National Human Genome Research Institute

Introduction and Goals of Meeting

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NHGRI

Foundation for the National Institutes of Health

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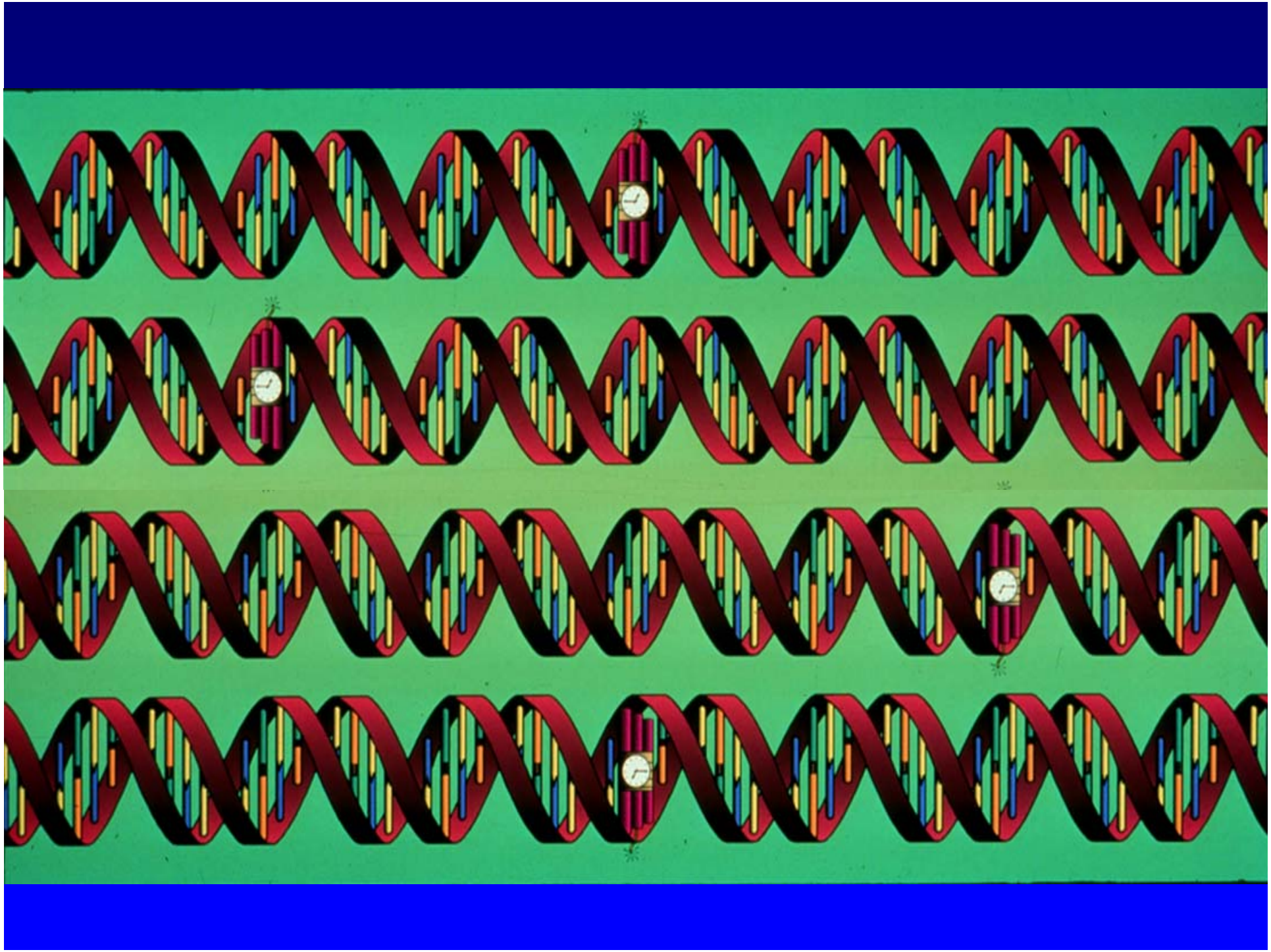
MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

J. D. Watson
F. H. C. Crick

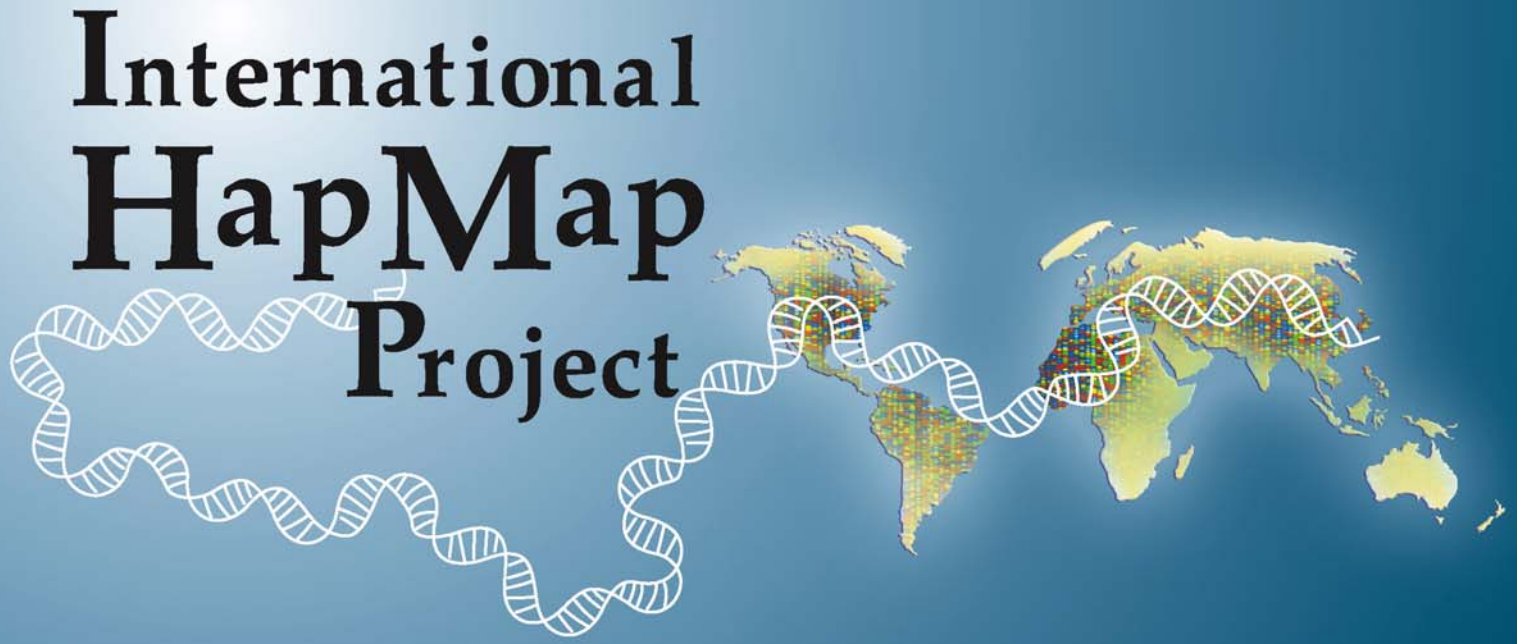
Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge.

April 2.



Whole Genome Association Approach to Common Disease: The View from 2002

- Identify all 10 million common SNPs
- Collect 1000 cases and 1000 controls
- Genotype all DNAs for all SNPs
- That adds up to 20 billion genotypes
- At 50 cents a genotype, that's $10 billion for each disease



www.hapmap.org

27 October 2005 | www.nature.com/nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

nature

THE HAPMAP PROJECT

Chapter and verse on human genetic variation

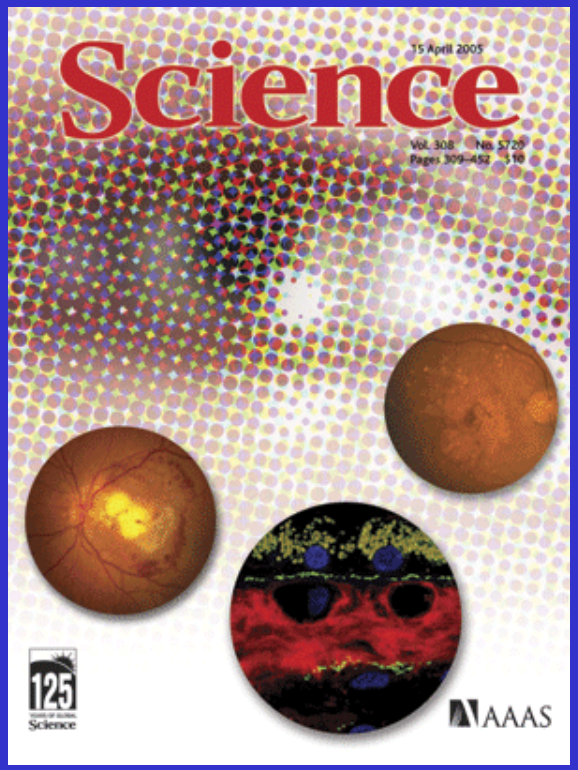
Whole Genome Association Approach to Common Disease in the HapMap Era

- Identify an optimum set of 300,000 tag SNPs
- Collect 1000 cases and 1000 controls
- Genotype all DNAs for all SNPs
- That adds up to 600 million genotypes
- Genotyping just dropped to $0.003, so that's $2 million for each disease, and that continues to drop

The First HapMap Success Story: Age-Related Macular Degeneration

Complement Factor H Polymorphism in Age-Related Macular Degeneration

Robert J. Klein,[1] Caroline Zeiss,[2*] Emily Y. Chew,[3*] Jen-Yue Tsai,[4*] Richard S. Sackler,[1] Chad Haynes,[1] Alice K. Henning,[5] John Paul SanGiovanni,[3] Shrikant M. Mane,[6] Susan T. Mayne,[7] Michael B. Bracken,[7] Frederick L. Ferris,[3] Jurg Ott,[1] Colin Barnstable,[2] Josephine Hoh[7†]



Two other risk variants have also been identified.

Together these account for a substantial fraction of the overall risk, and point to powerful new approaches to prevention and treatment.

nature genetics

Other early results From HapMap

Variant of transcription factor 7-like 2 (*TCF7L2*) confers risk of type 2 diabetes

Struan F A Grant[1], Gudmar Thorleifsson[1], Inga Reynisdottir[1], Rafn Benediktsson[2,3], Andrei Manolescu[1], Jesus Sainz[1], Agnar Helgason[1], Hreinn Stefansson[1], Valur Emilsson[1], Anna Helgadottir[1], Unnur Styrkarsdottir[1], Kristinn P Magnusson[1], G Bragi Walters[1], Ebba Palsdottir[1], Thorbjorg Jonsdottir[1], Thorunn Gudmundsdottir[1], Arnaldur Gylfason[1], Jona Saemundsdottir[1], Robert L Wilensky[4], Muredach P Reilly[4], Daniel J Rader[4], Yu Bagger[5], Claus Christiansen[5], Vilmundur Gudnason[2], Gunnar Sigurdsson[2,3], Unnur Thorsteinsdottir[1], Jeffrey R Gulcher[1], Augustine Kong[1] & Kari Stefansson[1]

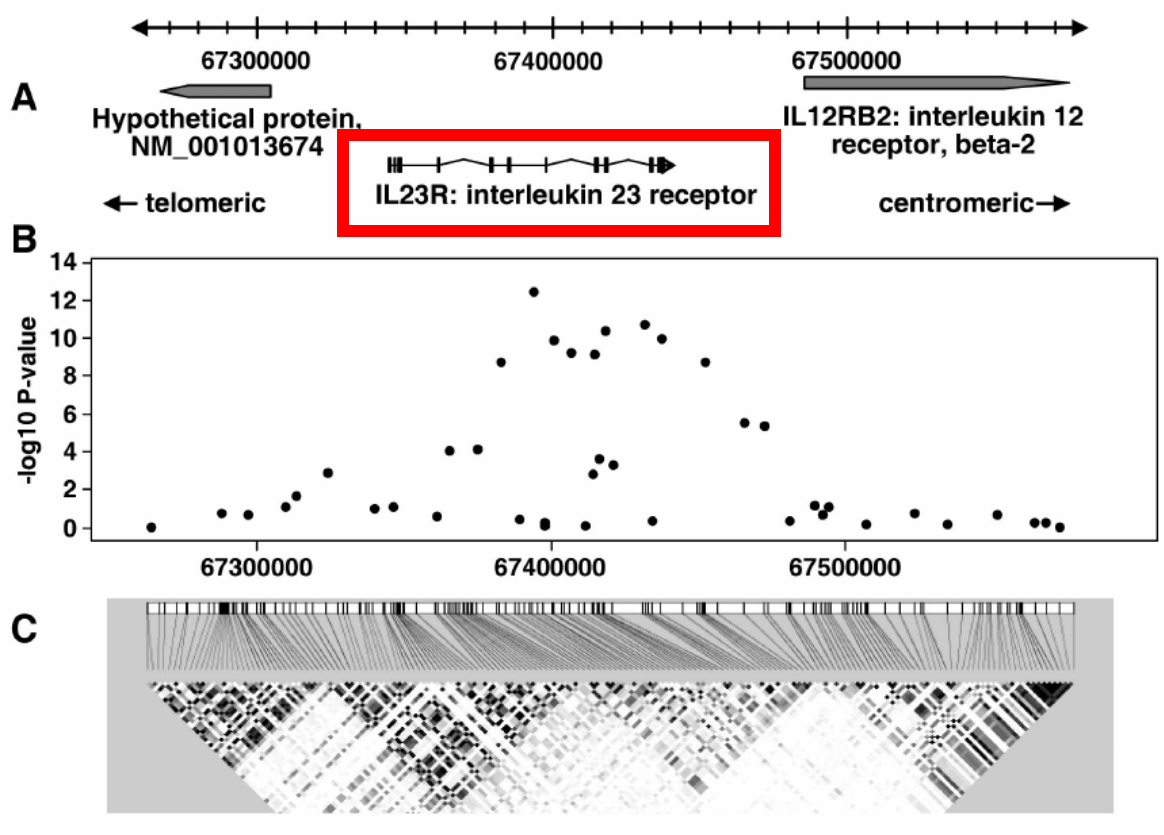
A common variant associated with prostate cancer in European and African populations

Laufey T Amundadottir[1,12], Patrick Sulem[1,12], Julius Gudmundsson[1,12], Agnar Helgason[1], Adam Baker[1], Bjarni A Agnarsson[2], Asgeir Sigurdsson[1], Kristrun R Benediktsdottir[2], Jean-Baptiste Cazier[1], Jesus Sainz[1], Margret Jakobsdottir[1], Jelena Kostic[1], Droplaug N Magnusdottir[1], Shyamali Ghosh[1], Kari Agnarsson[1], Birgitta Birgisdottir[1], Louise Le Roux[1], Adalheidur Olafsdottir[1], Thorarinn Blondal[1], Margret Andresdottir[1], Olafia Svandis Gretarsdottir[1], Jon T Bergthorsson[1], Daniel Gudbjartsson[1], Arnaldur Gylfason[1], Gudmar Thorleifsson[1], Andrei Manolescu[1], Kristleifur Kristjansson[1], Gudmundur Geirsson[3], Helgi Isaksson[2], Julie Douglas[4], Jan-Erik Johansson[5], Katarina Bälter[6], Fredrik Wiklund[6], James E Montie[7], Xiaoying Yu[8], Brian K Suarez[9], Carole Ober[10], Kathleen A Cooney[7,11], Henrik Gronberg[6], William J Catalona[8], Gudmundur V Einarsson[3], Rosa B Barkardottir[2], Jeffrey R Gulcher[1], Augustine Kong[1], Unnur Thorsteinsdottir[1] & Kari Stefansson[1]

Sciencexpress Report

A Genome-Wide Association Study Identifies *IL23R* as an Inflammatory Bowel Disease Gene

Richard H. Duerr,[1,2] Kent D. Taylor,[3,4] Steven R. Brant,[5,6] John D. Rioux,[7,8] Mark S. Silverberg,[9] Mark J. Daly,[8,10] A. Hillary Steinhart,[9] Clara Abraham,[11] Miguel Regueiro,[1] Anne Griffiths,[12] Themos Dassopoulos,[5] Alain Bitton,[13] Huiying Yang,[3,4] Stephan Targan,[4,14] Lisa W. Datta,[5] Emily O. Kistner,[15] L. Philip Schumm,[15] Annette Lee,[16] Peter K. Gregersen,[16] M. Michael Barmada,[2] Jerome I. Rotter,[3,4] Dan L. Nicolae,[11,17] Judy H. Cho[18]*



Turbocharging genetic analysis of common disease: The Genetic Association Information Network (GAIN)

- An unprecedented public-private partnership between
  - NIH
  - The Foundation for NIH
  - The private sector: Pfizer, Affymetrix, Perlegen, Abbott
  - The Broad Institute of Harvard/MIT
- Project announced February 8, 2006
- Applications (more than 30) received May 9, 2006
- Peer review: July 2006
- Technical Analysis Group (TAG) then looked at the highest scoring projects in much more detail
- GAIN Steering Committee made priority decisions Sept. 6, 2006
- FNIH Board approved choices October 5, 2006
- Projects announced October 10, 2006 at ASHG meeting
- Kickoff meeting November 29-30, 2006

Goals of the Meeting

- To survey the field of genome-wide association studies, and derive appropriate lessons for GAIN
- To share details of the study design and analysis plans for the six studies chosen for GAIN 1.0
- To clarify GAIN policies and procedures
- To resolve quality control and database issues
- To anticipate unique opportunities for cross-study analyses of genotypes and phenotypes
- To encourage the development of an open and scientifically stimulating scientific consortium for the GAIN project