A202 ANTI-TNF-α THERAPY MONITORING IN CHRONIC RHEUMATIC DISEASES BY CYTOMETRIC PROFILING OF PERIPHERAL BLOOD CELLS

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Ankylosing spondylitis (AS) is a chronic inflammatory disorder mainly affecting the axial skeleton and belongs to a group of rheumatic diseases known as spondyloarthritides. Anti-tumour necrosis factor (TNF)-α (tumour necrosis factor) biologicals, which aim to block the disease-associated proinflammatory activity of this cytokine, have been successfully applied for treatment of rheumatoid arthritis (RA) and AS as well. Unfortunately, only a subgroup of around 60% of patients is successfully responding to this treatment and up to now, there are no useful biomarkers available for predicting a beneficial clinical response to the cost-intensive TNF-α therapies. The aim of the present study was to monitor treatment of AS patients over time with

a multiparametric approach, called cytometric profiling, which allows immunoscoping of hundreds of immunophenotypic parameters at the single cell level. Fifty different monoclonal antibodies were combined to 10 different staining cocktails, which allowed the detection of all major leucocyte populations and their activation state in a few millitres of peripheral blood. Protocols applied include seven colour stainings that will allow the detection of up to 12 parameters. This strategy combines the generation of hypothesis-based and hypothesis-generating knowledge. The huge amount of data generated per measurement made it necessary to develop appropriate bioinformatic solutions for data storage, data normalisation and retrieval of differentially expressed parameters.

Here the authors present first preliminary data generated in a cohort of 10 AS patients 4, 8 and 12 weeks after starting treatment. Patterns of immunophenotypic parameters could be determined by bioinformatic tools originally applied to array-based transcriptome studies. The authors approach revealed cytometric signatures that indicate a successful treatment of patients. Neutrophils, monocytes and NK cells could identified as cellular sensitisers responding to TNF-α blockade. Altogether, this study demonstrates the value of our cytometric profiling approach to reveal patterns of parameters that generally possess higher predictive and diagnostic power than solitary ones. Moreover, this approach will help to disclose hitherto unknown disease-associated parameters, which may be helpful to identify new pathophysiology- and therapy-related mechanisms.