Background: Juvenile Idiopathic Arthritis (JIA) is a chronic pediatric inflammatory disease that shows many differences compared to adult-onset arthritis. The different clinical manifestations, the assessment and the management of JIA is the reason that the transition from childhood to adulthood is an important multidimensional process that emphasizes a lot of aspects.

Objectives: To describe the long-term outcome of JIA.

Methods: Five-hundred and twenty patients affected by JIA and referred to a transition care rheumatology tertiary centre were considered between 1999 and 2019. The outcome assessment included remission, disease duration, medications, number of prosthesis implantation, pregnancies, mortality and social integration (employment status and educational level).

Results: A hundred and thirty-six (28%) males and 382 (73%) females were included; 157 (30%) patients were lost to follow up. The mean age of the patients was 27 (18-57) years, with a mean age at onset of 8 years and an average disease duration of 19 years. Subtypes of JIA at disease onset included 252 (48%) oligoarthritis, 134 (26%) polyarthritis, 64 (12%) systemic arthritis, 22 (4%) psoriatic arthritis, 43 (8%) enthesitis related arthritis and 1 (0.1%) undifferentiated arthritis. Ninety-three (18%) patients suffered of uveitis. Ninety-five implant prosthesis and 16 arthrodesis were recorded. At follow up 198 (38%) patients were on remission of which 107 (20%) off medication. Among the 322 patients still on medication, 84 (16%) were under treatment with oral steroids, 226 (43%) with SDMARDs and 249 (40%) with bDMARDs. Five deaths (1%) occurred in this cohort. Two hundred and thirty-five subjects were still followed, not only because of the continuation of the study, but also because of the transition to adulthood, which is a crucial period for these patients. The transition age was considered after the age of 16 years old. The key word for the management of this cohort was the multidisciplinary approach towards each patient, with the collaboration of other specialists (ophthalmologist, orthopedic, dermatologist, gastroenterologist, obstetric and psychologist).

Conclusion: In the era of biologic therapy the long-term outcome of JIA underwent an outstanding improvement regarding a lot of variables. Two hundred and thirty-two patients were still followed, only not because of the continuation of the biological therapy, but also for a multidisciplinary care even during remission. JIA often persists over the adulthood, therefore the long term follow-up and care of these patients needs to be conducted by a rheumatologist expertized in JIA in collaboration with other specialists.

Disclosure of Interests: None declared

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A PILOT PROTEOMIC ANALYSIS OF PLASMA BIOMARKERS IN IGA VASCULITIS

S. Demir1, M. Sardan1, I. Yet1, E. Sag1, V. Bilginer1, O. Celikbicak1, S. Ozcn1.

1Hacettepe University Faculty of Medicine, Department of Pediatric Rheumatology, Ankara, Turkey; 2Hacettepe University Faculty of Medicine, Department of Bioinformatics, Ankara, Turkey; 3Hacettepe University Faculty of Medicine, Department of Chemistry, Ankara, Turkey.

Background: Iga vasculitis/ Henoch Schönlein Purpura (IgAV/HSP) is the most common vasculitis of childhood, characterized by the IgA1 immune deposits in the small vessels. Although it is very common, the understanding of its molecular pathogenesis is still very limited.

Objectives: We aimed to analyse plasma proteomes of IgAV/HSP patients using nano liquid chromatography – tandem mass spectrometry (nLC-MS/MS) to investigate the disease pathogenesis.

Methods: IgAV/HSP was diagnosed according to the Ankara criteria in 2008 (1). Five active IgAV/HSP patients and two age and gender-matched healthy controls were enrolled in this pilot study. Serum samples from subjects were collected on the same day of IgAV/HSP diagnosis and before steroid or other immunosuppressive treatment initiated. Sample preparation was carried out using PreOomics IST Kit. We investigated the alteration of serum proteome using the nano LC-MS/MS approach. Bruker raw files were analyzed using the proteomics software Max Quant (1.6.7.0). The human reference proteome set from UniProt was used to identify proteins. Proteomic data were analyzed with PerSeus 1.6.7.0.

Results: The data file includes peptide and protein identification, accession numbers, protein and gene names, sequence coverage and label free quantification (LFQ) values of each sample. 345 proteins were reported per sample. Identifications from the reverse decay database, identified by site only and known contaminants were excluded. Data were log transformed. Two sample T-test was performed between groups. We identified 23 significantly different expressed proteins (Table 1). Mainly the differentially expressed proteins were in the Ig and complement pathway, innate immune inflammatory,