**Identification of the distribution of HLA alleles in the Brazilian population and in neurological phenotypes possibly associated with autoimmunity**

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**Introduction**: The Human Leucocyte Antigen (HLA) genes, located at chromosome 6p21.3, are involved in susceptibility to more than 100 diseases of inflammatory, infectious and autoimmune nature [1]. With a density of single nucleotide polymorphisms (SNPs) significantly higher than most regions, HLA is among the most polymorphic regions of the human genome and presents considerable diversity among populations. Despite the importance of identifying and linking HLA types to the clinical condition there are very few databases that are dedicated to characterize HLA alleles in various populations. The knowledge about​​ autoimmune encephalitis has undergone a real revolution in recent years, since its recognition as an etiology of several severe acute and chronic neurological conditions has only been widely determined in the last 5 years. Autoimmune encephalitis is an inflammatory disorder characterized by a subacute impairment of short-term memory, psychiatric features and seizures. It is often associated with a variety of other neurological symptoms, and its differential diagnosis is wide, leading to challenges in its recognition. It used to be regarded as a rare disease, usually paraneoplastic and with poor prognosis. However, with the recent recognition of membrane-surface directed antibodies, it is now known that in a substantial proportion of patients there is no association with any malignancy and there is a good prognosis if treated. Sequencing the HLA region can provide critical insight into various immune disorders. There are no studies investigating the role of HLA in autoimmune encephalitis. Therefore, this study aims to identify HLA alleles distribution in Brazilian population (300 control subjects) and to identify a possible association between HLA alleles and autoimmune encephalitis (300 patients).

**Material and Methods:** To date, we have collected 300 samples of the control group and approximately 50 samples of the patients group. The HLA genotyping has been performed through Trusight HLA v2 Sequencing Panel, Illumina. This panel provides an assay to obtain ultrahigh resolution sequencing of 11 HLA Loci (Class I HLA-A, -B, -C; Class II HLA-DRB1/3/4/5, -DQA1, -DQB1, -DPA1, -DPB1) and the prepared libraries are loaded directly onto a MiSeq System for sequencing. The HLA locus is sequenced with paired-end 2 × 150 bp reads and the generated data are analyzed with TruSight HLA Assign 2.0 software.

**Results:** This is an ongoing study and currently, we are performing sequencing of the samples already collected and getting good quality data. The Q30 read quality scores are on average above 86.6%. We will evaluate the association of the HLA variants with risk of autoimmune encephalitis using a logistic regression model assuming additive effects of allele dosages on a log-odds scale.

**Discussion/Conclusion:** When the works is concluded, we hope to discover specific haplotypes that are predisposing to autoimmune encephalitis. In addition, our data will also be compared to that generated by high density SNP panels in the same sample and in other population, helping to establish a high resolution map of the HLA region in the Brazilian population, which will be made publically available at www.bipmed.org. Overall our study will contribute to a better understanding of the role of HLA variants in health and disease.

**Referências:** [1] Trowsdale J *et al*., Annu Rev Genomics Hum Genet 14:301, 2013.

Supported by: FAPESP, CNPq.