MICROARRAY ANALYSIS DETECTING SMALL CHANGES IN GENE EXPRESSION SHOWS INVOLVEMENT OF BONE REMODELING IN OSTEOARTHRITIS

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Differences in gene expression between bone from osteoarthritic (OA), normal (CTL) and osteoporotic (OP) individuals were studied in bone samples from 40 matched pairs of patients using competitive hybrdization to 19K oligonucleotide microarrays printed on glass slides. All analyses were performed in R using *SPOT* for image processing and *limma* for normalization and linear models. The data were characterised by small expression ratios and duplicate scans, done at different PMT voltage, were used to improve identification of regulated genes. 1.2 fold changes on arrays were reliably identified and confirmed by RT-PCR as 2 fold or more. A number of genes involved in the Wnt signalling pathway, known to be involved in bone remodelling and altered in OP, were identified as differentially expressed in OA bone. A subset of Wnt pathway genes were differentially expressed between male and female OA compared to CTL bone samples. These findings indicate the importance of altered bone remodelling in the pathogenesis of OA. Ability to identify key genes with small fold changes was crucial.