# Basic science, clinical abstract awardees honoured

At this evening's Networking Platform event, first authors from six basic science and six clinical research abstracts will each receive awards for achieving the highest overall scoring from an expert review panel. Each of the winners below will receive 1,000 euros.

## Basic science abstract winners

**Anne Musters, MD,** of the Amsterdam Rheumatology and Immunology Center/Academic Medical Center is receiving an award for her paper on the predictive role of dominant B-cell receptor (BCR) clones in the peripheral blood of individuals at risk for rheumatoid arthritis (abstract OP0204). She and her associates sought to validate that BCR clones in the peripheral blood of patients with specific autoantibodies and arthralgias and no clinically evident synovial inflammation predicted the imminent onset of clinical symptoms of RA. They found that the number of dominant BCR clones was increased in RA-risk individuals who developed arthritis within 3 years, compared with RA-risk individuals who did not. No individuals who were BCR-clone negative developed RA during that time period. They also found that a higher number of dominant BCR clones correlated with higher risk of arthritis, and that association was highly significant.


Dr. Musters

**Mohammad Hussein Al-Mossawi, BMBCh, DPhil,** of the Nuffield department of orthopaedics, rheumatology, and musculoskeletal sciences, University of Oxford (UK), is receiving a prize for leading a study on the genotypic effects of interleukin-7 receptor (IL-7R) polymorphism on monocyte protein surface expression and soluble IL-7R release (abstract OP0286). The study results indicated that monocytes upregulate IL-7R expression and soluble IL-7R secretion after lipopolysaccharide treatment in a manner that is functional and genotype and TNF-alpha dependent. They also showed that spondyloarthritis synovial monocytes express IL-7R, suggesting preactivation. The investigators noted that "these data draw attention to an unappreciated key myeloid role for ankylosing spondylitis risk variants at IL-7R."


Dr. Al-Mossawi

**Elena López-Isac, PhD,** of the Institute of Parasitology and Biomedicine López-Neyra, Spanish National Research Council, Granada, Spain, is being honoured for leading a study on the genetic component of systemic sclerosis (abstract OP0282). She and her associates performed a large meta–genome-wide association study of 26,679 genotyped individuals of European ancestry. Dr. López-Isac and her colleagues found 23 loci that reached the genome-wide significance level, with 12 of them being new associations that involved novel pathways in the pathophysiology of the disease, and confirmed several risk loci that had been previously reported.


Dr. López-Isac

**Marialbert Acosta-Herrera, PhD,** of the Institute of Parasitology and Biomedicine López-Neyra, Spanish National Research Council, Granada, Spain, is receiving a prize for her study to identify shared genetic etiologies among systemic autoimmune diseases (abstract OP0283). She and her associates performed a large-scale meta-analysis of four autoimmune diseases in individuals of European descent: rheumatoid arthritis, systemic lupus erythematosus, systemic sclerosis, and myositis. They identified 27 genome-wide significant independent loci with at least two diseases leading the association, including five unreported shared risk loci: NAB1, KPNA4-ARL14, DGQK, LIMK1, and PRR12.


Dr. Acosta-Herrera

**Sam R. Finlay,** is a PhD student at the Institute of Infection, Immunity and Inflammation, Glasgow, UK, and is being honoured for his paper on the role of human synovial tissue macrophages in the remission of rheumatoid arthritis (abstract OP0269). He and his colleagues studied the subpopulation of CD206+MerTK+ synovial tissue macrophages that predominates in RA patients in sustained remission. They hypothesised that activation of CD206+MerTK+ human synovial tissue macrophages contributes to the resolution of inflammation and found that CD206+MerTK+ macrophages, which predominate in RA patients in remission, have a Gas6-mediated negative feedback mechanism that limits production of tumour necrosis factor.


Mr. Finlay

**Louise M. Topping**, a PhD student at the Centre for Biochemical Pharmacology, William Harvey Research Institute, Barts, and the London School of Medicine and Dentistry, Queen Mary University of London, is receiving an award for her study on the therapeutic potential of anti-ROS-CII 3–loaded microvesicles in an in vivo model of arthritis (abstract OP0260). Anti-ROS-CII 3 is a single-chain variable fragment antibody specific to collagen II modified by reactive oxygen species. The investigators first determined that anti-ROS-CII 3–loaded microvesicles localised specifically in the arthritic joint and then determined that they were able to deliver anti-inflammatory therapeutics. They found through in vivo studies that using anti-ROS-CII fused to anti-inflammatory therapeutics led to a significant reduction in knee swelling.


Ms. Topping

## Clinical abstract award winners

**Cecilie Heegaard Brahe, MD,** of the Copenhagen Center for Arthritis Research and the Center for Rheumatology and Spine Diseases, Rigshospitalet, Glostrup, Denmark, is receiving a prize for her study on dose tapering and discontinuation of biologic disease-modifying antirheumatic drugs (bDMARDs) (abstract OP0038). She and her colleagues studied a cohort of patients with rheumatoid arthritis in sustained remission whose bDMARDs were tapered according to a set clinical guideline and stopped if the tapering was successful. Negative IgM-rheumatoid factor predicted successful discontinuation. A maximum of one bDMARD, male gender, and low baseline MRI combined inflammation and combined damage scores were independent predictors for successful tapering.


Dr. Heegaard Brahe

**Ippei Miyagawa, MD, PhD,** of the University of Occupational and Environmental Health, Kitakyushu, Japan, is being honoured for his paper on the selection of optimal biologic DMARDs, based on characteristic lymphocyte phenotypes, for treating psoriatic arthritis (abstract OP0321). He and his associates evaluated the therapeutic response of patients in whom the optimal bDMARD was strategically chosen based on the results of peripheral lymphocyte analysis and compared it with that of patients in whom the standard biologic product was used based on the 2011 and 2015 EULAR recommendations. At 6 months of therapy, the rate of low disease activity achievement was significantly higher in the strategic bDMARD treatment group.


Dr. Miyagawa

**Guoqi Cai,** a PhD candidate at Menzies Institute for Medical Research, University of Tasmania, Hobart, Australia, is receiving an

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# Machine learning predicts RA radiologic damage

For the first time, researchers have applied a machine-learning algorithm to develop a prediction model of radiological damage in RA patients based on genetic data. The result of this Spanish study will be presented on Friday afternoon at the Clinical Science Session, "Big Data for Musculoskeletal Research."

"Rheumatoid arthritis is a condition that can be associated with increased disability and premature mortality," said Dr. Luis Rodriguez-Rodriguez of the Hospital Clínico San Carlos in Madrid. "In the past few years, several factors have been associated with disease progress, but there are still no predictive models that have been implemented for routine use in clinical practice."

The purpose of the study was to develop and create a predictive RA prognosis model that could help health professionals determine the course of the disease in a particular patient, allowing for the creation of an optimal plan for his/her treatment. "We used radiological damage [Sharp/van der Heijde score] as a surrogate marker for disease severity, using demographic, clinical, and genetic variables as predictors," Dr. Rodriguez-Rodriguez said. "The genetic data [polymorphisms] were obtained from the ImmunoChip platform. We then employed machine-learning algorithms to develop the model."

Dr. Rodriguez-Rodriguez

The study was a cooperative effort and included patients from three rheumatology clinics in Madrid and one in Santander, Spain.

The model was created using patient data from three of the clinics and externally validated using data from the fourth. "We were able to identify several sets of variables able to predict the radiological damage with a low mean error," which was around 3.5 points of the Sharp/van der Heijde score, Dr. Rodriguez-Rodriguez stated. "Then we tested those sets of variables in the patients from the fourth clinic. A moderate increase in the mean error was observed [around 5.5 points of the Sharp/van der Heijde score]."

It is significant that this is the first time a RA patient prediction model has analysed the genetic basis of outcomes using a machine-learning algorithm. "We have not only developed a tool that may assist healthcare professionals in the management of RA patients," Dr. Rodriguez-Rodriguez explained, "but have also identified a set of polymorphisms that may play a role in the radiological damage of this condition and point to genes that could become targets of new rheumatoid arthritis management drugs."

He noted that his group is "optimistic about being able to implement this model in clinical practice, but still face a long road ahead as we need to validate it in different populations."

The presentation will be a draw for rheumatologists, data scientists, basic scientists, and those with an interest in the field, according to Dr. Rodriguez-Rodriguez, who added that "attendees will gain knowledge about practical use of these techniques, which will hopefully provide them with ideas and inspiration for their own projects. They also might be interested in working with our group, expanding our collaborative network."

Dr. Rodriguez-Rodriquez and his 10 coauthors represent Hospital Clínico San Carlos (Madrid), Hospital de la Princesa e IIS-IP (Madrid), Hospital de La Paz (Madrid), Hospital Marqués de Valdecilla (Santander), Hospital La Fe (Valencia, Spain), Instituto López-Neyra (Granada, Spain), and CIMNE (Madrid).

Dr. Rodriguez-Rodriguez has no financial disclosures of interest.

**CLINICAL SCIENCE SESSION**

Big Data for Musculoskeletal Research

Friday 15:30 – 17:00
Hall 7.2

# Shared genetic variants reported across four autoimmune diseases

Genome-wide association studies have emerged as a powerful tool to identify genetic variants associated with single diseases. When they are used across diseases, in a meta-analysis, these studies can reveal shared pathophysiological mechanisms, and in turn suggest novel therapeutic approaches.

On Friday morning, Marialbert Acosta-Herrera, PhD, of the Institute of Parasitology and Biomedicine Lopez-Neyra, Granada, Spain, will present on a genome-wide meta-analysis in four systemic autoimmune diseases: systemic sclerosis, systemic lupus erythematosus, idiopathic inflammatory myopathies, and rheumatoid arthritis. Dr. Acosta-Herrera's abstract received a basic science award from EULAR.

Dr. Acosta-Herrera said in an interview that her research group chose these four diseases because they are rheumatologic conditions with connective tissue involvement, share some genetic loci that had been previously reported, and have high comorbidity and high rates of familial clustering.

"Our main goal was to analyse simultaneously, and in a systematic fashion, the shared genetic variants associated with disease susceptibility," she said, noting that this was the first time such an analysis was performed for systemic seropositive musculoskeletal immune-mediated inflammatory diseases as a group.

Dr. Acosta-Herrera and her colleagues assessed about 4,600 cases of rheumatoid arthritis and about 3,400 controls; 3,200 cases of systemic lupus erythematosus and 8,800 controls; more than 2,200 cases of systemic sclerosis and more than 4,400 controls; and about 1,600 cases of myositis and 3,200 controls. They looked at about 6.5 million single-nucleotide polymorphisms across the diseases and identified 26 significant independent loci shared among at least two of them. The cases used in the study derived from populations of European descent.

The loci revealed in the meta-analysis mapped in transcription factor binding sites, promoter and enhancer histone marks, and DNase cleavage hotspots in immune cell lines, as well as in epithelial and epidermal cell lines, Dr. Acosta-Herrera said.

Dr. Acosta-Herrera

Among the 26 shared loci identified in the study, 10 of the associations are new for systemic sclerosis, 8 for lupus, 8 for RA, and 20 for myositis.

While most of the signals revealed in the study map to known susceptibility loci in autoimmune disease, Dr. Acosta-Herrera said five had never been reported before for any of the analysed diseases.

"The shared risk variants and their likely target genes are functionally enriched in immune cells like B and T lymphocytes, T-helper cells, T CD8+, natural killer, and monocytes, showing the most relevant cells among these conditions," she said.

Dr. Acosta-Herrera said the findings have implications for the potential use of some rheumatoid arthritis therapies in the other three diseases, for which few or no therapies exist.

"In the case of sclerosis, lupus, and myositis, we are talking about relatively rare diseases," she said. "One of the main advantages of analysing these data with rheumatoid arthritis is that drug repositioning among them could be possible, allowing therapies for RA to be considered in these diseases."

In addition, "being able to identify new genes associated with disease susceptibility may eventually lead to better patient stratification based on molecular and genetic information, not just clinical manifestations," she said

The European Union, and the governments of Spain and Andalusia, Spain, helped fund Dr. Acosta-Herrera's research.

**ABSTRACT SESSION**

From gene to function

Friday 10:15 – 11:45
Emerald