1st session of International Theoretical & Practical School on Quantitative Genetics

"Using whole-genome data in plant breeding: GWAS and Genomic Selection
to genetically characterize key traits in large germplasm collections"

July 2018, VIR, St Petersburg

Program

Registration : Sunday, July 22nd, 09h00-9h30 – The hall "Rhozovyi zal"					
Time/Day	9h30-11h	11h-11h30	11h30-13h	13h-14h	14h-17h30
Sunday, July 22nd The hall Pompeyskii zal	Lecture of Prof. Dmitriy Afonnikov "Analysis of the leaf hairiness in wheat: from high-throughput phenotyping to computational modeling of trichome development" (Institute of Cytology and Genetics, Novosibirsk)	***Coffee break***	Lecture of Prof. Vladimir Brukhin, "Genomic analysis of apomixes and its molecular-genetic regulation" (Dobzhansky Center for Genome Bioinformatics, St. Petersburg)	***Lunch***	14:00-15:30 The School Sponsor's presentation (OOO "Albiogen"): Nazar Samarov and Irina Makarenko "Illumina: genomic technologies in agriculture" **15:30 -16:00 Coffee break** 16:00-17:00 Visit to the Vavilov Institute 18:00-21:00 Welcome Party (boat, River Fontanka, 105)

	8:30-11:00	11:00-11:30	11:30-13:00	13:00-14:00	14:00-17:30
Monday July 23rd **The hall Rhozovyi zal**	**General introduction:** « Genetics of quantitative resistance to *Verticillium* wilt in *M. truncatula* » as a redline of the course. -*Theory*: RCBD and Linear Mixed Models, LMM analysis with R. - -*'How to?' guided practice:* Getting started with R: Generalities about the R environment: interface, data import, basic syntax, graphics. - *Guided practice on case study #1*: RCBD applied to genetic analysis of quantitative traits (heterosis, ploidy).	***Coffee break***	**How to make the best of large-scale phenotyping raw datasets: Focus on some useful experimental designs for GWAS and biostatistics with R** -*Theory*: Augmented Block Designs; Power of tests and independence concepts. - *Guided practice on case study #2*: Augmented-block designs for large-scale genotype collection evaluation. -*ePosters presentation*	***Lunch***	-*'How to?' guided practice:* R for semi-beginners: How to organize your data in a spreadsheet? How to analyse data quality? How to draw nice & informative graphs with R? **15:30 -16:00 Coffee break** - *'By yourself' practice to code an analysis:* * *Case study #3*: RCBD applied to plant quantitative genetics studies. * *Case study #4*: Augmented-block designs for GWAS. - *ePosters presentation*
	8h30-11h	11h-11h30	11h30-13h	13h-14h	14h-17h30
Tuesday July 24th **The hall Rhozovyi zal**	**How to deal with large-scale SNP raw datasets : Focus on some useful bioinformatics pipelines** *(no computational practice)*	***Coffee break***	**Analysis of genetic structure of populations** - *Theory and case study* : Presentation of basic concepts of popular methods for pop. structure, using SNPs or SSRs. - *ePosters presentation*	***Lunch***	**Analysis of genetic structure of populations, relationships with covariates and geography** **15:30 -16:00 Coffee break** - *Guided practice on case study*: Analysis of genetic structure of populations in the model legume *Medicago truncatula.* - *ePosters presentation*

	8h30-10h30	10h30-11h	11h-12h30	12h30-13h30	13h30-17h
Wednesday July 25th **The hall Rhozovyi zal**	**Genome Wide Association Study (GWAS)** - *Theory*: Linkage disequilibrium (LD), General Linear Models (GLM)	***Coffee break***	- *Guided practice on case study*: GWAS on agronomical traits in legumes with GLM and LD analysis. - *ePosters presentation*	***Lunch***	Section of quantitative PCR (Helicon) **15:30 -16:00 Coffee break**
	8h30-11h	11h-11h30	11h30-13h	13h-14h	14h-17h30
Thursday July 26th **The hall Rhozovyi zal**	**Genome Wide Association Study (GWAS)** - *Theory*: Mixed Linear Models (MLM) including population structure and kinship.	***Coffee break***	**Genome Wide Association Study (GWAS)** - *Guided practice on case study*: GWAS on agronomical traits in legumes with MLM and kinship computation. - *ePosters presentation*	***Lunch***	**Genomic Selection (GS)** - *Theory*: Principle of GS, Breeding Values, Heritability **15:30 -16:00 Coffee break** - *Guided practice on case study*: Computation of Best Linear Unbiased Estimator (BLUEs), Best Linear Unbiased Predictor (BLUPs), Pedigree vs. Kinship matrix, Imputation. - *ePosters presentation*
	8h30-10h30	10h30-11h	11h-12h30	12h30-14h	14h-17h30
Friday July 27th **The hall Rhozovyi zal**	**Genomic Selection (GS)** - *Theory:* One-step models using G-BLUP and RR-BLUP models. - *Guided practice on case study*: genomic prediction of agronomical	***Coffee break***	**Genomic Selection (GS)** - *Theory and case study*: One-step and two-step models. Cross Validation, Accuracy. Factors affecting GS, optimization of training populations.	***Lunch***	**Plant GWAS and GS Challenge.** *'By yourself' practice on complex case studies: GWAS and GS on agronomical traits in crops.* **15:30 -16:00 Coffee break**

	traits of interest in crop species	- *Guided practice on case study:* Accuracy computation for genomic prediction of agronomical traits of interest in crop species, using different GS models. - *ePosters presentation*	**Using whole-genome data in plant breeding: promises, challenges and limits.** GWAS *and/or* GS, MAS, functional validation of candidate genes. **Questions and Open Discussion.** **Delivery of certificates**