CREA Research Centre for Genomics and Bioinformatics and Haifa University organize :

Wheat Genetics and Genomics workshop

TOPIC:

The course will present selected topics in genetics and genomics of cereals and will enable participants to take advantage of emerging genetic tools and the completed genome sequences of most cereal crops.
Laptop is required for every student

SPEAKERS:

Prof. Assaf Distelfeld
Full Prof. at Haifa University, Director of Institute of Evolution, awarded with «Premio Rita Levi Montalcini -2021»

Dr. Hanan Sela
Research Associate at Haifa University

DATE:
23-24 june 2022

VENUE:
CREA-Genomica e Bioinformatica
Via S. Protaso, 302 – Fiorenzuola d'Arda

TIMING:
9-12 - 13-18

CREA Research Centre for Genomics and Bioinformatics – 29017 Fiorenzuola d'Arda (PC)
https://www.crea.gov.it/web/genomica-e-bioinformatica
0523 983758 –
erica.mica@crea.gov.it

COURSE PROGRAM AND DETAILS:

SPEAKERS:

Prof. Assaf Distelfeld **Email:** adistelfe@univ.haifa.ac.il
Dr. Hanan Sela **Email:** hans@evo.haifa.ac.il

ADDRESSED TO:

PhD Students

CONTENT AND ASSIGNMENTS:

lesson #	Topic	Assignment
1	Introduction to wheat genetics	Lecture
2	QTL mapping	Hands-on practice
3	Reference genomes	Lecture
4	From QTL to genes	Hands-on practice
5	The domestication BTR genes	Lecture
6	VEP analysis	Hands-on practice
7	Wild wheat diversity	Lecture
8	Allelic diversity database (GWAS)	Hands-on practice
9	Gene annotation	Hands-on practice
10	Population genetics	Lecture
11	Population genetics	Hands-on practice
12	Final discussions	

QTL mapping: Marker platforms pros & cons ; Construction of genetic maps of polyploid wheat; Dealing with high marker density and homeology; Mapping of quantitative traits to genetic maps (QTL mapping); Using the ICIMapping software to construct a genetic map and to map the brittle rachis trait (BTR) in a mapping population.
From QTL to genes: Exploring the gene space of QTLs using online databases; Gene annotation; Validating VEP by PCR; Looking for variation in genes using PCR and sequencing; Tools for PCR design in polyploid wheat. Gene Expression database;
VEP analysis: Variant effect prediction; Generation of variation (VCF) files from sequencing data (demonstration, not practice); using VCF flies to conduct VEP; Interpreting VEP results; Limitations of VEP;
Wild wheat diversity: Introduction to wild emmer (Triticum dicoccoides) the progenitor of cultivated wheat; wild emmer geographic distribution; Population structure of wild emmer; Conservation of wild emmer; Using wild emmer in breeding.
Allelic diversity database (GWAS): Using NCBI (sequence read archive) SRA database to study diversity of species; Generating VCF files representing the diversity of species; Using VCF files to conduct genome wide association scan (GWAS) to associate variation with traits; Practice will be done using the GAPIT R package and TASSEL.
Population genetics lecture and practice: Inferring population structure using genomic data, e.g PCA, STRUCTURE, DAPC, Neighbor joining trees) ; Estimates in population structure and their evolutionary meaning (Fst, linkage disequilibrium, LD, Tajima); Practice with real data of wild emmer population.

NOTES:

The course will include both a theoretical and a practical part, for this reason it is highly recommended a laptop for each student. The course is structured to provide time for informal discussions and exchange between the participants.