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Balanced amplification

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Experimental amplification of genomic material for analysis can introduce quantitative changes that make direct comparisons problematic. In an Advanced Online Publication in Nature Biotechnology, Makrigiorgos *et al.* describe a method that they call 'balanced PCR', for faithful amplification of two genomes (*Nature Biotechnology*, 5 August 2002, doi:10.1038/nbt724). The technique uses oligonucleotides that contain both common and unique DNA sequences to 'tag' each genomic DNA sample. The distinct genome samples are then pooled together and amplified simultaneously by PCR using the common DNA tag sequence. The sample material can be separated using the unique individual genomic tags. Makrigiorgos *et al.* validated this approach in a number of experimental systems and used microarray hybridization to follow the effects of amplification procedures. This technique will be useful for analysis when material is limiting, for example following laser-capture microdissection or for pre-implantation diagnosis.

References

1. Genetic analysis using genomic representations.

2. *Nature Biotechnology*, [http://www.nature.com/nbt/]