position papers, to identify relevant collaborations and even to consolidate consortia or projects and share efforts on the most strategic issues.

The GCIRC needs volunteers to lead, co-lead or simply contribute to these groups. The GCIRC will do its best to facilitate these interactions, and the next tangible sign of this effort will be the renewal of the GCIRC website with improved functionalities, to come soon.

Etienne Pilorgé,

GCIRC Secretary - Treasurer

Activity/ News of the association:

Next GCIRC board meeting

The next GCIRC executive board meeting will take place in Paris on March 18, 2020. All GCIRC members may contact either their national board member (see <http://gcirc.org/presentation.html>) or the GCIRC Secretariat (mail: contact@gcirc.org) to share any suggestion regarding the future activities of the association.

Welcome to New GCIRC members

We have the pleasure to welcome a new member, Prof Wancang SUN, rapeseed breeder from Gansu Agricultural University, China.

GCIRC at the Canola Week, Saskatoon, Canada, 4-5 December 2019

The Canola days took place in Saskatoon, Canada, on December 4th & 5th, 2019, “to get the latest information on industry priorities, production challenges, breeding and genomics, digital technologies and new opportunities affecting this valuable crop!”. The organizers invited GCIRC Secretary-treasurer Etienne Pilorgé to present the last evolutions of the association and future possibilities for enhanced interactions. Further information on the presentations made during these two days will be given in the next issues of this newsletter.

Collecting the 15th IRC presentations, let us go on!

To the attention of the participants to the 15th IRC in Berlin, it is not too late to send us your presentations or posters as pdf files. They will be published on the new GCIRC website, coming soon.

Some highlights from the XVIII International Congress on Molecular Plant-Microbe Interactions (IS-MPMI) 2019

Suzana Stjelja, third-year PhD student at the Plant Biology Department at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden attended XVIII International Congress on Molecular Plant-Microbe Interactions (IS-MPMI) from July 14th to 18th in Glasgow, Scotland, with support of the GCIRC. She points out some highlights of the conference, with a special attention to potential applications to Clubroot/ *Plasmodiophora* studies, and more generally pathogens of Brassicaceae.

IS-MPMI
XVIII CONGRESS



July 14–18, 2019
Glasgow, Scotland

<< My PhD research has an emphasis on genomics of the soil-borne plant pathogen *Plasmodiophora brassicae* that attacks plants in the Brassicaceae family and causes characteristic root galls or clubroots. The clubroot disease is rapidly spreading throughout the world including Sweden and reducing yields of economically important Brassica crops. *P. brassicae* is very difficult to control because of its extremely resilient resting spores that can survive up to two decades in the soil and which no chemicals can target. As an obligate biotroph (it cannot be cultivated on media and only exist in the soil or in living plant cells) *P. brassicae* is a challenging organism to study. Many aspects of its life cycle, infection process and genetics still remain unknown. My research focuses on refining the *P. brassicae* genomic

information by using long-read PacBio sequencing data, performing genome comparisons among a range of different *P. brassicae* pathotypes and deciphering clubroot associated microorganism communities. The long-term objective is to provide better understanding of *P. brassicae* genetics and genomics and contribute with new information that may form the basis for improved means of plant protection.

Thanks to the GCIRC support, I was able to attend the IS-MPMI congress and acquire an overview and new insights into host-microbe interactions, genomics of plant pathogens and microbiome studies, topics that are essential for my ongoing PhD projects. Furthermore, in the congress poster session I had the opportunity to present my own research and discuss results achieved by PacBio sequencing of the *P. brassicae* nuclear and mitochondrial genomes. A friendly environment at the congress encouraged me to interact with fellow PhD students and researchers at all career levels and offered a valuable opportunity to create scientific networks.

Here I present a report of the IS-MPMI congress including summaries for:

- Recurrent hybridization introduces high genetic variability in crop pathogen, a fascinating talk revealing importance of recombination and hybridization for evolution of fungal wheat pathogens. This study was of special interest for me because presented methods and findings may be applied to investigate genome-wide variation among *P. brassicae* pathotypes.
- Two poster presentations with focus on the Brassica pathogens, *Alternaria brassicae* and *P. brassicae*.
- Reproducibility in Science, a workshop that highlighted issues concerning re-use of scientific data and provided a range of valuable tools and workflows which facilitate data management and data sharing.): Dr. Benjamin Schwessinger (Research School of Biology, The Australian National University, Canberra, Australia) addressed challenges arising when reproducing, replicating and re-using our own or someone else's data. The slides he presented are accessible at https://figshare.com/articles/Reproducibility_for_Everyone_workshop_slides_ICMPMI2019/8874506

Recurrent hybridization introduces high genetic variability in crop pathogen (Concurrent session 15, July 17): Dr. Eva H. Stukenbrock (University of Kiel, Germany) presented findings from comparative population genomic studies on economically important fungal pathogens from *Zymoseptoria* species. These studies demonstrated the importance of recombination and recurrent hybridization for the emergence of new genetic variation in the pathogen genomes.

Zymoseptoria tritici and *Z. ardabiliae* are recently diverged sister species that evolve in highly dissimilar environments with non-overlapping hosts. *Z. tritici* causes septoria leaf blotch on wheat that is cultivated in agricultural systems while *Z. ardabiliae* infects wild grasses. *Z. tritici* has a sexual and asexual state and its haploid genome (40 Mb) comprises 21 chromosomes of which 8 are accessory chromosomes¹. Due to highly variable accessory chromosomes, large structural variation in the core chromosomes and extensive nucleotide diversity, the *Z. tritici* genome has remarkable levels of genetic variation. In order to identify mechanisms that contribute to this genetic variation Stukenbrock and Dutheil² investigated genome-wide patterns of recombination rates through linkage disequilibrium among single nucleotide polymorphisms (SNPs) in *Z. tritici* and *Z. ardabiliae*. They reported overall high recombination rates as well as higher recombination hotspot frequency and the occurrence of stronger hotspots in *Z. tritici* compared to *Z. ardabiliae*. When mapped to coding sequences, more than 50% of the *Z. tritici* hotspots co-localized with exons. This finding indicated that the recombination hotspots

in coding regions might be under selection because they enable fast emergence of new alleles and allele combinations essential for evolution of the wheat pathogen in agricultural environment.

Dr. Stukenbrock and her team generated full genome alignments and estimated distribution of intra- and interspecific genetic variation in order to further analyze highly variable regions (HVRs). Multiple genome alignments were based on de novo assemblies of 26 genomes from five *Zymoseptoria* species, sequenced with Illumina (short-read) and PacBio (long-read) technologies. After comparing coordinates between the alignments by projecting the alignments against the reference genome of *Z. tritici*, SNPs were identified. Analysis of intraspecific genetic variation showed a variable pattern with high peaks of variation restricted to short regions along the *Z. tritici* chromosomes. Furthermore, these polymorphic HVR windows included two or more distinct haplotypes. This high local variation was validated on two independent *Z. tritici* assemblies, generated by Illumina and PacBio and the haplotypes were confirmed by PCR amplification. To address the origin of the HVRs, Dr. Stukenbrock hypothesized that distinct haplotype patterns in the *Z. tritici* genome could be a product of introgression or gene flow between closely related species. This hypothesis was tested by generating a phylogenetic tree for every 1 kb window along the genome. Each window was classified as “monophyletic”, if sequences of the *Z. tritici* isolates clustered together or “nonmonophyletic”, if the *Z. tritici* sequences clustered with the sister species. A majority of the nonmonophyletic windows correlated with coordinates of the HVRs, suggesting that the regions with high local variation and distinct haplotypes most likely originate from introgression and recurrent hybridization between *Zymoseptoria* species. When investigating functional relevance of the genomic regions with introgression signatures, it was found that protein-coding genes were not enriched in these regions. However, it seems that fast evolving genes with “high effect” mutations and transposable elements are located in the introgressed regions.

The findings presented by Dr. Stukenbrock were recently published³, providing a prominent example of how high recombination rate and recurrent hybridization enable pathogens to rapidly evolve and overcome new host resistances. By demonstrating that genome alignments generated from de novo genome assemblies (and not by mapping reads to a reference genome) are necessary to recover highly divergent regions from genomic data, this study provides valuable guidelines for performing comparative population genomic analysis on other pathogens, including plasmodiophorids. Levels and distribution of genetic variation among *P. brassicae* pathotypes and mechanisms contributing to variation are poorly understood. Active genes coding meiotic-related proteins in the *P. brassicae* e3 nuclear genome were recently identified⁴. This finding suggests that the recombination events are possible in the *P. brassicae* genome. Further studies are necessary to investigate whether recombination might have an important role in evolution of *P. brassicae*.

Investigating the molecular interactions of *Plasmodiophora brassicae* with *Arabidopsis thaliana* through a genome-wide association study and gene expression analysis^[1]_{SEP}] (Poster 853-P2): J. Ochoa (Institute of Plant Genetics, Poland) presented a poster on resistance and susceptibility to clubroot disease caused by *Plasmodiophora brassicae*. More than 140 *Arabidopsis* accessions were infected with a P1b pathotype predominant in Poland. *Arabidopsis* accessions were screened for absence/presence of clubs and DNA was extracted from samples (hypocotyl and upper parts of roots) collected at 19 dpi. DNA was used for quantitative PCR to estimate relative infection levels based on the pathogen gene (Pb18S) and the host gene (AtSK11). Screening and quantitative PCR identified twelve resistant *Arabidopsis* accessions. These accessions were used for genome-wide association analysis (GWAS) and results showed a significant peak on a SNP next to the RPB1 resistance locus, previously identified in

the Arabidopsis accessions Tsu-0 and Ze-0. GWAS analysis of Arabidopsis susceptible accessions indicated a larger number of genes. T-DNA knockout lines were created for selected gene candidates. Validation of resistance caused by the RPB1 locus as well as evaluation of T-DNA knockout lines and gene expression analysis (RNA-Seq) are ongoing.

Whole-genome analyses reveal novel pathogenic features of the necrotrophic pathogen—*Alternaria brassicae* (Poster 849-P2) : Dr. Sivasubramanian (National AgriFood Biotechnology Institute, India) presented a poster with focus on *Alternaria brassicae*, a fungal pathogen that causes leaf blight/spot disease of Brassica crops. The disease is economically important, causing 10-70% yield losses worldwide and with no known source of resistance among cultivated Brassica species.

By using Nanopore sequencing, Dr. Sivasubramanian and his team described *A. brassicae* whole-genome assembly (34 Mb) with 50% GC content, 11,593 predicted genes and 9.33% repeats. They were first to report dispensable chromosomes in *A. brassicae*. Annotation procedure predicted various effectors, secondary metabolites and carbohydrate-active enzymes some of which were solely present in *A. brassicae*. Most of the predicted effectors were common among *Alternaria* genus indicating a broad mechanism of pathogenesis. Synteny analysis between six *Alternaria* species identified a genetic basis for exclusive production of Destruxin B, a known pathogenicity factor coded by a secondary metabolite cluster. Two genes from this cluster coding for the key enzymes, the DtxS1 (nonribosomal peptide synthetase) and DtxS3 (aldo-keto reductase), were absent from all other species except *A. brassicae*. In addition, seven secondary metabolite gene clusters, including a cluster coding for HC toxin were identified on otherwise gene sparse and repeat rich dispensable chromosomes. Among six *Alternaria* species, the *A. brassicae* genome has the highest repeat content and abundant transposable elements. Moreover, a significant overlap was found between repeat-rich regions and regions with effectors and secondary metabolites.

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Value chains and regional news

- **USA: opening a new oilseed crushing plant in Montana**

Reported by US Canola Association newsletter of January (<https://www.uscanola.com/newsletter/canola-quick-bytes-january-2020/>): “In early 2020, the largest oilseed crushing plant in Montana is scheduled to open. Montana Specialty Mills will crush organic canola, non-GMO canola and flax, grown by farmers in Western Canada and the northern U.S. plains. It will crush up to 10,000 bushels per day or 225 tons of oilseeds.” Meaning an initial capacity of 70000 tons a year for a still small market of organic and non-GMO canola.

- **Germany: UFOP report on global market Supply: Sustainable Intensification of arable Production for Food Security and Climate Protection**

“Climate change dictates more productivity and efficiency while taking the requirements of sustainable production into account at the same time. Biofuels from cultivated biomass play a leading role when these are being produced according to the legal specifications of the Renewable Energy Directive (RED II), emphasizes the UFOP” . <https://www.ufop.de/english/news/sustainable-intensification-arable-production-food-security-and-climate-protection/>

- **Cooking with Canola oil**

Reported by US canola Association newsletter “Canola Quick Bytes” of January 2020, the Canadian website canolainfo.org, offering information to consumer and specially” hundreds of recipes made with heart-smart canola oil” in English, Spanish, French, Chinese and Korean. <https://www.canolainfo.org/recipes/find-canola-oil-recipes.php>

- **Canola: boosting canola and peas protein ingredients**

Reported by Food ingredient 1st website on Jan 14th, 2020 : « Canada’s Merit Functional Foods, in consortium with seed processor Pitura Seeds and health brand The Winning Combination, has raised new capital to rapidly expand its ability to meet market demand for plant-based proteins and by-products, including trending peas and canola. » The co-investment comes from the super cluster Protein Industries Canada (PIC), an industry-led, non-profit organization that aims to boost Canada’s market viability as a global source of plant protein ingredients ». Merit uses the Burcon Nutras Science’s technology, developed for more than 19 years and is currently building its plant-based protein processing facility, where it will produce what is marketed as the “world’s first high-purity, non-GMO canola protein.” Read more on <https://www.foodingredientsfirst.com/news/pea-and-canola-boost-funding-will-merit-functional-foods-to-expand-disruptive-plant-protein-technology.html>

- **Pakistan OSR oil imports: [Pakistan: Oilseeds and Products Update](#)**

USDA, Foreign Agricultural Service news Dec 27th, 2019: “Rapeseed imports are up ten percent from a year ago at 907,485 metric tons, while imports of soybean oil and palm oil are up 60

percent and four percent respectively. The imports offset the lower domestic cotton production. Pakistan remains one of the world's largest vegetable oil importers."

- **Ukraine-China:** [Ukraine Signed A Rapeseed Meal Export Protocol with China](#)

From USDA Foreign Agriculture Service news: USA GAIN Reports from Monday, December 23rd, 2019: "Ukraine signed a Protocol for veterinary and phytosanitary requirements for exports of rapeseed meal to China. This agreement will further stimulate rapeseed processing in Ukraine."

- **France:** drop in winter OSR acreage

Sowings of cereals and rapeseed show a general decline, in "a context of bad weather which makes the estimates of areas uncertain", said on December 10th the statistical service of the French Ministry of Agriculture (Agreste).

"The winter cereal acreage would reach 6.55 Mha in 2020, 5% down compared to 2019 and 7.8% compared to the 2015-19 average. Winter rapeseed would see its acreage shrink to 1.049 Mha (- 4.9% compared to 2019). In detail, the soft winter wheat sole would reach 4.729 Mha, down 4.8% over one year and 5.6% compared to the 2015-19 average. Winter rapeseed sole would drop 4.9% year-on-year and 26.8% from the 2015-19 average, to 1.049 Mha, the lowest since 2002.

- **Russia**

During the Canola days, Dec 2019, Sergey Tuchin, from the German Seed Alliance, reported that Russia planted nearly 1.9 million ha rapeseed in 2019 , mainly as spring OSR (about 80%) and 20% winter oilseed rape for a production of 2.2 MT, and eyes expansion to over 4.9 million by 2024. For longer term, the potential acreage in the Northern West and Siberian territories is considerable, ranging about 115Mha and offering good opportunities for spring OSR, only possible oil crop in these regions. Rapeseed fits well in cereal rotations and is oriented to export after processing in Russia, targeting in future the Chinese market with productions of Siberia and far East. Average yields are still low, less than 1.5t/ha due to low input practices in most regions and dry conditions, and technical challenges remain important.

Scientific news

Publications:

BREEDING

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Upcoming International and national events

3-5 February 2020. iCROP2020. Crop modelling for Agriculture and Food Security under Global Change. Montpellier, France.

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9-12 February 2020. World congress on oils and fats. Sidney, Australia.

www.wcofsydney2020.com



26-29 April 2020. AOCs Annual Meeting. Montreal, Canada.

<https://annualmeeting.aocs.org/>



6-10 September 2020. 32nd Annual Meeting AAIC Association for the Advancement of Industrial Crops. Bologna, Italy.

www.aaic.org



Abstract Submission Deadline: April 20, 2020

27-30 September 2020. Brassica 2020, Saskatoon, Canada.

<http://cruciferseq.ca/Brassica2020>

29 September – 1st October 2020. IOBC-WPRS Working Group "Integrated Control in Oilseed Crops", Rennes, France.

<http://www.iobc-wprs.org/events/index.html>



24-27 September 2023. 16th International Rapeseed Congress, Sydney, Australia.

www.irc2023sydney.com



We invite you to share information with the rapeseed/canola community: let us know the scientific projects, events organized in your country, crop performances or any information of interest in rapeseed/canola R&D.

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