

Ruth Hershberg - Curriculum Vitae

Contact and personal information

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Employment

2012- : Assistant Professor, Department of Genetics, The Ruth and Bruce Rappaport Faculty of Medicine, Technion, Israel

2006-2011: Postdoctoral fellow in the lab of Prof. Dmitri Petrov at Stanford University.

Education

2001-2006: PhD student in computational molecular biology in the lab of Prof. Hanah Margalit.: Prokaryotic gene regulation – insights through sequence and genomic analyses – The Hebrew University of Jerusalem. PhD received summa cum laude.

1999-2001: M.Sc. student in Microbiology in the lab of Prof. Hanah Margalit – The Hebrew University of Jerusalem.

1996-1999: B.Sc. studies in life sciences – The Hebrew University of Jerusalem.

Selected fellowships and honors

2015: Elected by the Israeli Society of Microbiology (ISM) to serve as a committee member.

2014: Elected by the Society of Molecular Biology and Evolution (SMBE) board to serve on the Editorial board of the Society's journal, Genome Biology and Evolution (GBE).

2014: German-Israeli Foundation for Scientific Research and Development (GIF) Young Scientist Grant.

2013: Research Award from the Henri Gutwirth Fund for the Promotion of Research

2012-2017: Shillman Fellow, as part of the Technion's Robert J. Shillman Career Advancement Chair

2012-2016: European Commission Career Re-Integration (CIG) grant

2012-2014: Yigal Allon Fellowship for outstanding starting junior faculty awarded by the Israeli Council for Higher Education

- 2008-2010: Stanford Genome Training Program (SGTP) fellowship.
- 2006-2008: EMBO long-term fellowship.
- 2006: Hebrew University Medical school faculty prize for excellence received for PhD thesis.
- 2006: PhD awarded **summa cum laude**.
- 2003-2006: Yeshaya Horowitz excellence scholarship for complexity science.

Publications

(C: number of citations according to Google Scholar).

The total number of citations received by all my peer-reviewed papers is currently 2901 (March 2017). H-Factor 14

- 28) Avrani S, Bolotin E, Katz S and **Hershberg R** (2017) Rapid genetic adaptation during the first four months of survival under resource exhaustion. *Molecular Biology and Evolution* (In press).
- 27) **Hershberg R** (2016) Human host range of *Mycobacterium tuberculosis*. *Nature Genetics*. 48: 1453-1454 (Invited News and Views Article).
- 26) Bolotin E and **Hershberg R** (2016) Bacterial intra-species gene loss occurs in a largely clocklike manner mostly within a pool of less conserved and constrained genes. *Scientific reports*. 6:35168.
- 25) Ostrow SL and **Hershberg R** (2016) The somatic nature of cancer allows it to affect highly constrained genes. *Genome Biology and Evolution*. 8(5):1614-1620
- 24) Lan Y, Rosen G* and **Hershberg R*** (2016) Marker genes that are less conserved in their sequences are useful for predicting genome-wide similarity levels between closely related prokaryotic strains. *Microbiome*, 4:18 (Co-last authors, co-contributing authors). C:4
- 23) **Hershberg R** (2016) Codon usage and translational selection. In: Kliman RM (ed.), Encyclopaedia of Evolutionary Biology, Vol. 1, pp. 293-298. Oxford: Academic Press. (Book chapter)
- 22) Ostrow SL[†], Simon E[†], Prinz E, Bick T, Shentzer T, Nagawkar SS, Sabo E, Ben-Itzhak O, **Hershberg R*** and Hershkovitz D* (2016) Variation in KRAS driver substitution distributions between tumor types is determined by both mutation and natural selection. *Scientific reports*. 6:21927 (†Equal contributors, *Co-last authors, co-contributing authors). C:2
- 21) **Hershberg R** (2015) Mutation – the engine of evolution: studying mutation and its role in the evolution of bacteria. *Cold Spring Harbor Perspectives in Biology*. 7(9): a018077. (Review) C: 5
- 20) Bolotin E and **Hershberg R** (2015) Gene loss dominates as a source of genetic variation within clonal bacterial species. *Genome Biology and Evolution*. 7(8): 2173-2187. C: 8
- 19) Field W and **Hershberg R** (2015) Alarming high segregation frequencies of quinolone resistance alleles within human and animal microbiomes are not explained by direct clinical antibiotic exposure. *Genome Biology and Evolution*. 7(6):1728-1742 C: 4
- 18) Reichenberger ER, Rosen G, Hershberg U* and **Hershberg R*** (2015) Prokaryotic nucleotide composition is shaped by both phylogeny and the environment. *Genome Biology*

- and Evolution*. 7(5): 1380-1389. (*Co-last authors, co-contributing authors, article highlighted by the journal (same issue pages 1390-1391). C: 11
- 17) Ostrow SL, Barshir R, DeGregori J, Yeger-Lotem E and **Hershberg R** (2014) Cancer evolution is associated with pervasive positive selection on globally expressed genes. *PLoS Genetics*. 10(3): e1004239. (Article was featured in the Research Highlight section of *Nature Reviews Genetics*). C: 36
 - 16) Lan Y, Morrison C, **Hershberg R***, and Rosen G* (2014) POGO-DB - a database of Pairwise-comparisons Of Genomes and conserved Orthologous genes. *Nucleic Acids Research*. doi: 10.1093/nar/gkt1094 (*Co-last authors, co-contributing authors). C: 10
 - 15) Katz S and **Hershberg R** (2013) Elevated mutagenesis does not explain the increased frequency of antibiotic resistant mutants in starved aging colonies. *PLoS Genetics*. 9(11): e1003968. C: 14
 - 14) Lawrie DS, Messer, PW, **Hershberg R**, and Petrov DA (2013) Strong Purifying Selection at Synonymous sites in *D. Melanogaster*. *PLoS Genetics* 9(5): e1003527. C: 71
 - 13) **Hershberg R**, and Petrov DA (2012) On the limitations of using ribosomal genes as references for the study codon usage: a rebuttal. *PLoS One*, 7(12): e49060. C: 12
 - 12) **Hershberg R** and Petrov DA (2010) Evidence that mutation is universally biased towards AT in bacteria. *PLoS Genetics* 6:(9): e1001115 (Article was featured with a perspective in *PLoS Genetics*, and selected as a ‘must read’ article by Faculty of 1000). C: 198
 - 11) **Hershberg R** and Petrov DA (2009) General rules for optimal codon choice. *PLoS Genetics* 5(7):e1000556 (Article was featured in the Research Highlight section of *Nature Reviews Genetics*). C: 109
 - 10) **Hershberg R***, Lipatov M*, Small PM, Sheffer H, Niemann S, Homolka S, Roach JC, Kremer K, Petrov DA, Feldman MW, Gagneux S (2008) High Functional Diversity in *M. tuberculosis* Driven by Genetic Drift and Human Demography. *PLoS Biology* 6(12):e311 (*Equal contributors. Article was featured as a *Science Magazine* Editor’s Choice). C: 422
 - 9) **Hershberg R** and Petrov DA (2008) Selection on codon bias. *Annual Reviews in Genetics* 42:287-99. (Review) C: 442
 - 8) Padalon-Brauch G, **Hershberg R**, Elgrably-Weiss M, Baruch K, Rosenshine I, Margalit, H, Altuvia S (2008) Small RNAs encoded within genetic islands of *Salmonella typhimurium* show host-induced expression and role in virulence. *Nucleic Acids Research*. 36(6):1913-27. C: 155
 - 7) **Hershberg R**, Tang H, Petrov DA (2007) Reduced selection leads to accelerated gene loss in *Shigella*. *Genome Biology*. 8(8):R164. C: 53
 - 6) **Hershberg R**, Margalit H (2006) Co-evolution of transcription factors and their targets depends on mode of regulation. *Genome Biology*. 7(7):R62 (Article was featured in the “What the papers say” section of *Bioassays*). C: 36
 - 5) **Hershberg R**, Yeger-Lotem E, Margalit H (2005) Chromosomal organization is shaped by the transcriptional regulatory network. *Trends in Genetics*. 21(3):138-42. C: 67
 - 4) Zlotorynski E, Rahat A, Skaug J, Ben-Porat N, Ozeri E, **Hershberg R**, Levi A, Scherer, SW, Margalit H, Kerem B (2003) Molecular basis for expression of common and rare fragile sites *Mol. Cell. Biol.* 23(20):7143-7151. C: 188
 - 3) **Hershberg R**, Altuvia S, Margalit H (2003) A survey of small RNA-encoding genes in *Escherichia coli*. *Nucleic Acids Research* 31(7):1813-1820. C: 264

- 2) Argaman L*, **Hershberg R***, Vogel J*, Bejerano G, Wagner EGH, Margalit H, Altuvia S (2001) Novel small RNA-encoding genes in the intergenic regions of *Escherichia coli*. *Current Biology* 11(12):941-950. (*Equal contributors, cover article). C: 716
- 1) **Hershberg R**, Bejerano G, Santos-Zavaleta A, Margalit H (2001) PromEC: an updated database of *Escherichia coli* mRNA promoters with experimentally identified transcriptional start sites. *Nucleic Acids Research*. 29(1):277. C: 74

Selected talks

- The 8th Congress of the Federation of the Israel Societies for Experimental Biology – FISEB (ILANIT), Eilat, Israel, February 20-23, 2017, “From Boom to bust - the dynamics of bacterial adaptation under prolonged resource limitation”
- Genome Evolution Conference, Weizmann Institute, Rehovot, Israel, November 1-3, “From Boom to bust - the dynamics of bacterial adaptation under prolonged resource limitation”
- ISME (International Society for Microbial Ecology) 16th International Symposium on Microbial Ecology, Montreal, Canada, August 20-26, 2016, “The antibiotic independent evolution of antibiotic resistance”
- The Allied Genetics Conference (TAGC), Orlando, Florida, July 13-17, 2016, “The antibiotic independent evolution of antibiotic resistance”
- EMBL symposia: New Model Systems for Linking Evolution and Ecology, EMBL, Heidelberg, Germany, May 8-11, 2016, “The antibiotic independent evolution of antibiotic resistance”
- NYU-TICC Workshop, The Ruth and Bruce Rappaport Faculty of Medicine, Technion, Israel, December 7-8, 2015, “Studying cancer through an evolutionary prism”.
- Third Annual Broad-ISF Cell Circuits Symposium, Konrad Adenauer Conference Center, Jerusalem, Israel, June 8-10, 2015, “Cancer evolution is associated with pervasive positive selection on the most central gene functions”
- SMBE Satellite Meeting on Mutation, Repair and Evolution, Indiana University campus of Bloomington, Indiana, USA, May 11-14, 2015, “Antibiotic resistance mutations are poor markers of mutation rates”
- ISM (Israel Society of Microbiology) annual meeting, Bar-Ilan Israel, February 17-18 2015: “Alarming high frequencies of Quinolone resistance within human and animal microbiomes are not explained by clinical antibiotic exposure”
- The 7th Congress of the Federation of the Israel Societies for Experimental Biology – FISEB (ILANIT), Eilat, Israel, February 10-13 2014: “Elevated mutagenesis does not explain the increased frequency of antibiotic resistant mutants in starved aging colonies”
- IBS (Israeli Bioinformatics Symposium), Beer Sheva, Israel, June 27 2013: “Breast cancer is associated with pervasive positive selection on globally expressed genes”
- IBECC (International Biannual Evolution and Cancer Conference, San Francisco, USA, June 12-16 2013: “Breast cancer is associated with pervasive positive selection on globally expressed genes”
- IBM clinical genomic analysis workshop, Haifa, Israel, June 2 2013: “Breast cancer is associated with pervasive positive selection on globally expressed genes”
- ISM (Israel Society of Microbiology) annual meeting, Bar-Ilan Israel, February 18-19 2013: “Stress-induced evolution of antibiotic resistance”
- SMBE, Dublin, Ireland, June 23-26 2012: “Towards a Genome-wide understanding of bacterial mutation”
- Fred Hutchinson Cancer Research Center, Seattle, USA, February 22 2011: “Disentangling the Determinants of Genome Evolution”
- The University of California, Los Angeles (UCLA), Los Angeles, USA, February 10 2011: “Disentangling the Determinants of Genome Evolution”

- The University of Colorado, Denver, USA, February 1 2011: “Disentangling the Determinants of Genome Evolution”
- GeorgiaTech, Atlanta, USA, January 27 2011: “Disentangling the Determinants of Genome Evolution”
- Emory University, Atlanta, USA, January 25 2011: “Disentangling the Determinants of Genome Evolution”
- Penn State University, State College, USA, January 18 2011: “Disentangling the Determinants of Genome Evolution”
- The Weizmann Institute of Science, Rehovot, Israel December 20 2010: “Disentangling the Determinants of Genome Evolution”
- Technion - Israel Institute of Technology, Haifa, Israel, December 19, 2010: “Disentangling the Determinants of Genome Evolution”
- The University of Michigan, Ann Arbor, USA, October 28 2010: “Disentangling the Determinants of Genome Evolution”
- Second Bay Area Population Genomics Conference, Berkeley, USA, March 13 2010: “Evidence that mutation is universally AT biased”
- SMBE, Barcelona, Spain, June 5-8 2008: “Severely reduced selection leads to high functional diversity in *Mycobacterium tuberculosis*”
- MRC Laboratory of Molecular Biology, Cambridge, UK, April 6 2006: “Insights into the design and evolution of transcription regulatory networks”
- 6th Biopathways meeting, ISMB, Glasgow, Scotland, July 29-30 2004: “Chromosomal organization is shaped by the transcription regulatory network. “

Selected additional academic activities

- Associate Editor of Genome Biology and Evolution
- Committee Member of the Israeli Society of Microbiology (ISM)
- Co-organizing The first Pearl Seiden International meeting in Life Sciences: From synthetic biology to discovery and applications”, which took place December 9-10, 2015 at the Technion.
- Chairing sessions in ISM (Israeli Society of Microbiology) and SMBE (Society for Molecular Biology and Evolution) 2014 meetings
- Reviewing articles for Nature, Science, Nature Genetics, Nature Communications, PLoS Biology, PLoS Genetics, Genome Research, PLoS Computational Biology, Molecular Biology and Evolution, Genome Biology and Evolution, Theoretical Population Biology, Journal Of Molecular Evolution, Molecular Systems Biology, eLife, Scientific Reports, and Biology Letters
- Establishing an ‘advancing women in science’ program at the Technion – Israel Institute of Technology Faculty of Medicine (Together with Prof. Asya Rolls and Prof. Estee Kurant)
- Invited consultant - Army Research Office Microbiology Workshop “Bacterial Adaptation to New Environments”, Arlington, VA, September 29-30, 2008
- Consulting Israeli Molecular Pathologists on the introduction of Next Generation Sequencing Technologies (NGS) into clinical screening of tumors.