

Alan Howard Schulman

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1. Personal

Born: May 11, 1957 at Newark, New Jersey, USA
 Citizenship: Finland, USA
 Residence: Helsinki, Finland
 Languages: English (native); Finnish (written, spoken; exam 1988); basics of Spanish, French, German

2. Education and Degrees

1979-1986 **Yale University, Department of Biology**, New Haven, Connecticut USA. Program in Cell and Developmental Biology. **Ph.D.** (1986); **M.Phil.**(1982); **M.S.** (1981)
Title of Dissertation: The detection of sequences similar to leghemoglobin genes in the genomes of non-leguminous plants
 1975-1979 **Duke University**, Durham, North Carolina, USA. A.B., Botany.

3. Present Positions

Professor of Plant Biotechnology Luke Natural Resources Inst. Finland (MTT then successor) 01/01 à present.
Group Leader, Institute of Biotechnology, University of Helsinki 09/95 à present
Adjunct Professor (Docent), Plant Molecular Biology, Division of Genetics, University of Helsinki 11/94 à present

4. Previous Positions

Senior Fellow, Academy of Finland. Named for 5-year post, resigned to take permanent position 08/00 à 12/00
Senior Researcher, Institute of Biotechnology, University of Helsinki 01/90 à 09/95
Researcher, Institute of Biotechnology, University of Helsinki 09/88 à 12/89
Visiting Scientist, Department of Genetics, University of Helsinki 08/86 à 09/88

5. Research Profile

My group works to elucidate retrotransposon replication and their role in generating genomic diversity. We apply retrotransposon display methods we developed as genetic markers in breeding, biodiversity, and evolutionary studies in both temperate and tropical crops and train researchers worldwide in their use. We have actively developed and applied genomic tools for map-based cloning of genes conferring biotic and abiotic stress resistance as well as grain quality traits. We are active in barley, birch, Saimaa ring seal, and *Striga* genome sequencing projects and in defining the *Vicia faba* gene space.

Current	Ph.D.	Maitry Paul	<i>BARE</i> control on the whole-plant level. Expected 2019.
Current	Ph.D.	Jaakko Tanskanen	Molecular evolution of <i>BARE</i> retrotransposons 6 papers, Exp. 2019.
Current	M.Sc.	Marijke Iso-Kokkila	Genetic variation in drought response and transpiration in barley
2018	M.Sc.	Laura Vottonen	eQTL mapping of vicine and convicine in <i>Vicia faba</i>
2016	Ph.D.	Elitsur Yaniv	Positional Cloning of <i>Yr15</i> from wild emmer wheat (co-supervisor).
2012	Ph.D.	Marko Jääskeläinen	Translation and assembly of <i>BARE</i> retrotransposons.
2012	Ph.D.	Chang Wei	The Transcriptional Regulation of Retrotransposon <i>BARE</i>
2009	Ph.D.	Teija Tenhola-Roninen	Rye Doubled Haploids –Production and Use in mapping Studies
2006	Ph.D.	Marjo Serenius	Population structure of <i>Pyrenophora teres</i> , the causal agent of net blotch of barley
1998	M.Sc.	Eva Sirén	Characterization of the <i>BARE-1</i> LTR Terminator Function
1997	Ph.D.	Annu Suoniemi	Retrotransposons as Active and Major Components of the Barley Genome.
1995	M.Sc.	Marko Jääskeläinen	Starch synthesis and starch synthases in developing Bomi and <i>shx</i> barley
1994	M.Sc.	Tiina Arna	Cloning of a cDNA for the barley retrotransposon <i>BARE-1</i> .
1991	M.Sc.	Tarjaleena Tuomi	Cloning and expression of <i>waxy</i> -like genes in barley <i>Hordeum vulgare</i> L. grain endosperm.

6b. Trained Postdocs and Research Fellows: 37 from 22 countries

Postdocs: Mashhood Alam Chaudhary (India), Wei Chang (PRC), Marko Jääskeläinen (FI) Ruslan Kalendar (UKR), Jan Buchmann (CH), Cédric Moisy (F), François Sabot (F), Carlos Vicient (ES), Caroline Stuart-Rogers (UK).
Research Fellows: Benjamin Laduc (IS,) Ian Vogel (CZ), Violetta Kotseruba (RU), Viktor Tokan (CZ), Asmaa Abdel-Ghany (EG), Marwa Ghonaim (EG), Tatiana Zachepilo (RU), Krzysztof Stawujak (PL), Andrej Trebichalský (SK), Hande Demir (TR), Natali Paramonova (LV), Doungous Oumar (CM), Ilva Trapina (LV), Mary Jayne Manrique (PH), Marco Vukich (I) Ahmed Mansour Mohamed Mansour (EG), Gábor Gyulai (HU), Babak Abdollahi Mandoulakani (IR), Andrej Benjak (Austria), Svetlana V. Boronnikova (Russia), Alena Gajdošová (Slovakia), Petr Smykal (CZ), Kaisa Kajala (UK), Angelika Zuk (LV), María Pilar Vallés Brau (ES), Kristiina Antonius-Klemola (FI), Elisenda Ramallo Flaquer (ES), Alex Baumel (F)

7. Teaching Experience

International, 10 courses on genomics, plant breeding, molecular markers, molecular biology, bioethics, around the world; **Domestic**, 5-6 postgraduate student lectures per year since 1990 on plant molecular biology, genomics, and use of genomics in breeding.

8. Most Important Foreign Visits

--Childhood, education, and training in the USA: 1957--1986

9. Most Important Acknowledgements and Awards

Knight, First Class, Order of the Lion of Finland (for scientific contributions, 2010); Marquis Who's Who in the World (27th Edition à); John Spangler Nicholas Prize for the Outstanding Doctoral Candidate, 1987

10. Scientific Expert Positions

Academic Committees: ViPS (Viikki Plant Science Centre; Board member, 2018à; member 2015à) Board Member, Doctoral Program in Plant Sciences (Helsinki) 2005à; VRGO (Viikki Research Group Organization)

Editorial Boards, Scientific Journals: Editor, *Theoretical and Applied Genetics*; Editor, *Functional and Integrative Genomics*; Editor, *Agronomy*; former Editor, *Genomics Reports* 2001—2006; former Editor, *Genetica*, *Genome Letters* (ceased pub. 2003); former Editorial Board member, *Rebase Reports*

Management Committees: Board Member, EPSO (European Plant Science Organization), 2016à; NaPPI (phenotyping infrastructure) Finland (2015à) Member of IOC, Barley Genome Net 2006à; Founding Member, European Triticeae Genomics Initiative 2005à; Secretary (2016à) and Board Member (2004à), International Barley Genetics Symposium; Management Committees for COST Actions (2001à) 851, TD0801, FA1208, FA1306, FA0806; Plant GEM 2009à 2012

Coordination Roles: EU FP7 Project Tritigen: Workpackage coordinator; Network Coordinator, COST Network: TritiGen: Triticeae genomics for the advancement of key European crops 30 countries, 71 laboratories, 124 scientists; 05/07—04/11; Network Coordinator, ESF Network: Retrotransposons: their impact on organisms, genomes and biodiversity 01/00—12/03; Project Coordinator for an Academy of Finland Genome Research Program project 01/95—12/97, 01/98—12/00; Project Coordinator, NKJ Starch Collaboration c. 16 persons, 4 labs; 01/94—12/96; Project Coordinator, Nordic Starch Collaboration 01/90—06/94; c. 30 persons, 7 labs, USD \$5.8 million budget

Doctoral and Master's Evaluations: 21 for Ph.D as examiner since 1995, 2 for M.Sc

Professorial Evaluations: 10 (Helsinki (6), Univ. Uppsala, Haifa, Beersheva, Michigan) since 2000

Fellowship and Grant Evaluations: Evaluator, IRCSET Irish postdoctoral fellowships, Leverhulme Trust London, UK, WellcomeTrust Slovenian Ministry of Education, Science, and Sport, Austrian National Science Fund FWF, Norwegian National Science Foundation FUGE, Israel Science Foundation, Danish Ag. Res. Council, National Science Foundation USA, BBSRC, UK, Academy of Finland

Institutional Evaluations: Div. Plant Sci., Univ. Dundee 2010; Outside evaluator, Integrative Life Science (ILS) Doctoral Program (Helsinki)

Reviews for Scientific Journals: Austr J Agric Res, Biological Journal of the Linnean Society, Biology Letters, Royal Society, Genetica, Genetics, Genome, Hereditas, Molecular Biology and Evolution, Molecular and General Genomics, Nature Comm., Nature Genetics, Nature Scientific Reports, Physiologia Plantarum, The Plant Cell, The Plant Journal, Plant Molecular Biology, Plant Molecular Biology Reporter, Plant Physiology, PNAS, Theor and Appl Genet, Science, Trends Plant Sci, etc.

Scientific Positions of Trust: MTT *ad hoc* committee to plan new Food & Biotechnology Division ~120 persons; Member, Board of Doctoral Program in Plant Science (Univ. Helsinki) 2014à; Advisory Panel for Annual Plant Genomics Congress (London) 2012à; Expert advisor, Gene Technology Board statements on GMO status, 2007à; National Advisory Board on food, agro, bio -thematic programs of EU FP7 2006à; Scientific Advisor, EU HealthGrain project 2007-2010; Founding Member, International Barley Sequencing Consortium 2006à; MTT Food & Biotechnology Strategy Committee, 10 year plan 2006—2007; Member, Scientific Advisory Board, Boreal Plant Breeding Ltd. 2001—2005; Member, Maize Genetics Cooperation 1981à

11. Current Outside Collaborations

NorFab consortium (faba bean genomics, 8 partners, 4 countries); ClimBar consortium (climate change genomics, 9 partners, 7 countries); Barley Genome Network (6 partner institutions and countries); International Rye Sequencing Consortium (40 partners worldwide; co-PI on project); *Striga japonica* sequencing project (in charge of TE annotation); *Vigna unguiculata* sequencing project (in charge of TE annotation)

12. Conferences Organized

27 international conferences since 1990, total of 2500 participants. Recent: Plant Biology Europe 2018

13. Professional Organizations

Finnish BioBio Society, International Barley Genetics Symposium OC; AAAS; EPSO

14. Seminars: 70 invited seminars since 2008.

15. Outside Funding (last 10 years):

Current: "Retrotransposon and gene interactions in barley under drought stress (RetroStress)", Academy of Finland, 516,194 €, 2018-2022; "PapuGeno, Genomic tools for faba bean (*Vicia faba* L.) improvement for food and protein security" Academy of Finland, 589,000 €, 2016-2020, "NORDFAB: Protein for the Northern Hemisphere", Innovation Fund Denmark, 2016-2021, 96,590 €, "ClimBar: An integrated approach to evaluate and utilise genetic diversity for breeding climate-resilient barley". **Recent:** FACCE-ERA-NET+, 2014-2017, 297,000 €, "Multiply Mobile Elements: Retrotransposon Cell-to-Cell movement", Academy of Finland 2013-2017, 636,000 €, "Enhancing development of water-use efficient crops & production methods to dry and saline conditions" 2013-2016, ICI-MFA, Finland (capacity building with FCRI, Egypt), 94,000 € Genomic response to drought in a natural laboratory" (ecogenomics) 2010-2013, Academy of Finland, 559,000 € "TriticeaeGenome: Genomics for Triticeae improvement" (physical map construction, linkage to genetic map, and use, barley & wheat) 2008-2012, FP7, 283,000€ JGI barley genome sequencing project (money from & to USA partners); "Genome hitch-hiking and the parasitic dynamics of Cassandra, a novel group of retrotransposons", Academy of Finland, 2008-2011, 407,000 €, "TritiGen: Triticeae Genomics for the Advancement of Essential European Crops", COST network (Coordinator, 70 labs, 2007-2011, 495,000 € for all; "EXBARDIV: Genomics-Assisted Analysis and Exploitation of Barley Diversity", ERA-NET Plant Genomics Research, 2007-2010

16. Publications (141 total publications of which 98 peer-reviewed articles, incl. Nature (3), Nature Genetics (1), Nature Reviews Genetics (3), Nature Communications (2) PNAS (2), Plant Cell (1), New Phytologist (1); Genome Research (2), Plant Journal (4). 28 books or book chapters, 4 publications aimed at the agricultural sector, 3 newspaper articles aimed at the general public, 3 patents or disclosures, 1 doctoral dissertation.

Metrics, 06.09.2018: Google Scholar: 250 records, 12063 citations, **h-Index=50**. Web of Science: 98 records, 7595 citations, **h-index=40**. Scopus Orcid **h-index=42**, 8116 citations. Research Gate: **RG Score 39.28, h-index 50** (95th percentile)

Google Scholar list: <https://scholar.google.fi/citations?user=O3fzsjIAAAJ&hl=en>

PDFs for most publications available at: <http://www.biocenter.helsinki.fi/bi/genomedynamics/publications.html>

Key Publications:

1. Klymiuk V et al. 2018. Cloning of the wheat Yr15 resistance gene sheds light on the plant tandem kinase-pseudokinase family. *Nat Comm* 9: 3735 (**IF=12.35**), 03.10.2018
2. Mascher M et al. 2017. A chromosome conformation capture ordered sequence of the barley genome. *Nature* 544: 427-433. Cover photo. (**IF=38.138**)
3. Salojärvi J et al. 2017. Adaptive Landscape and Population Genomics of Silver Birch. *Nat Genet.* 49(6): 904-912. (**IF=31.616**)
4. Jääskeläinen, M., Chang, W., Moisy, C., Schulman, A.H. 2013. Retrotransposon *BARE* displays strong tissue-specific differences in expression. Cover photo. *New Phytol.* doi: 10.1111/nph.12470.13 (**IF=6.89**)
5. Chang W, Jääskeläinen M, Li S-P, Schulman AH. 2013. *BARE* retrotransposons are replicated and translated via distinct RNA pools. *PLoS One* 8: e72270. doi:10.1371/journal.pone.0072270. Online 06.08.2013. (**IF=3.73**)
6. International Barley Genome Sequencing Consortium, Mayer KF, Waugh R, Brown JW, Schulman A, Langridge P, Platzer M, Fincher GB, Muehlbauer GJ, Sato K, Close TJ, Wise RP, Stein N. 2012. A physical, genetic and functional sequence assembly of the barley genome. *Nature* 491:711-716. (**IF= 36.23, 717 citations**)
7. Int Brachypodium Initiative. 2010. Genome sequencing and analysis of the model grass *Brachypodium distachyon*. *Nature* 463: 763-768 doi:10.1038/nature08747 (**IF= 36.23, 1056 citations**)
8. Kalendar, R., Tanskanen, J., Chang, W., Antonius, K., Sela, H., Peleg, O., Schulman, A.H. 2008. *Cassandra* retrotransposons carry independently transcribed 5S RNA. *Proc. Natl. Acad. Sci. USA:* 105: 5833-5838 (**IF=10.56**)
9. Wicker, T., Sabot, F., Hua-Van, A., Bennetzen, J.L., Capy, P., Chalhoub, B., Flavell, A.J., Leroy, P., Morgante, M., Panaud, O., Paux, E., SanMiguel, P. & Schulman, A.H. 2007. A unified classification system for eukaryotic transposable elements. *Nature Rev. Genet.* 8: 973-982. doi:10.1038/nrg2165 (**IF=43.23, 1275 citations**)
10. Shirasu, K., Schulman, A.H., Lahaye, T. & Schulze-Lefert, P. 2000. A contiguous 66 kb barley DNA sequence provides evidence for reversible genome expansion. *Genome Res.* 10: 908-915 (**311 citations**)
11. Kalendar, R., Tanskanen, J., Immonen, S., Nevo, E. & Schulman, A.H. 2000. Genome evolution of wild barley (*Hordeum spontaneum*) by *BARE-1* retrotransposon dynamics in response to sharp microclimatic divergence. *Proc. Natl. Acad. Sci. USA* 97(12): 6603-6607. (**IF=10.56, 576 citations**)