P64. CHARACTERIZATION OF GENOMIC PROFILE OF BLADDER CANCER: ARRAY-COMPARATIVE GENOMIC HYBRIDIZATION AS A HIGH-THROUGHPUT APPROACH

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Introduction: Bladder cancer (BC) is a solid tumor with high recurrence rates. It is the sixth tumor with the highest incidence and the eighth one with the highest mortality in the world. Since the prognostic tools currently available have limitations in identifying subgroups of patients at increased risk for recurrence or progression after treatment, we needed to increase knowledge of the genetic changes associated with the BC. The aim of this study was to characterize the genomic profile of bladder tumors using a whole genome technique, array-Comparative Genomic Hybridization (aCGH).
Materials and methods: Bladder tumor samples were obtained from 28 patients when they performed a transurethral resection of bladder tumor (TURBT), and aCGH was done using an Agilent oligonucleotide microarray 4 × 180K. The controls used were bladder tissue samples from non- cancer donors. Clinical data from the patients were registered and histopathological information analyzed.
Results: With this whole genome approach, we verified that our samples presented few genomic imbalances. In these preliminary results, we did not verify a pattern of chromosomal alterations, as, we did not find imbalances in more than 20% of patients. Besides that, the chromosomes with more frequent copy number gains were 1, 11, 13, 18 and 21 and the chromosomes with more frequent copy number losses were 1, 6, 10, 13, 20, 21, 22 and X. In addition, the sizes of aberrations detected for the same chromosome were often variable between patients.
Conclusions: In conclusion, we found that with this approach we identified some chromosomal regions altered in bladder cancer comparing to normal tissues. Thus, could be mapped fundamental genes related to disease initiation and progression. The correlation between molecular and clinical-pathological data will be essential to recognize accepted biomarkers with possible diagnostic and prognostic interest.

P65. INFLUENCE OF HISTOCHEMICAL STAINS ON DNA OBTAINED FROM FFPE SAMPLES

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Introduction: Formalin fixed, paraffin embedded (FFPE) samples are used for diagnostic and prognostic purposes. Histopathological analysis frequently includes not only histomorphological evaluation but also histochemical and molecular studies. In some cases FFPE samples are scarce and it is necessary to use the same histological section for histochemical analysis and DNA extraction. In molecular pathology labs this is a common practice, allowing the analysis of DNA specifically from altered cells. However, histochemical techniques use reagents that may induce chemical modifications on DNA. To perform a literature review about the influence of histochemical stains on DNA integrity.
Materials and methods: PubMed and Research Gate were used to survey original articles published until December 2017.
Results: For this review articles about the analysis of DNA extracted from stained FFPE sections were considered. The studies demonstrated that: DNA extracted from sections stained with Azure B, toluidine blue and methyl green (MG) was successfully amplified by Polymerase Chain Reaction (PCR) whereas Mayer's hematoxylin stain inhibits the reaction. Another study demonstrated that DNA amplification by PCR had better results with eosin Y and MG stains comparatively to Mayer's hematoxylin and May-Grunwald. Banaschak et al. 2001, showed that DNA analysis by PCR and capillary electrophoresis was successful with Hematoxylin Eosin (HE), Periodic Acid Schiff (PAS), Azan and Perls stains. Phosphotungstic acid hematoxylin (PTHA) and Gomori stains had negative results. Two different studies concluded that DNA is refractory to HE stain as capillary electrophoresis demonstrated similar degradation to that of unstained samples and it was successfully amplified by PCR.
Conclusions: Histochemical analysis allows demonstration of cellular components whose alterations are typical from pathological conditions. These techniques encompass reagents that may alter biomolecules. Nevertheless, from the analyzed studies it is possible to conclude that DNA integrity is maintained in techniques such as Azure B, toluidine B, MG, eosin Y, HE, PAS, Azan and Perls. On the other hand, Mayer's hematoxylin, May-Grunwald, PTHA and Gomori resulted in inhibition of DNA amplification. Since this analysis was not performed in common routine techniques such as Masson's Trichrome and PAS-Alcian Blue, it is important to deepen the knowledge, performing new studies for future appliance.

P66. SEVERE INTELLECTUAL DISABILITY, ABSENT SPEECH, EPILEPSY AND CRANIOFACIAL DYSMORPHISMS IN A FEMALE PATIENT WITH A 3(P25.3) PROXIMAL INTERSTITIAL *DE NOVO* DELETION

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Introduction: Deletions at the distal portion of the short arm of chromosome 3 cause a recognizable syndrome with characteristic features, most frequently arising de novo and with breakpoints at band 3(p25). Interstitial deletions involving only sub-band 3(p25.3) are less frequently reported, and within this region two deletion areas can be defined: distal and proximal deletions.
Case report: We report a 24 year old female with global developmental delay (DD), severe intellectual disability (ID), absent speech, epilepsy and craniofacial dysmorphisms. Due to her severe ID, absent speech and dysmorphic features, she was initially considered an Angelman syndrome patient. However, array-CGH analysis revealed a *de novo* 1Mb interstitial deletion at band 3(p25.3) between positions 10,364,749 and 11,421,309 (hg19).
Discussion: The reported deletion overlaps with deletions previously reported in the most proximal area of region 3(p25.3), although there are only 5 patients reported in the literature with this imbalance. These patients present a common phenotype consisting of DD, ID, absent or poor speech and epilepsy or EEG anomalies. The commonly deleted region includes the 3 last coding exons of *SLC6A11* gene, *SLC6A1* gene and its antisense gene, *HRH1* gene and part of *ATG7* gene. Both *SLC6A* genes code for Gamma-aminobutyric acid (GABA) transporters, responsible from removing GABA from the synapse. *SLC6A1* gene is reported in OMIM Morbid Map as heterozygous mutations are responsible for myoclonic-atonic epilepsy