IRR IRF
Institute of Rheumatology Research
Institut für Rheumaforschung
Institut pour la recherche en rhumatologie

Epigenetic Inheritance in Ankylosing Spondylitis

Project details

Research Leader	PD Dr. Dr. med. Caroline Ospelt, Center of Experimental Rheumatology, Department of Rheumatology, University Hospital of Zurich
Participating Institutes	Department of Rheumatology, University Hospital of Zurich; Clinic of Reproductive Medicine, University Hospital of Zurich
Relevant conditions	ankylosing spondylitis
Project duration	1 year
Total project cost	140'000.-

What are the aims of this research?

The aim of our research is to find out whether patients with ankylosing spondylitis (AS) have differences in the epigenetic profile of their sperm cells compared to healthy individuals.

Studies identified several genetic risk loci which are associated with the risk to develop AS. However, these genetic risk loci can only explain a minor part of the heritability of AS, which is estimated to be >95%. This strongly suggests that other mechanisms, for instance epigenetics, mediate the heritability of AS.

Epigenetic modifications of the genome like DNA methylation and histone modifications do not alter the DNA sequence, as occurs with mutations, but they do determine whether a gene in a cell is expressed (transcribed) or whether it is silenced. Recent studies in animals and in humans suggest that pathologic conditions e.g. obesity or liver fibrosis can induce epigenetic changes in the male germline (sperm), which influence the susceptibility of the offspring to develop disease.

Why is this research important?

The results of this study will clarify the question of heritability of AS and will also be suggestive for other chronic inflammatory diseases with a high familial risk.

The results of the current study will determine whether patients with AS have an altered epigenetic profile in their germline cells or not. If we find differences in DNA methylation and/or histone modifications in patients versus controls, this indicates that indeed epigenetics might play a role in the heritability of AS and further studies can be initiated to determine how these changes are induced and whether they indeed influence the risk to develop AS in the offspring. If we don't find any significant changes we can exclude DNA methylation and histone modifications as mediators of heritability in AS.

How will the findings benefit patients?

It is easy to understand that the increased familial risk is a matter of concern for patients, since they want to know, whether they will give the disease to their children or not. Even though with the current study we will not be able to give an answer to this specific question to the patients yet, our results will significantly contribute to understand the mechanisms that lie behind the strong heritability of AS and will add another significant piece of data that will one day hopefully help to solve the riddle of why and how AS is inherited.