Guest Editorial

Diagnostic Array Comparative Genomic Hybridization

Is It Ready for Prime Time?

In this issue of *The Journal of Molecular Diagnostics*, we feature two articles that offer different perspectives on an emerging field of diagnostic technology. Comparative genomic hybridization (CGH) allows a simultaneous assessment of copy number across the whole genome. It involves the competitive hybridization of a reference and sample of interest to an immobilized target sequence. Imbalances caused by gene deletion or amplification will lead to fluorescently detectable signals on the array. This information in turn can be used to map regions of abnormality at a level of distinction that surpasses conventional karyotyping. Although metaphase chromosomes were the initial targets used in array CGH,¹ recent advances in array technologies use oligonucleotides, single-nucleotide polymorphisms, cDNAs, and bacterial artificial chromosomes, and offer the potential for higher resolution analysis.

Thus far, array CGH has been used extensively in research but is a relative newcomer to the diagnostic arena. In the two articles that follow, Bejjani and Shaffer² and Veltman and de Vries³ present two very different visions of how this technology may be used in the diagnostic setting. Bejjani and Shaffer have chosen to take a targeted approach, whereas Veltman and de Vries prefer whole-genome coverage. It remains to be seen which of these approaches will become more widely adopted in the clinical laboratory. A number of factors are likely to influence the choice of individual centers, including the cost relative to the incremental value gained by a broader coverage. Complicating factors such as copy number polymorphisms in normal individuals have only been described recently.^{4,5} Progress in our understanding of how wide the degree of variation is between individuals may also play a role in the evolution of array CGH.

Development of expression array analysis has preceded array CGH in terms of clinical uptake. Here, similar discussions occur regarding the utility and practicality of whole-genome expression characterization or the use of

smaller panels of significantly altered genes. Furthermore, expression of genes identified by array analysis as having prognostic or predictive value may be incorporated into even more targeted polymerase chain-reaction or immunohistochemical tests.⁶

We are at an exciting stage in the development of diagnostic array CGH. Increasing large-scale studies using this technology may ultimately demonstrate whether one approach, broad versus targeted analysis, is superior for the clinical laboratory. The discussion will continue as clinical laboratories evaluate the utility and potential of this application. However, at the outset one thing seems clear: diagnostic array CGH is likely to have broad and far-reaching implications for the diagnostic community.

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