CLINICAL CHARACTERISTICS AND GENETIC EXPRESSION IN A COHORT OF PATIENTS WITH FAMILY MEDITERRANEAN FEVER

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Background: Familial Mediterranean fever (FMF) is the most frequent mono genetic periodic fever syndrome and is characterized by recurrent episodes of fever, serositis, arthritis, dental manifestations and long-term renal complications (amyloidosis is the most important complication). The genetic mutation of the disease is found in the MEFV gene located on the short arm of chromosome 16 and is inherited in an autosomal recessive manner. It affects the populations of the Mediterranean basin and is diagnosed according to the clinical evaluation.

Objectives: To describe the clinical characteristics of a cohort of patients with FMF and to study the different genetic mutations located in the MEFV gene.

Methods: Retrospective descriptive study of patients treated in our Hospital (2008-2018), with FMF diagnosis and MEFV gene mutation. The data was obtained through the review of medical records.

Results: We included 52 patients (29 men), mean age 41 years. The following mutation have been identified in alleles of the MEFV gene: Non-pathogenic in 34 patients (65%) (p202Q 73%, p148Q 17%, p.319K 6% and p339F 3%). Pathogenic in 18 patients (34%) (p.202Q 22%, eg 148 27%, pr.653H 5%, pn.694V 16%, pr.159T 5%). In 17% of the patients family history was documented. Elevated acute phase reactants in 41 patients (79%) (C Reactive Protein 75%, Globular sedimentation rate 65%). Echocardiography was performed in 14 patients, with diagnosis of pericardial effusion in 6 of them. Two patients develop renal amyloidosis, one of them (homozygous for the mutation 148Q) died due to this complication. 54% of patients use colchicine as initial treatment, achieving 50% good response with control of symptoms. 19% undergo treatment with glucocorticoids (0.5-1 mg/kg/day), needing to add methotrexate in 1 patient and hydroxychloroquine in another. Four also use biological therapy (1 tocilizumab, 2 anakinra, 1 canakinumab) and 2 thalidomide to control skin manifestations.

Conclusion: The genetic study confirms the diagnosis of FMF, allowing it to be differentiated from other SAIs. It also has prognostic value, depending on the mutation detected and if it affects one or both alleles. In our series, the most prevalent symptoms in patients with pathogenic mutations were fever, abdominal pain and arthralgias.

Disclosure of Interests: None declared

GENETIC EXPRESSION AND CLINICAL MANIFESTATIONS IN A COHORT OF PATIENTS WITH AUTOINFLAMMATORY SYNDROME

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Background: The autoinflammatory syndromes (SAI) encompass a set of diseases in which there is an alteration of the innate immune response, contrary to what occurs in autoimmune diseases, in which the origin is due to pathological changes in the adaptive immune response. These diseases have common symptoms such as fever, skin, joint and lung involvement, among others, so they can be difficult to diagnose and classify.

Objectives: To describe the clinical and genetic characteristics of a cohort of patients with autoinflammatory syndromes (SAI).

Methods: Retrospective descriptive study of patients seen in our Hospital (2008-2018), with a diagnosis of SAI. The data was obtained through the review of medical records.

We have included data from patients who present a positive genetic study, both for described and pathogenic mutations, as well as nonpathogenic mutations, but which present a clinical picture according to this pathology.

The most frequent clinical manifestations: Arthritis 77.5%, followed by high fever (> 39) 73.8%, myalgias 72.5%, abdominal pain 56.3%, exanthema 47.5%, arthritis 35%, pericarditis 28.8%, headache 21.3%, pharyngitis 21.3% and canker sores 20%. The onset of the picture was a fever in 59 patients (73.8%) accompanied by cutaneous manifestations in 51.2% of the cases, with the rest of the symptoms being variable depending on the mutation studied.

The most affected joints were: Metacarpophalangeal in 18 patients (22.8%), ankles in 15 patients (18.8%), proximal interphalangeal in 3 (3.9%), hips in 2 patients (2.5%) and knees in 2 patients (2.5%). Elevated acute phase reactants were found in 53 patients (66.8%), with high sedimention velocity in 56.3% and C reactive protein in 63.3%. The initial treatment was based on colchicine in 45% of the cases, needing to add corticosteroids in 25% of the patients. 10.1% required drugs modifying the disease, being the most frequent methotrexate (74.25%).

Sixteen patients (20%) required biological therapy, being the most used anakinra (12.5%), followed by etanercept (2.5%) and canakinumab (2.5%). In the period of time analyzed, 3 patients died due to causes unrelated to the SIA.

Conclusion: -The results obtained are consistent with what exists in the medical literature.

Disclosure of Interests: None declared

GENOMIC PROFILING OF INFLAMMATION-RELATED GENES IN NEURO-BEHÇET SYNDROME: A PRELIMINARY ITALIAN STUDY

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Background: Behçet Syndrome (BS) is a chronic vasculitis characterized by a wide spectrum of clinical manifestations, including the rare nervous system involvement. The most frequent clinical manifestations: Arthralgias 77.5%, followed by high fever (> 39) 73.8%, myalgias 72.5%, abdominal pain 56.3%, exanthema 47.5%, arthritis 35%, pericarditis 28.8%, headache 21.3%, pharyngitis 21.3% and canker sores 20%. The onset of the picture was a fever in 59 patients (73.8%) accompanied by cutaneous manifestations in 51.2% of the cases, with the rest of the symptoms being variable depending on the mutation studied.

The most common SAI in our center is the family Mediterranean fever, followed by the TRAPS. The most frequent mutation was the MEFV (P.R202Q), followed by the MEFV (p.E148Q).

With our study we want to reflect the variety of symptoms presented by patients with SAI diagnosed in adulthood. Despite the great variability, the most frequent symptoms are arthralgias, fever greater than 39 °C and myalgias.

The most used treatment in this type of patients is colchicine and respond to this positively in most cases.

Disclosure of Interests: None declared


involvement, known as “Neuro-BS” (NBS) [1-3]. BS inflammatory features were studied in several genetics studies with focus on single nucleotide polymorphisms (SNPs) of genes involved in inflammation and immune response [4,5]. A very few papers assessed the mutual state of NBS patients and this characterization was limited to a small number of SNPs [3].

**Objectives:** The aim of this study was to analyse the genetic background of a homogenous group of Italian NBS (parenchymal form) to genotype some SNPs of inflammation-related genes.

**Methods:** NBS patients were extracted from our database and retrospectively studied. Molecular characterization was performed for a subset of 20 NBS patients and 42 sex-matched healthy controls (HC) via: a) bioinformatics consultation for SNPs selection and primer design; b) SNPs genotyping: DNA extraction, PCR amplification, direct sequencing; c) DNA variant analysis using similarity search tool and specific software. In a second phase of analysis, a group of 30 BS patients without neurological involvement (no-NBS) was also genotyped. The odds ratio (OR) was calculated to assess the strength of BS association for each genotype.

**Results:** NBS patients subset was formed by 14 males and 6 females with mean age equal to 44.20 (±10.73) years. Six SNPs were considered eligible for molecular analysis and genotyped. Our results underlined the major role of ERAP1 rs17482078 GA genotype was absent in control group, while its frequency was equal to 10% for the patients (p-value<0.05). rs17482078 GA frequency was higher in NBS patients compared to no-NBS patients (p-value<0.01). No statistically significant differences were found for other SNPs of ERAP1 neither for IL-10 and STAT4 polymorphisms when NBS patients and controls were compared.

**Conclusion:** Our results reported for the first time the genotype distribution of several susceptibility loci in a group of Italian NBS patients. The data suggest a possible association between ERAP1 rs17482078 and NBS. Larger analyses were required to verify our preliminary findings.

**REFERENCES**