Resource Summary Report

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Wellcome Trust Case Control Consortium

RRID:SCR_001973
Type: Tool

Proper Citation

Wellcome Trust Case Control Consortium (RRID:SCR_001973)

Resource Information

URL: https://www.wtccc.org.uk/

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Description: Consortium of 50 research groups across the UK to harness the power of newly-available genotyping technologies to improve our understanding of the aetiological basis of several major causes of global disease. The consortium has gathered genotype data for up to 500,000 sites of genome sequence variation (single nucleotide polymorphisms or SNPs) in samples ascertained for the disease phenotypes. Analysis of the genome-wide association data generated has lead to the identification of many SNPs and genes showing evidence of association with disease susceptibility, some of which will be followed up in future studies. In addition, the Consortium has gained important insights into the technical, analytical, methodological and biological aspects of genome-wide association analysis. The core of the study comprised an analysis of 2,000 samples from each of seven diseases (type 1 diabetes, type 2 diabetes, coronary heart disease, hypertension, bipolar disorder, rheumatoid arthritis and Crohn's disease). For each disease, the case samples have been ascertained from sites widely distributed across Great Britain, allowing us to obtain considerable efficiencies by comparing each of these case populations to a common set of 3,000 nationally-ascertained controls also from England, Scotland and Wales. These controls come from two sources: 1,500 are representative samples from the 1958 British Birth Cohort and 1,500 are blood donors recruited by the three national UK Blood Services. One of the questions that the WTCCC study has addressed relates to the relative merits of these alternative strategies for the generation of representative population cohorts. Genotyping for this main Case Control study was conducted by Affymetrix using the (commercial) Affymetrix 500K chip. As part of this study a total of 17,000 samples were typed for 500,000 SNPs. There are two additional components to the study. First, the WTCCC award is part-funding a study of host resistance to infectious diseases in African populations. The same approach has been used to type 2,000 cases of tuberculosis (TB) and 2,000 cases of malaria, as well as 2,000 shared controls. As well as addressing

diseases of major global significance, and extending WTCCC coverage into the area of infectious disease, the inclusion of samples of African origin has obvious benefits with respect to methodological aspects of genome-wide association analysis. Second, the WTCCC has, for four additional diseases (autoimmune thyroid disease, breast cancer, ankylosing spondylitis, multiple sclerosis), completed an analysis of 15,000 SNPs designed to represent a large proportion of the known non-synonymous coding SNPs across the genome. This analysis has been performed at the WTSI using a custom Infinium chip (Illumina). Data release The genotypic data of the control samples (1958 British Birth Cohort and UK Blood Service) and from seven diseases analyzed in the main study are now available to qualified researchers. Summary genotype statistics for these collections are available directly from the website. Access to the individual-level genotype data and summary genotype statistics is by application to the Consortium Data Access Committee (CDAC) and approval subject to a Data Access Agreement. WTCCC2: A further round of GWA studies were funded in April 2008. These include 15 WTCCC-collaborative studies and 12 independent studies be supported totaling approximately 120,000 samples. Many of the studies represent major international collaborative networks that have together assembled large sample collections. WTCCC2 will perform genome-wide association studies in 13 disease conditions: Ankylosing spondylitis, Barrett's oesophagus and oesophageal adenocarcinoma, glaucoma, ischaemic stroke, multiple sclerosis, pre-eclampsia, Parkinson's disease, psychosis endophenotypes, psoriasis, schizophrenia, ulcerative colitis and visceral leishmaniasis. WTCCC2 will also investigate the genetics of reading and mathematics abilities in children and the pharmacogenomics of statin response. Over 60,000 samples will be analyzed using either the Affymetrix v6.0 chip or the Illumina 660K chip. The WTCCC2 will also genotype 3,000 controls each from the 1958 British Birth cohort and the UK Blood Service control group, and the 6,000 controls will be genotyped on both the Affymetrix v6.0 and Illumina 1.2M chips. WTCCC3: The Wellcome Trust has provided support for a further round of GWA studies in January 2009. These include 5 WTCCC-collaborative studies to be carried out in WTCCC3 and 5 independent studies, across a range of diseases. Many of the studies represent major international collaborative networks that have together assembled large sample collections. WTCCC3 will perform genome-wide association studies in the following 4 disease conditions: primary biliary cirrhosis, anorexia nervosa, pre-eclampsia in UK subjects, and the interactions between donor and recipient DNA related to early and late renal transplant dysfunction. The WTCCC3 will also carry out a pilot in a study of the genetics of host control of HIV-1 infection. Over 40,000 samples will be analyzed using the Illumina 660K chip. The WTCCC3 will utilize the 6,000 control genotypes generated by the WTCCC2.

Abbreviations: WTCCC

Synonyms: Wellcome Trust Case-Control Consortium (WTCCC)

Resource Type: data or information resource

Defining Citation: PMID:17554300

Keywords: gene, genomic, genetics, microarray, genome-wide association study, snp, genome-wide association, blood, dna, genotype, variation, genome, sequence variant, copy

number variation, genetic variation, phenotype, disease

Related Condition: Bipolar disorder, Coronary artery disease, Crohn's disease, Rheumatoid arthritis, Type 1 diabetes, Type 2 diabetes, Hypertension, Control, Multiple sclerosis, Breast cancer, Ankylosing spondylitis, Autoimmune thyroid disease, Malaria, Tuberculosis, Inflammatory bowel disease, Barrett's esophagus, Esophageal adenocarcinoma, Glaucoma, Ischemic stroke, Pre-eclampsia, Parkinson's disease, Psychosis endophenotypes, Psoriasis, Schizophrenia, Ulcerative colitis, Visceral leishmaniasis, Primary biliary cirrhosis, Anorexia nervosa, Human immunodeficiency virus, Renal transplant dysfunction, Diabetes

Funding: Wellcome Trust ;
Bill and Melinda Gates Foundation ;
Wellcome Trust Sanger Institute; Hinxton; United Kingdom

Availability: Access to summary data and individual-level genotype data is available by application to the Wellcome Trust Case Control Consortium Data Access Committee. Access to data will be granted to qualified investigators for appropriate use.

Resource Name: Wellcome Trust Case Control Consortium

Resource ID: SCR_001973

Alternate IDs: nif-0000-10551

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250410T064807+0000

Ratings and Alerts

No rating or validation information has been found for Wellcome Trust Case Control Consortium.

No alerts have been found for Wellcome Trust Case Control Consortium.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 209 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

McGrail C, et al. (2025) Genetic Discovery and Risk Prediction for Type 1 Diabetes in Individuals Without High-Risk HLA-DR3/DR4 Haplotypes. Diabetes care, 48(2), 202.

Crouch DJM, et al. (2025) Bayesian Effect Size Ranking to Prioritise Genetic Risk Variants in Common Diseases for Follow-Up Studies. Genetic epidemiology, 49(1), e22608.

Wang JT, et al. (2024) FastBiCmrMLM: a fast and powerful compressed variance component mixed logistic model for big genomic case-control genome-wide association study. Briefings in bioinformatics, 25(4).

Metayer C, et al. (2024) Folate Metabolism and Risk of Childhood Acute Lymphoblastic Leukemia: A Genetic Pathway Analysis from the Childhood Cancer and Leukemia International Consortium. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 33(9), 1248.

Haque MA, et al. (2024) Genome-wide association study identifies genomic regions associated with key reproductive traits in Korean Hanwoo cows. BMC genomics, 25(1), 496.

Collins KE, et al. (2024) Donor genetic burden for cerebrovascular risk and kidney transplant outcome. Journal of nephrology, 37(6), 1643.

Chen X, et al. (2024) Classification of Schizophrenia, Bipolar Disorder and Major Depressive Disorder with Comorbid Traits and Deep Learning Algorithms. Research square.

Kozlowska J, et al. (2024) Unveiling new genetic insights in rheumatoid arthritis for drug discovery through Taxonomy3 analysis. Scientific reports, 14(1), 14153.

Hoffmann M, et al. (2024) Network medicine-based epistasis detection in complex diseases: ready for quantum computing. Nucleic acids research, 52(17), 10144.

McGrail C, et al. (2024) Genetic association and machine learning improves discovery and prediction of type 1 diabetes. medRxiv : the preprint server for health sciences.

Elgamal RM, et al. (2024) Circulating pancreatic enzyme levels are a causal biomarker of type 1 diabetes. medRxiv : the preprint server for health sciences.

Tang DY, et al. (2024) SEEI: spherical evolution with feedback mechanism for identifying epistatic interactions. BMC genomics, 25(1), 462.

Li Q, et al. (2024) An expression-directed linear mixed model discovering low-effect genetic variants. Genetics, 226(4).

Zhao Z, et al. (2024) Controlling for polygenic genetic confounding in epidemiologic association studies. bioRxiv : the preprint server for biology.

Hernangomez-Laderas A, et al. (2023) Sex bias in celiac disease: XWAS and monocyte eQTLs in women identify TMEM187 as a functional candidate gene. Biology of sex

differences, 14(1), 86.

McGrail C, et al. (2023) Genetic discovery and risk prediction for type 1 diabetes in individuals without high-risk HLA-DR3/DR4 haplotypes. medRxiv : the preprint server for health sciences.

Hoffmann M, et al. (2023) Network medicine-based epistasis detection in complex diseases: ready for quantum computing. medRxiv : the preprint server for health sciences.

Sergouniotis PI, et al. (2023) From genetic variation to precision medicine. Cambridge prisms. Precision medicine, 1, e7.

Jeon S, et al. (2023) Evaluating Genomic Polygenic Risk Scores for Childhood Acute Lymphoblastic Leukemia in Latinos. medRxiv : the preprint server for health sciences.

Lakiotaki K, et al. (2023) Automated machine learning for genome wide association studies. Bioinformatics (Oxford, England), 39(9).