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Education & Training

1988–1990	Georg-August-Universität, Göttingen, Germany	Vordiplom	Biology
1990–1991	University of California, San Diego, CA	–	Biology
1991–1992	Georg-August-Universität, Göttingen, Germany	–	Biology
1992–1993	Columbia University, New York, NY	M.A.	Molecular Genetics
1993–1996	Columbia University, New York, NY	M.Ph.	Statistical Genetics
1996–2000	Columbia University, New York, NY	Ph.D.	Statistical Genetics

Research Focus

To what degree do we inherit predisposition to disease, life expectancy, and personal skills, predilections, and behaviors? What are the specific genetic factors involved in shaping these characteristics? To address these questions, Dr. Göring's research group works on two aspects of genetic epidemiology, the development of statistical methods for genetic analysis and the application of those methods to well-designed human datasets.

On the methodological front, one current project of Dr. Göring's research group is to develop ways to localize and identify rare genomic variants with strong phenotypic impact on complex traits in extended pedigree samples. Specifically, his research group is taking advantage of genotyped rare variants from whole genome sequence data to phase and impute missing genotype data, and they are developing methods for assessing the phenotypic effect of unique chromosome segments (found only in a single pedigree founder and his/her descendants) on disease and disease-related quantitative risk factors.

On the applied front, Dr. Göring's research group is involved in several studies that integrate genotypic data and other "omics" technology-generated data to unravel trait etiology. A recent project involved the search for differences in gene expression between schizophrenic individuals and controls. His research group examined the expression patterns of case and control lymphoblastoid cell lines (from both European ancestry and African American individuals) before and after stimulation with the neurotransmitter dopamine, with the hope that the identified differences reveal information about the etiology of schizophrenia.

Dr. Göring's group is also seeking to identify early metabolomic biomarkers for cardiovascular disease and type 2 diabetes. They are characterizing the metabolome of blood plasma samples using a highly sensitive separation methodology (untargeted two-dimensional gas chromatography approach coupled to time-of-flight mass spectrometry) to identify specific molecules or chemical signatures that predict elevated risk of disease onset. A recent metabolomic project was focused on large Mexican American families, and a current project involves Sikhs from India.

Publications

Articles

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2. **Göring HHH**, Ott J (1997) Relationship estimation in affected sib pair analysis of late-onset diseases. *Eur J Hum Genet* 5:69–77
3. Gieser L, Fujita R, **Göring HHH**, Ott J, Hoffman DR, Cideciyan AV, Birch DG, Jacobson SG, Swaroop A (1998) A novel locus (RP24) for X-linked retinitis pigmentosa maps to Xq26–27. *Am J Hum Genet* 63:1439–1447
4. Annunen S, Paassilta P, Lohiniva J, Perälä M, Pihlajamaa T, Karppinen J, Tervonen O, Kröger H, Lähde S, Vanharanta H, Ryhänen L, **Göring HHH**, Ott J, Prockop DJ, Ala-Kokko L (1999) An allele of COL9A2 associated with intervertebral disc disease. *Science* 285:409–412
5. Le Saux O, Urban Z, **Göring HHH**, Csiszar K, Pope FM, Richards A, Pasquali-Ronchetti I, Terry S, Bercovitch L, Lebwohl MG, Breuning M, van den Berg P, Kornet L, Ott J, de Jong PTVM, Bergen AAB and Boyd CD (1999) Pseudoxanthoma elasticum maps to an 820-kb region of the p13.1 region of chromosome 16. *Genomics* 62:1–10
6. **Göring HHH**, Terwilliger JD (2000) Linkage analysis in the presence of errors I: Complex-valued recombination fractions and complex phenotypes. *Am J Hum Genet* 66:1095–1106 [erratum in (2000) *Am J Hum Genet* 66:1472]
7. **Göring HHH**, Terwilliger JD (2000) Linkage analysis in the presence of errors II: Marker-locus genotyping errors modeled with hypercomplex recombination fractions. *Am J Hum Genet* 66:1107–1118 [erratum in (2000) *Am J Hum Genet* 66:1472]
8. **Göring HHH**, Terwilliger JD (2000) Linkage analysis in the presence of errors III: Marker loci and their map as nuisance parameters. *Am J Hum Genet* 66:1298–1309
9. **Göring HHH**, Terwilliger JD (2000) Linkage analysis in the presence of errors IV: Joint pseudomarker analysis of linkage and/or linkage disequilibrium on a mixture of pedigrees and singletons when the mode of inheritance cannot be accurately specified. *Am J Hum Genet* 66:1472–1478

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12. **Göring HHH**, Terwilliger JD, Blangero J (2001) Large upward bias in estimation of locus-specific effects from genome-wide scans. *Am J Hum Genet* 69:1357–1369
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14. Hsueh W-C, **Göring HHH**, Blangero J, Mitchell BD (2001) Replication of linkage to quantitative trait loci: Variation in location and magnitude of the LOD score. *Genet Epidemiol* 21 (Suppl 1):S473–S478
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