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NIDDK IBD Genetics Consortium Repository
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Introduction
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The NIDDK IBD Genetics Consortium DNA and cell line repository was started in 2003. Its goal is to establish a large collection of samples and linked phenotype information, which will be of broad value both to the Consortium investigators and to the scientific community at large. Since it began, the Consortium has been prospectively recruiting a combination of cases, controls, and trios at six sites throughout North America. Phenotyping has been performed using a well-defined, standardized protocol, and lymphoblastoid cell lines have been established for each subject. The resulting DNA samples have already been utilized by the Consortium to complete various association studies, including genome-wide association studies using dense genotyping arrays.

When subjects are recruited, their samples are sent to Rutgers where lymphoblastoid cell lines are created; after these have been established, DNA samples for research are then available through Rutgers. Phenotype data for each subject are collected by the Consortium's Data Coordinating Center (DCC). This data product contains phenotype data for all subjects with DNA samples available as of November 2007 (n = 4,761).

Study Cohorts
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As noted above, the Consortium has recruited a combination of cases (affected with IBD), unrelated controls and trios (a small number of trios also contain one or more additional affected siblings). This data product contains data on 2,349 independent cases (i.e., at most one from each family), 833 unrelated controls, and 690 complete trios. Since recruitment is ongoing, and since this data product includes all subjects for which DNA is currently available, several partial trios are also included.

When possible, an affected subject's unaffected spouse or co-residential partner was recruited to serve as a control. The resulting pairing between case and control is recorded in the variable "spouse" in the phenotype file. Other controls were recruited from among a case's friends, from patients with

unrelated conditions, or from the community.

A detailed description of the inclusion/exclusion criteria may be found in the Consortium phenotyping manual, provided with this package. Note that although all sites are open to recruiting subjects from any racial/ethnic background, one site has focused especially on recruiting African-American subjects, while another has focused on recruiting subjects from Puerto Rico.

Contents

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This data product contains the following files:

- README.txt (this file)
- phenotyping-manual.pdf (phenotyping manual)
- phenotyping-forms.pdf (phenotyping forms)

- phenotype data
 - phenotypes.xpt (SAS XPORT format)
 - formats.xpf (SAS XPORT file containing formats for file above)
 - phenotypes.sas (SAS command file to generate formats)
 - phenotypes.txt (tab-delimited ASCII format)
 - phenotypes-codebook.txt (codebook)

- pedigree file
 - pedfile.xpt (SAS XPORT format)
 - pedfile.txt (tab-delimited ASCII format)
 - pedfile-codebook.txt (codebook)

- DNA sample file
 - dna-samples.xpt (SAS XPORT format)
 - dna-samples.txt (tab-delimited ASCII format)
 - dna-samples-codebook.txt (codebook)

The pedigree file indicates the familial relationships among subjects (control subjects are excluded from this file). The DNA sample file provides the linkage between the subject ID and the sample IDs used to identify the DNA samples which reside at Rutgers.

Relevant Publications

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[1] C. Abraham and J. H. Cho. Functional consequences of nod2 (card15) mutations. *Inflamm Bowel Dis*, 12(7):641-650, 2006. PMID: 16804402.
- [2] C. Abraham and J. H. Cho. Bugging of the intestinal mucosa. *N Engl J Med*, 357(7):708-710, 2007. PMID: 17699823.
- [3] J.-P. Achkar, T. Dassopoulos, M. S. Silverberg, J. A. Tuvlin, R. H. Duerr, S. R. Brant, K. Siminovitch, D. Reddy, L. W. Datta, T. M. Bayless, L. Zhang, M. M. Barmada, J. D. Rioux, A. H. Steinhart, R. S. McLeod, A. M. Griffiths, Z. Cohen, H. Yang, G. P. Bromfield, P. Schumm, S. B. Hanauer, J. H. Cho, and D. L. Nicolae. Phenotype-stratified genetic linkage study demonstrates that *ibd2* is an extensive ulcerative colitis locus. *Am J Gastroenterol*, 101(3):572-580, 2006. PMID: 16542294.
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- [7] T. Dassopoulos, G. C. Nguyen, A. Bitton, G. P. Bromfield, L. P. Schumm, Y. Wu, A. Elkadri, M. Regueiro, B. Siemanowski, E. A. Torres, F. J. Gregory, S. V. Kane, L. E. Harrell, D. Franchimont, J.-P. Achkar, A. Griffiths, S. R. Brant, J. D. Rioux, K. D. Taylor, R. H. Duerr, M. S. Silverberg, J. H. Cho, and A. H. Steinhart. Assessment of reliability and validity of *ibd* phenotyping within the national institutes of diabetes and digestive and kidney diseases (niddk) *ibd* genetics consortium (*ibdgc*). *Inflamm Bowel Dis*, 13(8):975-983, 2007. PMID: 17427244.
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- [10] R. H. Duerr. Genome-wide association studies herald a new era of rapid discoveries in inflammatory bowel disease research. *Gastroenterology*, 132(5):2045-2049, 2007. PMID: 17484895.
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