Panel Testing for Breast Cancer Risk Assessment: is it just because we can rather than should?

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Since the identification of BRCA1 and BRCA2 a number of other genes have been reported to be associated with an increased risk of breast cancer. Many of these genes have now appeared on commercial massively parallel sequencing (MPS) panels and are increasingly used for assessing breast cancer risk in women who developed disease at unusually young ages. Apart from BRCA1 and BRCA2 where there is considerable evidence associated with disease risk as well as strategies to mitigate the effects of mutation carriage there is little if any information about the consequence mutations in the more recently identified breast cancer susceptibility genes. This includes knowledge about the histopathology conferred by the loss of expression of a particular gene, the influence of environmental factors on disease risk as well as the most effective treatment strategies for disease prevention or disease treatment. For many of the genes listed on commercial panels knowledge about disease frequency in affected populations compared to control populations is lacking thereby undermining the veracity of breast cancer susceptibility claims.

To help address the shortfall in information about some of the more recently identified genetic risk factors to breast cancer we undertook a study of 2000 cases and 2000 controls to estimate the prevalence of mutations in a panel of genes that are commonly included in commercial testing. The results reveal that MPS panel testing must continue under a research setting so that more information can be gathered to understand what is meant by the term “genetic predisposition” to breast cancer for a large proportion of genes that are currently under scrutiny. At present only four genes can be used unequivocally in a diagnostic setting for the assessment of genetic risk of disease in most countries.