Syllabus, DNA to Population 2022

Prof. Nir Ohad, Dr. Tzachi Hagai, Dr. Yariv Wine and Prof. Martin Kupiec,

The course is a mixture of frontal classes and discussion of papers read by the students. Four different subjects are taught, encompassing genetics of various organisms/models. This is a Midrasha Course for MSc and PhD students, but it is elective for 3rd year students after consultation with Martin.

Grade: There will be an exam on all the material taught in class, and about the papers read by the students.

This year's subjects are:

Nir Ohad: 24/2, 3/3. 10/3/22.

"The relation between plant reproduction and Epigenetic regulation "

Papers included are:

1) Mutations in the FIE and MEA Genes That Encode Interacting Polycomb Proteins Cause Parent-of-Origin Effects on Seed Development by Distinct Mechanisms The Plant Cell, Vol. 12, 2367–2381,(2000)

Optional Background for Session 1:

A mutation that allows endosperm development without fertilization PNAS 1996

- 2) Regulation of stem cell maintenance by the Polycomb protein FIE has been conserved during land plant evolution. Development 2009
- 3) A single homeobox gene triggers phase transition, embryogenesis and asexual reproduction. Nature Plants 2016

Optional Paper for Session 3:

The Polycomb group protein CLF emerges as a specific tri-methylase of H3K27 regulating gene expression and development in Physcomitrella patens. Biochimica et Biophysica Acta 2016

17/3: Purim

Tzachi Hagai: 24/3, 31/3. 7/4/22

"Host-pathogen co-evolution"

1) Evolutionary arms race at the coding sequence level Paper and review:

Protein kinase R reveals an evolutionary model for defeating viral mimicry, Elde et al, Nature, 2009

Evolutionary Landscapes of Host-Virus Arms Races, Tenthorey et al, Annual Review of Immunology, 2021

- 2) Coding versus non-coding evolution Contrasts between adaptive coding and noncoding changes during human evolution, Haygood et al, PNAS, 2007
- 3) Transcriptional evolution of innate immune response Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages, Schroder et al, PNAS, 2012

PESAH

Yariv Wine: 28/4 (5/5 Yom Haatzmaut) 12/5, 19/5. "B cells and antibody evolution on the fast track"

- 1) Weinstein et al. 2009. "High-Throughput Sequencing of the Zebrafish Antibody Repertoire". Science 324 (5928), 807-810. [doi: 10.1126/science.1170020]
- 2) Wang et al. 2014. "B-cell repertoire responses to varicella-zoster vaccination in human identical twins". Proc Natl Acad Sci U S A. 13;112(2):500-5. [doi: 10.1073/pnas.1415875112]
- 3) Aizik et al. 2021. "Antibody Repertoire Analysis of Tumor-Infiltrating B Cells Reveals Distinct Signatures and Distributions Across Tissues". Frontiers in Immunology. 19;12:705381. [doi: 10.3389/fimmu.2021.705381].

Martin Kupiec: 26/5, 2/6, 9/6/22.

"DNA damage response and homologous recombination in yeast"

- 1) Introduction to yeast biology and to homologous recombination
- 2) How do you search for homology?
- 2a) Agmon et al. (2013) Effect of nuclear architecture on the efficiency of double-strand break repair. Nat Cell Biol.15:694-699.
- 2b) Marcomini et al (2018) Asymmetric Processing of DNA Ends at a Double-Strand Break Leads to Unconstrained Dynamics and Ectopic Translocation. Cell Reports 24, 2614–2628.
- 3) Chromosomal structure in the response to DSBs
- 3a) Mine-Hattab, J. and R. Rothstein (2012) Increased chromosome mobility facilitates homology search during recombination. Nat Cell Biol. 14:510-517.
- 3b) Nuclear F-actin and myosins drive relocalization of heterochromatic breaks. Caridi CP, D'Agostino C, Ryu T, Zapotoczny G, Delabaere L, Li X, Khodaverdian VY, Amaral N, Lin E, Rau AR, Chiolo I. Nature. 2018

Jul;559(7712):54-60. doi: 10.1038/s41586-018-0242-8. Epub 2018 Jun

20.PMID: 29925946

Additional interesting review: Zimmer C, Fabre E (2019) Chromatin mobility upon DNA damage: state of the art and remaining questions. Curr Genet. 2019 Feb;65(1):1-9. doi: 10.1007/s00294-018-0852-6.The repair of broken chromosomes.