Dear Colleagues,

I am writing on behalf of a multi-IC planning group (Stephen Chanock, NCI; Katrina Gwinn-Hardy, NINDS; Thomas Lehner, NIMH; Christopher O'Donnell, NHLBI; James Ostell, NLM; and myself) to inform you of plans for the second multi-IC symposium on Application of Genomic Technologies to Population-Based Studies, on May 22-23, 2007, this year focusing on "Facilitating Collaboration in Genome-Wide Association Studies."

As you may remember, we conducted a similar symposium last June, which arose from conversations with many of you about approaches to promoting the application of genomic technologies, such as genotyping and sequencing, to large-scale population studies. Materials and recommendations from that symposium were posted on an internal NIH website, http://www.genome.gov/Pages/Extranets/PopulationGenomicsTraining/ . Considerable progress has been made in addressing those recommendations, as described at (http://www.genome.gov/Pages/Extranets/PopulationGenomicsTraining/summary.cfm) and in the attached PDF document. Undoubtedly this progress summary is incomplete, focusing as it does on efforts known primarily to a small group of us. Additional input and comments are eagerly sought-- we would like this site to become an NIH-wide resource for applying genomic technologies to population studies, and we'll need your help to make it as useful as possible.

For this year's symposium we will use a similar approach and format as last year, with an NIH-accessible website, a several-hour opening "primer" session, and a full day of panel discussions by representatives of various ICs with experience in genome-wide association studies. NHGRI will again host the symposium, which will be held on Tuesday afternoon, May 22 from about 2-5:30PM, and Wednesday, May 23 from about 8:30AM-5:30PM, at the North Bethesda Marriott Conference Center on Marinelli Road.

Building on last year's experience, we will try to accommodate a slightly larger number of attendees. Registration for each session will be open and will be on a first-come, first-served basis. Registration information will be available shortly and will also be provided on the symposium website.

The goal of the symposium, broadly defined, is to increase the productivity and efficiency of genome-wide association studies NIH-wide. The proposed objectives are:

1. To share early NIH-wide experience with GWA studies, including scientific and programmatic problems encountered and solutions employed

2. To identify approaches for facilitating collaboration across GWA studies for replication and follow-up studies (sequencing, function, etc)

3. To examine different models for data analysis and approaches for maximizing use of GWA data

Topics to be addressed in the May 22 "primer" session include:

1. Study design: initial and replication studies, power
2. Technologic issues in GWA and follow-up studies
3. Challenges in analysis: computing platforms, spurious associations
4. Dissemination and publication: what to publish, when and how
5. Data resources for GWA studies: caBIG, dbGaP, etc.

Five working groups drawn from across NIH will address the following topics during the May 23 full-day session:

1. Replication studies: What is the best approach for planning for replication studies (organized consortia, wide-open data access/sharing, built into initial study, other models)? Do these strategies differ by disease prevalence or anticipated effect size?

2. Cross-study analyses: How can we best facilitate cross-study/cross-phenotype GWA analyses, such as diabetes in stroke studies or depression in CVD studies?

3. Follow-up studies: How should one plan for follow-up studies (especially sequencing and functional studies) and what additional costs over what period should one anticipate?

4. Data sharing: What are the options for rapid data sharing (caBIG, dbGaP, individual websites) and the pros and cons of each?

5. Consent and approvals: What consent, IRB approvals, and community consultation are needed for broad data sharing as in caBIG and dbGaP?

The second day will be devoted primarily to discussion among all symposium participants, with only brief introductory panel presentations and reference to background materials as needed. Please let us know if you have suggestions for other topics that should be addressed in either the afternoon or full-day session.

The anticipated output of the symposium, in addition to a series of recommendations to the various ICs for issues to consider in designing, soliciting, and implementing these studies, is to increase the level of familiarity and understanding of GWA studies within NIH, and to develop actual collaborations within or across ICs for carrying out these studies.

We hope you'll reserve these dates on your calendars and that you'll join us on May 22-23 (as space permits, sorry...).

Teri Manolio for the multi-IC symposium planning group