

Reviewer's report

Title: Understanding environmental causes of disease: what can we expect from new concepts and technologies?

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Reviewer: Martyn T Smith

Reviewer's report:

The authors have responded well to my earlier critique and the paper seems better in structure and content.

Several important points still need to be addressed.

1) p. 11, second para – I would quibble with the authors' definition and description of genomics. The authors say genomics is the study of all of the genes in an organism. No one else I know of defines it as such although definitions differ. The American heritage dictionary defines Genomics as "The study of all of the nucleotide sequences, including structural genes, regulatory sequences, and noncoding DNA segments, in the chromosomes of an organism," which seems similar to the authors' definition but is not limited to genes which are increasing hard to define. Other dictionaries have similar definitions. The US EPA, on the other hand, takes a much broader approach defining Genomics as "The study of all the genes of a cell, or tissue, at the DNA (genotype), mRNA (transcriptome), or protein (proteome) levels." The latter seems more a definition of –omics than genomics in my view.

It is important to note, however, that the investigation of the roles and functions of single genes is a primary focus of molecular biology and is a common topic of modern medical and biological research. Research on single genes does not fall into the definition of genomics unless the aim of this genetic, pathway, and functional information analysis is to elucidate its effect on, place in, and response to the entire genome's networks. Hence, genotyping of candidate genes is molecular biology and not genomics. I therefore disagree that genomics can be divided into 3 areas that includes genotyping (sequencing may be a better term), transcriptomics (why not proteomics as well?) and epigenomics (defined later by the authors on p.13).

2) P.11 last sentence of 2nd para- The authors use Hunter (2006) as a reference for the power of proteomics to detect ovarian cancer using serum profiling – I thought the point of this editorial was to show that this approach was flawed and the approach has now been largely abandoned.

3) P.11. last line – SELDT-TOF/MS is not used in metabolomics as far as I am aware. Just prior to that the authors use Hunters editorial to define metabolomics –this seems inappropriate.

4) P.12 – 2nd and 3rd para – The authors describe genotyping as an omic technology, which it is not if it focuses on single genes, and the example given in para 3 of studies in DNA repair genes is inappropriate if one wishes to claim this is a genomic application to environmental health. I suggest rewriting paras 2 and 3.

5) P.18 – Conclusions – The authors claim that “The new omics can be extremely useful in tracing the history of such insults and to reflect the cumulative effect of different exposures.” They then propose two caveats. However, no examples are provided that support this conclusion in the text and I doubt -omics as defined by the authors will ever be useful for this purpose. Adductomics may do so but the authors do not discuss this approach or the idea of an exposome (C. Wild, 2005). The authors should delete or rewrite this last paragraph so that it better reflects the abstract and the papers' content.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Declaration of competing interests:

I declare that I have no competing interests