University of California San Francisco **Prepared: August 10, 2010**

CURRICULUM VITAE

Name: **Mark Seielstad**

Positions: Associate Professor
Department of Laboratory Medicine &
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Blood Systems Research Institute
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EDUCATION:

1988-92	Stanford University, Stanford, CA	**B.S.** with Honors, Biological Sciences
1988-92	Stanford University, Stanford, CA	**A.B.** Classical Studies
1992-98	Harvard University, Cambridge, MA	**Ph.D.** Biology
1998-00	Harvard School of Public Health, Boston, MA	postdoctoral fellowship

PRINCIPAL POSITIONS HELD:

2000-01	Harvard School of Public Health	Research Associate	Population Genetics
2002-04	Harvard School of Public Health Dept. of Environmental Health	Assistant Professor (tenure track)	
2002-04	Genome Institute of Singapore	Group Leader	Population Genetics

2005-09	Genome Institute of Singapore	Associate Director	Human Genetics
2004-10	Genome Institute of Singapore	Senior Group Leader	Human Genetics

OTHER POSITIONS HELD CONCURRENTLY:

1994-96	Stanford University	Visiting Scholar	Genetics
1995	Addis Ababa University, Ethiopia	Visiting Scholar	Biology
2000-02	University of Khartoum, Sudan (Third World Academy of Sciences, Trieste, Italy)	Visiting Assistant Professor	
2005-08	Harvard School of Public Health Dept. of Genetics & Complex Diseases	Adjunct Assistant Professor	
2009-10	Harvard School of Public Health Dept. of Epidemiology	Adjunct Assistant Professor	

HONORS AND AWARDS:

1985	French Government -- *Société Honoraire de Français* Scholarship for study in France
1990-92	Classics Undergraduate Prizes, Stanford University (1990, 1991, and 1992)
1990	Lionel Pearson Award for study at the Intercollegiate Center for Classical Studies (Rome) and for archeological study in Tunisia and Turkey; Stanford University
1991	Travel Award for excavation work in Panakton, Greece and for archeological study in Jordan and Egypt; Stanford Dept. of Classics
1991	Howard Hughes Medical Institute Major Grant for thesis research on the molecular systematics of the butterfly genus, *Colias*, Stanford University Dept. of Biological Sciences
1994	U.S. National Science Foundation -- Graduate University for Advanced Studies,Yokohoma; Summer Research Fellowship at the Japanese National Institute of Genetics, Mishima
1994-98	Arthur Green Fund (Harvard University) Grants for field research in Sudan (1994 and 1998); Ethiopia (1995); and Thailand and Vietnam (1997-1998)
1996-98	L.S.B. Leakey Society Award for field research in Mali (1996); Thailand and Vietnam (1997-8)
1992-93	National Institutes of Health Genetics Trainee, Harvard University
1993-96	National Science Foundation Predoctoral Fellow
2000	National Research Service Award, National Institute of General Medical Sciences (F32 GM20425-01) (declined)
2000-02	Principal Investigator, Research Career Award, U.S. National Human Genome Research Institute (K22 HG00053-01; US$1,047,678) (2000-2002).
2002	The Keville-DePalma Founders Lecture; Salem State University, Salem, MA
2002	The Horning Lecture in the Humanities; Oregon State University, Corvallis, OR

KEYWORDS/AREAS OF INTEREST:

Human genetics, population genetics, genomics, genetic epidemiology, immunogenetics, autoimmunity, infectious diseases, immunology, type 2 diabetes, metabolism, evolution, anthropology.

PROFESSIONAL ACTIVITIES

PROFESSIONAL ORGANIZATIONS

Memberships

1998-now American Society of Human Genetics
1998-now Genetics Society of America
2002-now American Association for the Advancement of Science
2003-now Human Genome Organization (HUGO)
2007-now International Genetic Epidemiology Society

2009-now Illumina Genotyping Advisory Panel (unpaid)

SERVICE TO PROFESSIONAL PUBLICATIONS:

2005-now Ad hoc referee for *Science* (2 papers)*; Nature Genetics* (10 papers)*; The American Journal of Human Genetics* (11 papers)*; Genome Research* (5 papers)*; PLoSONE* (2 papers)*;* the National Science Foundation, Physical Anthropology Section; and the L.S.B. Leakey Society (a private funding agency for anthropological research)

2007-now	Editorial Board	*The HUGO Journal* (formerly: *Genomic Medicine*)
2008-now	Associate Editor	*Annals of Human Genetics.*
2009-now	Associate Editor	*BMC Medical Genetics*

INVITED PRESENTATIONS

KEYNOTE

The 2nd Annual Conference on Sex and Gene Expression of the Society for Women's Health Research. (March 8-11, 2001).
The Malaysian Society of Molecular Biology and Biochemistry. Bangi, Malaysia (August 17, 2006).
The Genes That Cause Autoimmune Disease. Federation of Clinical Immunology Societies Annual Meeting, San Diego (11th June 2007).
Mapping Human Genetic History in Asia. Opening Plenary. HUGO-Asia-Pacific meetings 2008, Cebu, the Philippines (2nd April 2008).
Mapping Human Genetic History in Asia. Special Plenary. Human Genome Meetings 2008 (HUGO), Hyderabad, India (28th September 2008).
Japan College or Rheumatology International Symposium, Tokyo, Japan (April 24th, 2009).

INTERNATIONAL

Trinational Workshop on Molecular Evolution, University of Munich (June 5-7, 1997).
Department of Biological Anthropology Colloquium, University of Cambridge, UK (June 19, 1997).
Department of Biology Seminar, Chiang Mai University, Thailand (November, 1997).
Department of Epidemiology Seminar, Beijing Medical University (November 8, 1999).
Department of Bio. Anthropology Seminar, University of Oxford (March 17, 2000).
Eijkman Institute for Molecular Biology, Jakarta, Indonesia (July 9, 2001).
Genome Institute of Singapore, Singapore (September 25, 2001).

Institute of Mathematical Sciences, Workshop on Population and Statistical Genetics; National University of Singapore (March 26, 2002).
6th Annual NUS-NUH Annual Scientific Meeting, Singapore (August 16, 2002).
Biomedical Research Council Symposium, Singapore (July 31, 2003).
3rd International Eijkman Symposium, Yogyakarta (Oct. 1, 2004).
5th HUGO Pacific Meeting, Pattaya, Thailand (November 18, 2004).
Royal Dutch Academy of Sciences Open Science Meeting, Yogyakarta (Sept. 28, 2005).
Institute of Mathematical Sciences, Workshop on Genomics, Singapore (Nov. 15, 2005).
Affymetrix User Group Meeting, Singapore (Nov. 12, 2006).
8th International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Bangkok (Nov. 30, 2006).
7th International Symposium on Host Genetic Epidemiology, Seoul National University (Dec. 8, 2006).
Symposium & Workshop on Forensic DNA, Jakarta (5th February 2007).
Illumina User Group Meeting, Siena, Italy (26th April 2007).
Center for Molecular Medicine, Karolinska Institutet, Stockholm (9th May 2007).
International Medical & Health Conference, Kota Bahru, Malaysia (25th May 2007).
Instituto Nacional de Medicina Genomica, Mexico City (4th September 2007).
Clinician Scientist Unit, National University Hospital, Singapore (29th October 2007).
Singapore Eye Research Institute, Singapore (31st October 2007).
Eijkman International Symposium, Bali (16th November 2007).
Indian Society of Human Genetics, Annual Meetings, Vishakhapatnam (12th February 2008).
Centre for Cellular and Molecular Biology, Hyderabad (14th February 2008).
1st Asia Pacific Inflammatory Bowel Disease Scientific Meeting & Postgraduate Course, Singapore (24th February 2008).
Illumina User Group Meeting, Cebu, the Philippines (31st March 2008).
Combined Analysis of Three Genome-Wide Scans Reveals Novel Loci Associated with Rheumatoid Arthritis. HUGO-Asia-Pacific meetings 2008, Cebu, the Philippines (5th April 2008).
The Population Genetics of SNPs and CNVs in Southeast Asian Populations. Affymetrix Integrated Genomics Solution Seminar. Singapore. (22nd September 2008).
Genome-Wide Studies for Chronic Diseases. The Singapore Epidemiology of Eye Diseases Symposium. (13th October 2008).
Korean National Institutes of Health, Seoul, Korea (April 27, 2009).
Genetics of Nasopharyngeal Carcinoma Workshop, National Cancer Centre, Singapore (February 20th, 2010)
Global Diabetes Consortium Meeting, Hong Kong (March 15, 2009).

NATIONAL

Division of Human Genetics Seminar, Washington University (March 22, 2000).
Seminar, Center for Human Genetics, University of California, San Francisco (Sept. 9, 2005).
Illumina User Group Meeting, San Diego (March 14, 2006).
Affymetrix User Group Meeting, Singapore (Nov. 12, 2006).
Program for Quantitative Genetics, Harvard School of Public Health, Boston, MA (October 27, 2009).
Session Chair, Program for Quantitative Genetics Annual Conference, Harvard University, Boston, MA (November 12, 2009).

ACADEMIC AND PUBLIC SERVICE

INSTITUTE SERVICE

2005-2009 Genome Institute of Singapore (GIS), Graduate Student's Committee. Provided mentoring and guidance for all graduate students within the Institute (N~50, advised by ~30 PI's). Attended weekly graduate student seminars and advised/critiqued students afterwards.

2004-now Liaison for the GIS and its Institutional Review Board, monitoring human subjects research. Advised PI's on their applications.

TEACHING and MENTORING

Affiliated with Biomedical Sciences (BMS) Graduate Program, UCSF
Expected affiliation with Biological and Medical Informatics (BMI) Graduate Program, UCSF

Currently advising one BMI student, Roxana Ordonez, an NSF-predoctoral fellow who has expressed an interest in continuing her Ph.D. research under my supervision (with Neil Risch, co-advisor).

POSTGRADUATE AND OTHER COURSES

1992 Teaching Assistant, Biological Sciences 2, Harvard University, Cambridge, MA
1996 Teaching Assistant, Molecular Biology Core (Science B-46), Harvard College, Cambridge, MA
2000 Lecturer, Course on Human Genome Diversity, ICGEB, Islamabad, Pakistan
2004 Course Director and Lecturer (2 lecturers, organized a graduate course of 20 lectures), Introduction to Genomics, Karolinska Institutet – National University of Singapore joint Ph.D. Program in Genetic and Molecular Epidemiology
2006 Course Director and Lecturer (2 lecturers, organized a graduate course of 20 lectures), Introduction to Genomics, Karolinska Institutet – National University of Singapore joint Ph.D. Program in Genetic and Molecular Epidemiology
2006 Lectured for graduate Molecular Biology Course at the Institute for Molecular and Cell Biology, Singapore (Byrappa Venkatesh, Course Director).
2008 Lectured for graduate Molecular Biology Course at the Institute for Molecular and Cell Biology, Singapore (Byrappa Venkatesh, Course Director).

PREDOCTORAL STUDENTS SUPERVISED

Dates	Name	Program or School	Role	Current Position
2002-2006	Methawee Srikummool	Chiang Mai University Ph.D.	co-advisor	postdoctoral fellow, Chiang Mai University, Chiang Mai, Thailand
2003-2007	Jatupol Kampuansai	Chiang Mai University Ph.D.	co-advisor	Assistant Professor, Chiang Mai University, Chiang Mai, Thailand
2008-now	Wibhu Kutanan	Chiang Mai University Ph.D.	co-advisor	
2006-now	Eileen Png	National University of Singapore, Ph.D.	advisor	
2007-now	Chee Seng Ku	National University of Singapore, Ph.D.	co-advisor	
2008-now	Rajkumar Dorajoo	ASTAR-Imperial University, London, Ph.D.	co-advisor	
2009-now	Rick T.H. Ong	National University of Singapore, Ph.D.	advisor	

POSTDOCTORAL FELLOWS DIRECTLY SUPERVISED OR MENTORED:

Dates	Name	Fellow	Faculty Role	Current Position
2004-2008	"Terry" KL Toh	postdoc	Research Supervision	Clinical Scientist, National University Hospital, Singapore
2005-2007	Jenny Hui Hui Tan	postdoc	Research Supervision	Instructor, Ministry of Education, Singapore
2006-now	Vikrant Kumar	postdoc	Research Supervision	
2009-now	Devindri Perera	postdoc	Research Supervision	

FACULTY MENTORING

K08 Faculty mentoring for and scientific collaborations with:

Adam Lauring, MD, PhD
NIH Clinician-Scientist Career Development Awardee (K08)
Assistant Adjunct Professor, Infectious Diseases
UCSF Department of Medicine &
Department of Microbiology and Immunology
600 16th Street
Genentech Hall, S-576
San Francisco, CA 94143-2280
Tel:(415) 502-6357
Fax:(415) 514-4112
Adam.Lauring@ucsf.edu

SUMMARY OF TEACHING HOURS:

2008-09 252 total hours of teaching
Formal classroom teaching hours: 12
Informal teaching hours: 250 hours, mentoring students and postdocs

2009-10 310 total hours of teaching
Formal classroom teaching hours: 10
Informal teaching hours: 300 hours, mentoring students and postdocs

2010-11 Total anticipated hours of teaching: 300.
Formal classroom teaching hours: 10
Informal teaching hours: 300 hours, mentoring students and postdocs

RESEARCH AND CREATIVE ACTIVITIES

RESEARCH AWARDS AND GRANTS:

CURRENT

1U01DK085545-01 (principal investigator) 9/20/09-7/31/14
NIH/NIDDK $46,536 direct year 01; $314,153 direct/yrs1-5
Identifying Variants Causal for Type 2 Diabetes in Major Human Populations

1R01DK080720-01A1 (co-investigator) 3/1/09-2/28/14
NIH/NIDDK $681,811 direct year 01; $2,358,691 direct/yrs 1-5
Genetic and Environmental Determinants of Type 2 Diabetes in Chinese Singaporeans

National Medical Research Council, Singapore (collaborator) 2008-2013
Translational Research Innovations in Ocular Surgery $3,600,000 direct year 01; $18,000,000 direct/yrs 1-5

National Medical Research Council, Singapore (collaborator) 2008-2011
Genome-wide case-control studies to identify genetic variants and gene-environment interactions involved in the pathogenesis of type 2 diabetes mellitus in Chinese, Malays and Asian Indians living in Singapore $500,000 direct year 01; $850,000 direct/yrs 1-3

NMRC/1111/2007 (co-investigator) 2007-2010
National Medical Research Council, Singapore
Environmental and genetic determinants of adiponectin in Chinese, Malays and Asian Indians, National Medical Research Council, Singapore $150,000 direct year 01; $425,000 direct/yrs 1-3

PAST

5R01CA104021-02 (co-investigator) 9/1/05-6/30/10
NIH/NCI $1,264,708 direct/yrs 1-5
Genetic determinants of postmenopausal breast cancer.

GIS/05-PB2101 (PI) 4/1/05-3/31/2009
Genome Institute of Singapore (GIS) intramural $2,983,900 direct/yrs 1-4
High-Throughput SNP Genotyping Facility

GIS/09-BR2102 (PI) 4/1/05-3/31/10
Genome Institute of Singapore Intramural Funding $5,979,847 direct yrs 1-6

N66001-08-C-2014 (PI) 5/1/08-8/31/09
DARPA (USA) $830,829 direct
Genetic Biomarkers for Prediction of Vaccine Response

W911QY-06-C-0085 (PI) 2006-2007

DARPA $325,000 direct/yr 1
Genetic Biomarkers for Prediction of Vaccine Response

Susan G. Komen Breast Cancer Foundation (co-investigator) 2004-2006
Genetic & environmental determinants of postmenopausal breast cancer
$952,057 direct

05/1/36/19/413 (co-investigator) 2006-2009
Biomedical Research Council, Singapore $886,250 direct/yrs 1-3
The Genetics of High Density Lipoprotein Cholesterol Metabolism

PEER REVIEWED PUBLICATIONS

1. **Seielstad** MT, Hebert JM, Lin AA, Underhill PA, Ibrahim M, Vollrath D, Cavalli-Sforza LL (1994) Construction of human Y-chromosomal haplotypes using a new polymorphic A to G transition. *Human Molecular Genetics,* **3**:2159-61.

2. Ruiz-Linares A, Nayar K, Goldstein DB, Hebert JM, **Seielstad** MT, Underhill PA, Lin AA, Feldman MW, and Cavalli-Sforza LL (1996) Geographic clustering of human Y chromosome haplotypes. *Annals of Human Genetics* , **60**:401-408.

3. Wells RS, **Seielstad** M, Bunce M, Tyan DB, Bekele E, and Parham P (1997) Cw*1701 defines a divergent African HLA-C allelic lineage. *Immunogenetics,* **46**:173-180.

4. Perez-Lezaun A, Calafell F, **Seielstad** M, Mateu E, Comas D, Bosch E, and Bertranpetit J (1997) Population genetics of Y-chromosome short tandem repeats in humans. *Journal of Molecular Evolution*, **45**:265-270.

5. **Seielstad** M, Minch E, and Cavalli-Sforza LL (1998) Genetic evidence for a higher female migration rate in humans. *Nature Genetics,* **20:**278-280.

6. **Seielstad** M, Bekele E, Ibrahim M, Touré A, and Traoré M (1999) A view of modern human origins from Y chromosome microsatellite variation. *Genome Research,* **9:**558-567.

7. Pritchard JK, **Seielstad** MT, Perez-Lezaun A, and Feldman MW (1999) Population growth of human Y chromosomes: a study of Y chromosome microsatellites. *Molecular Biology and Evolution,* **16:**1791-1798.

8. Jorde LB, Watkins WS, Bamshad MJ, Dixon ME, Ricker CE, **Seielstad** MT and Batzer MA (2000) The distribution of human genetic diversity: a comparison of mitochondrial, autosomal and Y-chromosome data. *American Journal of Human Genetics,* **66:**979-988.

9. Underhill PA, Shen P, Lin AA, Jin L, Passarino G, Yang WH, Kauffman E, Bonné-Tamir B, Bertranpetit J, Francalacci P, Ibrahim M, Jenkins T, Kidd J, Mehdi SQ, **Seielstad** MT, Wells RS, Piazza A, Davis RW, Feldman M, Cavalli-Sforza LL and Oefner PJ. (2000) The architecture of Y-chromosome biallelic haplotype diversity: an emerging portrait of mankind. *Nature Genetics,* **26:**358-361.

10. Su B, Xiao C, Deka R, **Seielstad** M, Kangwanpong D, Xiao J, Lu D, Underhill P, Cavalli-Sforza L, Chakraborty R and Jin L (2000) Y chromosome haplotypes reveal prehistorical migrations to the Himalayas. *Human Genetics,* **107:**582-90**.**

11. Y Ke, B Su, X Song, D Lu, L Chen, H Li, C Qi, S Marzuki, R Deka, P Underhill, C Xiao, M Shriver, J Lell, D Wallace, S Wells, M **Seielstad**, P Oefner, D Zhu, J Jin, W Huang, R Chakraborty, Z Chen, L Jin (2001) African Origin of Modern Humans in East Asia: A tale of 12,000 Y chromosomes. *Science* **292:**1151-1153.

12. Niu T, **Seielstad** M, Zeng X, Apffel A, Li G, Hahnenberger K, Xu X. (2001) Detection of novel ALAD gene polymorphisms using denaturing high-performance liquid chromatography. *Human Biology,* **73:**429-42.

13. Ardlie K, Lunetta K and **Seielstad** M (2002) Testing for population subdivision and association in four case-control studies. *American Journal of Human Genetics,* **71:**304-311.

14. Bereir RE, Mohamed HS, **Seielstad** M, El Hassani AM, Khalil EA, Peacock CS, Blackwell JM, Ibrahim ME. (2003) Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. *Genetica,* **119**:57-63.

15. **Seielstad** M, Yuldasheva N, Singh N, Underhill P, Oefner P, Shen P, Wells RS (2003) A novel Y-chromosome variant puts an upper limit on the timing of first entry into the Americas. *American Journal of Human Genetics,* **73:**700-705.

16. Chia KS, Lee JJM, Cheung P, Cheung KH, **Seielstad** M, Liu E (2004) Twin births in Singapore: a population-based study using the national birth registry. *Annals Academy of Medicine Singapore,* **33**:195-199.

17. Zhang C, Bailey DK, Awad T, Liu G, Xing G, Cao M, Valmeekam V, Retief J, Matsuzaki H, Taub M, **Seielstad** M, Kennedy GC. (2006) A whole genome long-range haplotype (WGLRH) test for detecting imprints of positive selection in human populations. *Bioinformatics* **22**:2122-8.

18. Teo YY, Fry AE, Clark TG, Tai ES, & **Seielstad** M. (2007) On the Usage of HWE for Identifying Genotyping Errors. *Ann Hum Genet.* **71**:701-3.

19. Besaggio D, Fuselli S, Srikummool M, Kampuansai J, Castrì L, Tyler-Smith C, **Seielstad** M, Kangwanpong D and Bertorelle G. Genetic variation in Northern Thailand Hill Tribes: origins and relationships with social structure and linguistic differences. (2007). *BMC Evolutionary Biology 7(Suppl 2):S12 doi:10.1186/1471-2148-7-S2-S12*

20. Plenge RM*, **Seielstad** M*, Padyukov L, Lee AT, Remmers EF, Ding B, Liew A, Khalili MSH, Chandrasekaran A, Davies LRL, Li W, Tan AKS, Bonnard C, Ong RTH, Thalamuthu A, Pettersson S, Liu C, Tian C, Chen WV, Carulli JP, Altshuler D, Alfredsson L, Criswell LA, Amos CI, Seldin MF, Kastner DL, Klareskog L, Gregersen PK. Genome-wide association study in rheumatoid arthritis identifies TRAF1-C5 as a new susceptibility locus (2007). *The New England Journal of Medicine* **357**:1199-209.
***equal contributions**

21. S Nejentsev, T Thye, J S Szeszko1, H Stevens, Y Balabanova, A M Chinbuah, M Hibberd, E van de Vosse, B Alisjahbana, R van Crevel, THM Ottenhoff, E Png, F Drobniewski, J A Todd, **M Seielstad**

and R D Horstmann. (2008) Analysis of association of the MAL/TIRAP variant and tuberculosis in 9,441 subjects from three populations. *Nature Genetics* **40**: 261 - 262.

22. Teo YY, Inouye M, Small KS, Fry AE, Potter SC, Dunstan SJ, **Seielstad** M, Barroso I, Wareham NJ, Rockett KA, Kwiatkowski DP, Deloukas P. (2008) Whole genome-amplified DNA: insights and imputation. *Nature Methods.* **5**:279-80.

23. Tan JT, Dorajoo R, **Seielstad** M, Sim XL, Ong RT, Chia KS, Wong TY, Saw SM, Chew SK, Aung T, Tai ES. (2008) FTO Variants Are Associated With Obesity in the Chinese and Malay Populations in Singapore. *Diabetes*. **57**:2851-7.

24. Raychaudhuri S, Remmers EF, Lee AT, Hackett R, Guiducci C, Burtt NP, Gianniny L, Korman BD, Padyukov L, Kurreeman FA, Chang M, Catanese JJ, Ding B, Wong S, van der Helm-van Mil AH, Neale BM, Coblyn J, Cui J, Tak PP, Wolbink GJ, Crusius JB, van der Horst-Bruinsma IE, Criswell LA, Amos CI, Seldin MF, Kastner DL, Ardlie KG, Alfredsson L, Costenbader KH, Altshuler D, Huizinga TW, Shadick NA, Weinblatt ME, de Vries N, Worthington J, **Seielstad M**, Toes RE, Karlson EW, Begovich AB, Klareskog L, Gregersen PK, Daly MJ, Plenge RM. (2008) Common variants at CD40 and other loci confer risk of rheumatoid arthritis. *Nature Genetics* **40**:1216-23.

25. Chen H, Toh TK, Szeverenyi I, Ong RT, Theng CT, McLean WH, **Seielstad** M, Lane EB. (2008) Association of Skin Barrier Genes within the PSORS4 Locus Is Enriched in Singaporean Chinese with Early-Onset Psoriasis. *Journal of Investigative Dermatology*. **129**:606-14.

26. Thuong NTT, Dunstan SJ, Chau TTH, Thorsson V, Simmons CP, Quyen NTH, Thwaites GE, Lan NTN, Hibberd M, Teo YY, **Seielstad** M, Aderem A, Farrar JJ and Hawn TR. (2008) Identification of Tuberculosis Susceptibility Genes with Human Macrophage Gene Expression Profiles. *PLoS Pathogens* **4**:e1000229.

27. Davila S, Hibberd ML, Dass RH, Wong HEE, Sahiratmadja E, Bonnard C, Alisjahbana B, Szeszko JS, Balabanova Y, Drobniewski F , van Crevel R, van de Vosse E, Nejentsev S, Ottenhoff THM, **Seielstad** M (2008) Genetic Association and Expression Studies Indicate a Role of Toll-Like Receptor 8 in Pulmonary Tuberculosis. *PLoS Genetics* **4**:e1000218.

28. Tai ES, Sim XL, Ong TH, Wong TY, Saw SM, Aung T, Kathiresan S, Orho-Melander M, Ordovas JM, Tan JT, **Seielstad** M. (2008) Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. *J Lipid Res*. **50**:514-20.

29. Ding B, Padyukov L, Lundström E, **Seielstad** M, Plenge RM, Oksenberg JR, Gregersen PK, Alfredsson L, Klareskog L. (2009) Different patterns of associations with anti-citrullinated protein antibody-positive and anti-citrullinated protein antibody-negative rheumatoid arthritis in the extended major histocompatibility complex region. *Arthritis Rheum.* **60**:30-8.

30. Lim LS, Tai ES, Aung T, Tay WT, Saw SM, **Seielstad** M, Wong TY. (2009) Relation of Age-related Cataract With Obesity and Obesity Genes in an Asian Population. *Am J Epidemiol.* **169**:1267-74.

31. Lee YC, Raychaudhuri S, Cui J, De Vivo I, Ding B, Alfredsson L, Padyukov L, Costenbader KH, **Seielstad** M, Graham RR, Klareskog L, Gregersen PK, Plenge RM, Karlson EW. (2009) The PRL -1149 G/T polymorphism and rheumatoid arthritis susceptibility. *Arthritis Rheum.* **60**:1250-4.

32. Tan JT, Dorajoo R, **Seielstad** M, Sim XL, Ong RT, Chia KS, Wong TY, Saw SM, Chew SK, Aung

T, Tai ES. (2008) FTO variants are associated with obesity in the Chinese and Malay populations in Singapore. *Diabetes*. **57**:2851-7.

33. Chen J, Zheng H, Bei JX, Sun L, Jia WH, Li T, Zhang F, **Seielstad** M, Zeng YX, Zhang X, Liu J. (2009) Genetic structure of the Han Chinese population revealed by genome-wide SNP variation. *Am J Hum Genet*. **85**:775-85.

34. Raychaudhuri S, Thomson BP, Remmers EF, Eyre S, Hinks A, Guiducci C, Catanese JJ, Xie G, Stahl EA, Chen R, Alfredsson L, Amos CI, Ardlie KG; BIRAC Consortium, Barton A, Bowes J, Burtt NP, Chang M, Coblyn J, Costenbader KH, Criswell LA, Crusius JB, Cui J, De Jager PL, Ding B, Emery P, Flynn E, Harrison P, Hocking LJ, Huizinga TW, Kastner DL, Ke X, Kurreeman FA, Lee AT, Liu X, Li Y, Martin P, Morgan AW, Padyukov L, Reid DM, **Seielstad** M, Seldin MF, Shadick NA, Steer S, Tak PP, Thomson W, van der Helm-van Mil AH, van der Horst-Bruinsma IE, Weinblatt ME, Wilson AG, Wolbink GJ, Wordsworth P; YEAR Consortium, Altshuler D, Karlson EW, Toes RE, de Vries N, Begovich AB, Siminovitch KA, Worthington J, Klareskog L, Gregersen PK, Daly MJ, Plenge RM. (2009) Genetic variants at CD28, PRDM1 and CD2/CD58 are associated with rheumatoid arthritis risk. *Nat Genet.* **41**:1313-8.

35. Teo YY, Sim X, Ong RT, Tan AK, Chen J, Tantoso E, Small KS, Ku CS, Lee EJ, **Seielstad** M, Chia KS. (2009) Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. *Genome Res.* **19**:2154-62.

36. **HUGO Pan-Asian SNP Consortium, Abdulla MA, Ahmed I, Assawamakin A, Bhak J, Brahmachari SK, Calacal GC, Chaurasia A, Chen CH, Chen J, Chen YT, Chu J, Cutiongco-de la Paz EM, De Ungria MC, Delfin FC, Edo J, Fuchareon S, Ghang H, Gojobori T, Han J, Ho SF, Hoh BP, Huang W, Inoko H, Jha P, Jinam TA, Jin L, Jung J, Kangwanpong D, Kampuansai J, Kennedy GC, Khurana P, Kim HL, Kim K, Kim S, Kim WY, Kimm K, Kimura R, Koike T, Kulawonganunchai S, Kumar V, Lai PS, Lee JY, Lee S, Liu ET, Majumder PP, Mandapati KK, Marzuki S, Mitchell W, Mukerji M, Naritomi K, Ngamphiw C, Niikawa N, Nishida N, Oh B, Oh S, Ohashi J, Oka A, Ong R, Padilla CD, Palittapongarnpim P, Perdigon HB, Phipps ME, Png E, Sakaki Y, Salvador JM, Sandraling Y, Scaria V, **Seielstad** M, Sidek MR, Sinha A, Srikummool M, Sudoyo H, Sugano S, Suryadi H, Suzuki Y, Tabbada KA, Tan A, Tokunaga K, Tongsima S, Villamor LP, Wang E, Wang Y, Wang H, Wu JY, Xiao H, Xu S, Yang JO, Shugart YY, Yoo HS, Yuan W, Zhao G, Zilfalil BA; Indian Genome Variation Consortium. (2009) Mapping human genetic diversity in Asia. *Science*. **326**:1541-5.
**** corresponding author**

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NON-PEER REVIEWED PUBLICATIONS AND OTHER CREATIVE ACTIVITIES:

Reviews & Commentaries

1. 'Whiffs of selection', (2000) *Nature Genetics* **26**:131-2 (News & Views).
2. Asymmetries in the maternal and paternal genetic histories of Colombian populations (2000) *American Journal of Human Genetics,* **67**:1062-1066 (Invited Editorial).
3. Review of *Microsatellites: evolution and applications*. Goldstein D and Schloetterer C, eds. for *Quarterly Review of Biology* (2001) **76:**74-5.
4. Ardlie K, Kruglyak L & **Seielstad** M (2002) Patterns of linkage disequilibrium in the human genome. *Nature Reviews Genetics,* **3:**299-309.

Book Chapters

5. **Seielstad** M (1998) Some effects of culture on genetic variation. in *Proceedings of the trinational workshop on molecular evolution.* M. Uyenoyama and A. von Haeseler, eds. Duke University Publications Group, Durham.
6. Ruvolo M and **Seielstad** M (2001) The apportionment of human diversity 25 years later. In *Thinking about evolution: historical, philosophical and political perspectives.* Singh, Krimbas, Paul and Beatty, eds. Cambridge University Press.
7. Srikummool M, Kangwanpong D, Singh N and **Seielstad** M (2001) Y-chromosomal variation in uxorilocal and patrilocal populations in Thailand. in *Genetic, Linguistic and Archaeological Perspectives on Human Diversity in Southeast Asia,* Jin L, Seielstad M, & Xiao C, eds. World Scientific Press, Singapore.

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8. *Genetic, Linguistic and Archaeological Perspectives on Human Diversity in Southeast Asia,* Jin L, **Seielstad** M, and Xiao C, eds. World Scientific Publishing, Singapore (2001).

Translation

9. Cavalli-Sforza, LL (2000) *Genes, Peoples, and Languages*, M. **Seielstad**, trans. Farrar, Straus & Giroux, New York.

OTHER CREATIVE ACTIVITIES:

Led and managed an effort to describe haplotype variation in three ethnic populations inhabiting Singapore (Chinese, Malays and Indians) and helped develop a website to distribute the data: http://www.nus-cme.org.sg/SGVP username: Reviewer; password: sgvp

ABSTRACTS:

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Seielstad, M, Minch, E, and Cavalli-Sforza, LL (1997) The apportionment of Y chromosome diversity. Cold Spring Harbor Laboratory Meetings on Human Evolution (talk).

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Seielstad M, L. Padyukov, B. Ding, L. Alfredsson, L. Klareskog & the EIRA Study Group (2007). Genomics of Common Diseases Conference, Hinxton, UK.

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A. Dellinger, T. L. Young, M. **Seielstad**, L. K. Goh, S. M. Saw, Y. J. Li. Significant Results of CNV Analysis of Myopia in Schoolchildren. American Society of Human Genetics Annual Meetings 2008.

V. Kumar, J. H. H. Tan, Y. Zhu, F. Yao, Y. Ruan, M. **Seielstad** Genome-wide analysis of structural variation by pair-end mapping. American Society of Human Genetics Annual Meetings 2008.

R. M. Plenge, S. Raychaudhuri, E. F. Remmers, A. T. Lee, L. Gianniny, L. Padyukov, L. A. Criswell, C. I. Amos, M. F. Seldin, D. L. Kastner, T. W. J. Huizinga, N. de Vries, J. Worthington, M. **Seielstad**, R. E. M. Toes, E. W. Karlson, A. B. Begovich, L. Klareskog, P. K. Gregersen, M. J. Daly, BRASS, EIRA, GENRA, NARAC, WTCCC. Meta-analysis of rheumatoid arthritis genome-wide association studies identifies common variants at CD40 and five other gene loci. American Society of Human Genetics Annual Meetings 2008.

RESEARCH PROGRAM

RESEARCH INTERESTS

My research centers on the identification of inherited variation that influences disease risk in humans. The hope is that this will lead to tangible improvements in public and individual health, via the identification of novel genes and pathways involved in the physiology of a particular disease process or non-disease phenotype. Neither of these rather lofty aims – the identification of disease related variation, nor the translation into clinical utility – has been realistic for complex diseases until just the last two or three years. But within this short period of time, an increasingly detailed understanding of the human genome sequence and the structure of variation within it have combined with dramatic improvements in the cost and throughput of SNP genotyping and DNA sequencing, to enable the identification of common variants underlying complex disease risk. Early results from these 'genome-wide association studies' (GWAS) have demonstrated both their feasibility, and their potential for identifying unexpected pathways of disease physiology – pathways that seem likely, in many cases, to be the targets of successful new therapies and predictive risk assessments.

During my time in Singapore, I have been fortunate to have designed and executed several such studies, each of which will lead directly to years of productive follow-up research. I have chosen to concentrate particularly on disorders of immunity and metabolism for several reasons. First is my belief that deaths from epidemics or famine are likely to have been among the two greatest selective forces in our evolutionary past. This leads to the expectation that the magnitude of genetic effects contributing to susceptibility to infection, autoimmunity, and metabolic disease is significant, and probably larger than for many other complex diseases that have so far proved refractory to genetic analysis. This should increase the likelihood of identifying relevant genes via population-based association studies, and should serve as a better testing ground for methodology that might then be more successfully applied to diseases with more subtle genetic etiologies. It also leads to the attractive hypothesis (which my research program aims to test) that our adaptations to survive infections and periods of food scarcity have left us maladapted to modern life in which infectious mortality has been sharply reduced by improvements in hygiene, antibiotics/antivirals, and vaccines; and in which an overabundance of food poses a greater threat to the health of a growing fraction of the global population, than does its scarcity. In addition to susceptibility to infections and overt autoimmune conditions; immune genes are now known to play key roles in many cancers, allergic and hyper-responsive disorders of rapidly increasing incidence such as asthma, metabolic disease/diabetes, as well cardiac and vascular disease. By using pathogens, vaccines, and autoimmune diseases as probes of functionally relevant immunogenetic variation, I believe we can gain a broader understanding of numerous other diseases that all converge in one way or another on the nexus of immune genes – and my research program at UCSF seeks to uncover the genetic underpinnings of both immune-related and metabolic diseases of humans.

At the present time, I have completed genome-wide association studies in:

1.) Tuberculosis
2.) Antibody response to Hepatitis B vaccination
3.) Rheumatoid Arthritis
4.) Psoriasis
5.) Ulcerative Colitis
6.) Type 2 Diabetes
7.) HDL- Cholesterol levels and other metabolic and biometric traits