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Microarray mix and match

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How valid is it to compare microarray data from different platforms and different laboratories? A recent study that takes a detailed look at this issue concludes that although inconsistencies can arise, steps can be taken to minimize them. The study also lays the ground for ongoing comparisons between platforms.

Using samples from the same two mouse tissues in each case, Kuo and colleagues assessed data from 10 microarray platforms. These included commercially available and 'home-made', one-dye and two-dye, and oligo and cDNA platforms.

The first comparison looked at five separate analyses of a single sample using the same platform. There was generally good consistency among replicates, although this was slightly lower for the home-made

platforms. Correcting for the quality of individual spots increased the consistency of results across all set-ups.

Next, the authors compared results across platforms and found much greater variability. However, the discrepancies were reduced by more careful matching of probes between platforms. Previous comparisons have matched probes according to their correspondence with the same gene. But Kuo *et al.* found that matching probes to the same exon resulted in much greater consistency. Using this approach, good consistency was seen among 8 of the 10 platforms. Again, spot filtering improved consistency in all cases.

A third comparison, using 3 of the 10 platforms, looked at the effects of doing the same experiment in different laboratories. Much less variability was seen than in the intra-platform comparison, suggesting that microarray performance is more or less equivalent in the hands of different groups.

Finally, Kuo *et al.* assessed how useful widely applied quantitative RT-PCR methods are for validating microarray results. Although quantitative RT-PCR results were generally consistent with microarray data, the correlation was far less reliable for genes that are expressed at low levels.

As well as pointing out where inconsistencies between existing platforms arise, this study provides a framework for future comparisons. By setting aside a plentiful supply of the biological samples they used, the authors aim to assess new gene-expression technologies as they emerge.

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ORIGINAL RESEARCH PAPER Kuo, W. P. *et al.* Sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. *Nature Biotechnol.* 2 July 2006 (doi:10.1038/nbt1217)
FURTHER READING Hoheisel, J. D. Microarray technology: beyond transcript profiling and genotype analysis. *Nature Rev. Genet.* 7, 200–210 (2006)