disseminated Bacillus Calmette-Guérin infection after vaccination resulting in multiple brain abscesses and pneumatoceles which is not common among the opportunistic infections seen in patients with HIES in the literature. Patient is in good health under control. However, male patient who also has also classical multisystem HIES as the first patient had no intracellular bacterial and Candida infections until today.

P057
Evaluation of protein expression profiles in patients with common variable immunodeficiency by proteomic approach

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Common Variable Immunodeficiency (CVID) is the most frequent primary immunodeficiency in adult. CVID is characterized by a marked decrease in serum immunoglobulins and high susceptibility to recurrent bacterial infections of the respiratory and gastrointestinal tracts. The clinical course of CVID can be complicated by autoimmune disorders, neoplasia, lymphoproliferative syndromes, or granulomas. Proteomics was defined as the study of complex biosystems (such as serum and tissues) in order to characterize content and changes in their proteome, induced by physiological or pathologic conditions. We used a proteomic approach to study protein expression profiles of serum samples from nine patients (5 males, 4 female), (age 12–59 years) with CVID, evaluated at the Division of Clinical Immunology and Allergy, University of Naples 'Federico II'. First, we compared their serum proteomes to control proteomes. Then, we evaluated changes in protein expression after one year of substitutive therapy with intravenous immunoglobulins. We used 2-D differential gel electrophoresis (2D- DIGE), that allows to separate proteins according to their charge and molecular weights. Taking advantage of fluorescent labelling of the samples, dedicated software platforms allow to identify quali-quantitative alterations in protein levels. Finally we performed Western Blot to validate data. Currently available results suggest that, compared to controls, patients before treatment show reduced levels of some proteins, already known in literature because of their relationships to infections and cancer. Besides, patients before treatment show higher serum levels of other proteins, which are correlated to inflammatory conditions. Finally, comparing proteome of these patients with CVID before and after 1 year of substitutive therapy, we observed that therapy actually modifies, and in many instances reverts the observed trends. Our preliminary data show that the serum proteome patterns of patients with CVID is different from control proteomes. These differences could characterize specific clinical phenotypes, representing evidence for evolution of immunodeficiency towards infective or neoplastic diseases. Furthermore, therapy with immunoglobulins is associated to a corrective trend of the patients' altered protein expression profiles, supportive of the effectiveness of substitutive therapy in patients with CVID.

P058
Familial hemophagocytic lymphohistiocytosis syndrome due to perforin-1 gene mutation. Clinical and molecular characteristics.

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Familial hemophagocytic lymphohistiocytosis (FHLH) is inherited in an autosomal recessive manner and characterized by proliferation and infiltration of hyperactivated macrophages and T-lymphocytes. FHLH is characterized by acute illness with prolonged fever and hepatosplenomegaly, cytopenias, and neurologic abnormalities. Perforin-1(PRF-1) mutations account for 20–40% of FHL cases. Perforin-1 has 70–75 kD and is one of the major cytolytic proteins of cytolytic granules. PRF1 is a pore-forming protein with a mechanism of transmembrane channel formation similar to component complement C9. We report the case of a 2-month-old girl, burned to consanguineous parents, who presented fever, hypoactive, hepatomegaly and splenomegaly. The initial analysis showed plaquetopaenia, anaemia, increased GPT, GGT and bilirrubin, coagulation alterations and increased levels of LDH and triglycerids. The bone marrow aspirated showed hemophagocytosis.

Methods: Mutation analysis of PRF-1 gene was performed by PCR and DNA direct sequencing. Perforin expression and NK receptors were analysed by flow cytometric analysis. Total PBMCs cytotoxicity assays with cell line k562 was peformed.

Results: Direct sequencing of individual exons of PRF-1 gene in the patient revealed a homozygous change of G445A in exon 2, this mutation resulted in a aminoacid change p.G149S. Parents DNA analysis revealed heterozygous mutation; furthermore, mother's DNA presented the A380C (p.N127T) polimorphism , localized also in exon 2. Patient and parents NK receptor expression, (NKG2C, NKG2A, NKG2D, ILT2, NKp30, NKp44, NKp46 and KIR) were normal. T and NK percentage of positive perforin cells were deficient in patient and with