Letters to the Editor

Expanded Publishing Model for Genetic Association Studies

To the Editors: While stressing the need to integrate epidemiology and biology for causal inference, new *CEBP* publication criteria will exclude the results of many genetic association studies (1). Clearly, editors must prioritize because journal pages are limited; at the same time, epidemiologists are able to measure thousands of genetic variants and potentially millions of gene-gene and gene-environment interactions. No single journal, or even the universe of existing journals, has the capacity to publish all worthy results. Selective publication will bias the accumulation of original data needed for research synthesis and knowledge integration.

We believe that research based on a complex disease model, in which the accumulation of many small effects may be as important as rare large effects, calls for an analogous publishing model. All results of well-conducted epidemiologic studies, not just those with the highest prior probability, largest effect size, or greatest statistical significance, should be made accessible to researchers in the field. Supplementing existing journals with alternative publication channels, such as open-access publishing on the Internet, can make this approach feasible. Special appeals, such as *CEBP* ''Null Results in Brief,'' should encourage researchers to publish ''null'' results based on sound epidemiologic study designs and analyses. In the long run, this approach will facilitate research synthesis and integration and support causal inference.

An expanded publishing model also honors *CEBP*'s traditional commitment to publishing completed studies regardless of the conclusions (2) while accommodating the results of ''broad investigations of the vast number of genes about which we know very little from the laboratory or epidemiology'' (3). Eliminating both the motive and the opportunity for post hoc inference based on selective reporting also has the potential to help replace ''data dredging'' with more constructive ''data mining,'' acknowledging the value of data-driven, hypothesis-generating research as well as traditional hypothesis testing.

For the last several years, these ideas have motivated the development and growth of the Human Genome Epidemiology Network, an open international collaboration committed to assessing the impact of human genome variation on population health (4). In addition to partnering with journals to publish systematic reviews, the Human Genome Epidemiology Network is currently developing guidance for meta-analysis of gene-disease associations and establishing a ''network of networks'' to lay groundwork for collaborative analyses (5). Expanded opportunities to publish results of creditable research will help build a more comprehensive knowledge based on human genes and disease.

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