Prediction of treatment response in rheumatoid arthritis patients using genome-wide SNP data.

Although a number of treatments are available for Rheumatoid Arthritis (RA), they do not work well for a substantial proportion of patients. Therefore, we would like to predict in advance the response to different treatments. We are analysing patient's inherited genetic data for single nucleotide polymorphisms (SNPs), these are a variation of a single base pair in DNA e.g. A to C, to see if they correlate with drug response. We are using a variety of statistical methods to see if they can predict treatment response, as measured by change in three different clinical markers (C-reactive protein, swollen joint count in 28 joints and erythrocyte sedimentation rate) over 3-6 months after starting treatment. We have analysed the data from patients receiving two different treatments: methotrexate, which is the first choice of treatment for RA, and tumour necrosis factor α inhibitors, which are usually prescribed to patients who do not benefit from previous treatments. So far, we have found that, using genetic data alone, we cannot predict the treatment response reliably enough for clinical decision-making. However, we can expect to be able to predict the treatment response better if we could analyse data from a larger number of patients. In addition, investigating biological markers of treatment response (such as gene expression or DNA methylation) rather than clinical measures might provide better insight into prediction of treatment response.