adenocarcinoma was quite high (19.5% and 9.6%, respectively). EGFR mutations were more common in women comparing with men, whereas ALK translocation was associated with younger age. High accuracy of ALK-detection by IHC allows using it for screening, however due to low PPV, ALK-positive IHC results should be verified by FISH.

**PO-337** PRELIMINARY OBSERVATIONS: ARRAY-COMPARATIVE GENOMIC HYBRIDIZATION AS A HIGH-THROUGHPUT APPROACH AGAINST BLADDER CANCER

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**Introduction** Bladder cancer (BC) starts when urinary bladder cells grow abnormally. It is a solid tumour with high recurrence rates. BC is the eighth tumour with the highest mortality and the sixth one with the highest incidence in the worldwide. Since the prognostic tools currently available have limited accuracy and acquired changes in specific genes are thought to be significant in the development of bladder tumours, we needed to improve the research in this field of genetic changes associated with the BC. The aim of this study was the characterisation of the genomic profile of bladder tumours using the array-Comparative Genomic Hybridization (aCGH) technique.

**Material and methods** Bladder tumour samples were acquired from 28 patients when they were submitted a transurethral resection of bladder tumour (TURBT). The aCGH was done using a Agilent oligonucleotide microarray 4 × 180K. Bladder tissue samples from non-cancer donors are used as controls. Histopathological information from the patients was analysed and clinical data registered.

**Results and discussions** A few genomic imbalances were verified, using aCGH – a whole genome technique. In these preliminary outcomes, we did not observe a pattern of chromosomal alterations, as, we did not find imbalances in more than 20% of patients. Moreover, the chromosomes with more frequent copy number losses were 1, 6, 10, 13, 20, 21, 22 and X and the chromosomes with more frequent copy number gains were 1, 11, 13, 18 and 21. Additionally, the sizes of aberrations detected for the same chromosome were often variable between patients.

**Conclusion** This approach allowed us to identify altered chromosomal regions in bladder cancer comparing to normal tissues. In this way, is possible to map fundamental genes related to disease initiation and progression. The correlation between molecular and clinical-pathological data will be fundamental to identify recognised biomarkers with possible diagnostic and prognostic interest.

**PO-338** RECURRENT GliobLASTOMA: A COMPLEX SCENARIO DOMINATED BY LOSS OF MMR PROTEINS

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**Introduction** Glioblastoma (GBM) is a highly malignant primary brain tumour of neuroepithelial origin. The presence of MMR defects is associated with GBM progression. The aim of this study was to evaluate the frequency of MMR alterations in GBM.

**Materials and methods** This study included 109 GBM patients, who underwent a surgical treatment at the Department of Neurosurgery of the University Hospital of Padua from 2002 to 2012. All the cases were included in a database of GBM patients with clinical information. The genetic alterations were detected by hypermethylation array, sequencing, and copy number analysis. The frequency of each MMR alteration was calculated.

**Results and discussion** In our cohort, 13.7% (15/110) of cases had an alteration in MMR genes. The most frequent alteration was the deletion of one allele of MMR genes (MSH2, MSH6, MLH1, and PMS2) in 11.7% (13/110) of cases. The presence of MMR alterations was associated with a shorter survival, while the loss of one allele of MMR genes was associated with a shorter survival and a higher tumour grade.

**Conclusion** The presence of MMR alterations is associated with a shorter survival in GBM. The loss of one allele of MMR genes is associated with a shorter survival and a higher tumour grade. These results suggest that the presence of MMR alterations is a prognostic factor in GBM and that the loss of one allele of MMR genes is a prognostic factor in GBM.