STREGA: a ‘How-To’ guide for reporting genetic associations

Thomas J. Hudson · David N. Cooper

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This issue of *Human Genetics* contains recommendations for reporting genetic association studies (Little et al. 2009). These have been framed as a statement and checklist entitled STrengthening the REporting of Genetic Association Studies (STREGA). The STREGA statement was developed by a panel of experts including epidemiologists, geneticists, statisticians, clinician scientists as well as journal editors. Joint publication in seven key journals in the field has required input from a total of 12 peer-reviewers who made their own valuable contributions to the statement, and coordination between several journal editors and publishers. STREGA represents an extension of STROBE (STrengthening the REporting of OBservational Studies in Epidemiology), which was published by several journals in 2007 (von Elm et al. 2007), and contains a checklist with 22 basic items such as title and abstract, study size, statistical methods, limitations and funding. The STREGA panel formulated its recommendations as additions to 12 items in the STROBE checklist that are specifically relevant to genetic association studies, including laboratory methods related to genotyping and allele-calling, genotyping accuracy, haplotype modeling, population stratification, relatedness between subjects, and statistical adjustments to allow for multiple hypothesis testing.

The STREGA authors have succeeded in producing a quality tool to assist authors. Trainees and authors preparing their first manuscripts reporting association studies will benefit not only by perusing the checklist, but also by delving into the accompanying discussion. The rationale for each recommendation is clearly stated, and refers to a series of key publications that describe the underlying issues such as the sorts of biases that can often be inadvertently introduced in genetic association studies. Although one may criticize the use of checklists for reporting a wide range of studies that differ quite widely with respect to design, methods, disease applications, etc., this approach offers many benefits to readers interested in interpreting the results of the thousands of genetic association studies reported every year, many of which lead to quite different conclusions being drawn. Although contradictory interpretations of studies with different designs, phenotype definitions, and populations are not wholly unexpected, transparency in reporting of study methods and results will enable users to develop an enhanced appreciation of the reasons underlying conflicting reports.

The editors of *Human Genetics* are pleased to endorse the STREGA statement. Our Instructions for authors will be revised to include a recommendation that authors refer to the guidelines when they are preparing manuscripts for publication. The instructions to peer-reviewers will suggest that manuscripts reporting genetic associations should follow STREGA recommendations, such that decisions to publish such manuscripts will be based on the quality of the study report, in addition to novelty and scientific merit. While the STREGA recommendations are not meant to be rigidly applied, authors of articles which appear to be of scientific value and that are considered to be deserving of publication, may still be asked to revise and resubmit articles along with the STREGA checklist, if peer-reviewers are of the opinion that the manuscript is incomplete in some

T. J. Hudson (✉)
Ontario Institute for Cancer Research, MaRS Centre,
South Tower, 101 College Street, Suite 800, Toronto,
ON M5G 0A3, Canada
e-mail: tom.hudson@oicr.on.ca

D. N. Cooper
Institute of Medical Genetics, Cardiff University,
Heath Park, Cardiff CF14 4XN, UK
e-mail: cooperDN@cardiff.ac.uk

way. If manuscripts become too long in the process, some of the accompanying information may always be posted on the Internet as part of the Supplementary Material Online. Springer, the publisher of *Human Genetics*, is happy to make the STREGA article freely available on the *Human Genetics* website: <http://www.springer.com/biomed/human+genetics/journal/439>.

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