analyses indicated that these mutations could be potentially pathogenic. Moreover, mutations in the ALKBH1 gene were also associated with nodal metastasis.

Conclusions: Our results suggest that ALKBH1 alterations were significantly associated with poor prognosis and may represent a new marker of prognosis in OSCC.

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61P Biomarkers EGFR, p53, IDH1 and MDM2 as prognostic indicators for overall survival of glioblastoma patients

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Background: Glioblastoma (GBM) is one of the deadliest cranial tumors occurring in adults. Various biomarkers have been tested for their significance in diagnosis, prognosis, and treatment of GBM. Some well-studied markers in GBM are Isocitrate dehydrogenase1 (IDH1), Murine double minute2 (MDM2), Epidermal Growth Factor Receptor (EGFR) and p53. The aim of this study was to investigate the protein expression of these markers in GBM patients of Pakistan.

Methods: A total of 51 surgically resected formalin-fixed paraffin-embedded specimens from patients diagnosed and treated at Aga Khan University Hospital were included in this study. Immunohistochemistry (IHC) for IDH1, MDM2, EGFR and p53 was performed using Dako EnVision System and respective monoclonal antibodies. Survival analysis was performed to check association of markers protein expression with prognosis in GBM patients.

Results: There were 36 males and 15 females in this study, with a median age of 48 at the time diagnosis. Overexpression of molecular markers was as follows: 55% for EGFR, 22% for p53, 79% for IDH1 and 85% for MDM2. We did observe that EGFR was significantly associated with increased age of our patients and with worse survival. Age >40 years was a predictor for worse prognosis as well.

Conclusions: EGFR overexpression and advanced age were worse prognostic indicators.

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62P Study on the role and mechanism of HAX-1 and S100A12 in promoting malignant progression of glioma

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Background: Glioma is the most common primary tumor of the human central nervous system. It is characterized by fast growth, strong invasion and impossible to complete surgical resection. Despite advances in tumor diagnosis and treatment, including surgery, radiotherapy and chemotherapy, the median survival for WHO Grade II gliomas is 5 years, for WHO Grade III gliomas is 2-3 years, and for WHO Grade IV gliomas is 14.6 months. The study of glioma cell formation mechanism is of great significance for the treatment of glioma. S100A12 expression was found to be highly correlated with glioma progression. Hax-1 protein has a variety of biological functions, such as anti-apoptosis, regulation of cell migration and endocytosis, and participates in invasion, metastasis and tumorigenesis in different types of tumors. However, there are few studies on the regulatory mechanisms of S100A12 and HAX-1 in glioma cells, and their mechanisms of action have not been fully analyzed.

Methods: To explore the effect and mechanism of S100A12 and HAX-1 genes on proliferation, invasion and migration of glioma cells and Lay the foundation for the study of glioma treatment. In this study, we carried out immunohistochemical investigation of S100A12 and HAX-1 in 81 glioma tissues to determine their expressions in glioma cells, and evaluate the clinical significance of S100A12 and HAX-1 in glioma patients. Futher we knockdown the S100A12 and HAX-1 by shRNA, and evaluated cell proliferation, cell migration and cell apoptosis by MTT, colony formation assay, transwell assay, flow cytometry assay and western blot.

Results: We found that S100A12 and HAX-1 were upregulated in tissues of glioma patients and the expressions were correlated to WHO stage. Further, we found that knockdown S100A12 inhibits the proliferation, migration and invasion of glioma cells through regulating cell apoptosis and EMT.

Conclusions: Both S100A12 and HAX-1 play vital roles in glioma progression, and may be important regulatory molecules for biological behaviors of glioma cell lines.

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63P Molecular markers as predictors of response to perioperative FLOT chemotherapy in gastric cancer

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Background: Perioperative FLOT chemotherapy has improved the prognosis in patients with locally advanced resectable gastric cancer (GC). However, in 80% of cases, the tumor is resistant to the therapy, and the patients are exposed to unnecessary toxicity and delayed surgical treatment. The aim of this study was to identify molecular predictive markers of efficacy of perioperative FLOT chemotherapy in patients with locally advanced resectable GC.

Methods: The retrospective study included 185 patients. All tumor samples were assessed for HER2 and microsatellite instability (MSI) status. Among all cases there were 45 patients with locally advanced $T_{2\text{-}4}N_{1\text{-}2}$ M_0 GC, who underwent a total or subtotal gastrectomy with D2 lymphadenectomy and perioperative chemotherapy with FLOT. MSI detection was performed using mononucleotide markers (NR21, NR24, NR27, BAT25, BAT26) by fragment analysis. HER2 gene amplification testing was performed using fluorescent in situ hybridization. Also 19 patients were tested for copy number changes of the FGFR1, FGFR2, KRAS, MET, EGFR, CCND1, MYC genes using multiplex-ligation probe amplification analysis. The endpoints were progression-free survival (PFS) and objective response rate (ORR).

Results: MSI was detected in 4.8% (9/185) of GC cases. Prevalence of HER2 amplification was 7.5% (14/185). PFS in patients with HER2-positive GC, receiving perioperative chemotherapy with FLOT (4/45), was significantly lower than in patients with HER2-negative GC: the median was 156 and 317 days, respectively ($p=0.0006$). There was no correlation between the alteration and objective response (OR) ($p=1.0$). PFS in GC patients with KRAS amplification (3/19) was significantly lower comparing to patients without KRAS amplification: the median was 98 and 327 days, respectively ($p<0.0001$). There was no association between an increase in KRAS copy number and ORR ($p=1.0$). For MSI and other studied markers no statistically significant correlation with PFS and ORR was found ($p>0.05$).

Conclusions: The presence of HER2 and KRAS amplification have been shown as promising predictive markers of the treatment failure in patients treated with perioperative FLOT chemotherapy for locally advanced resectable GC.

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64P Integrative immune transcriptomic classification could improve patient selection for precision immunotherapy in advanced gastroesophageal adenocarcinoma

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Background: Gastroesophageal adenocarcinoma (GEA) treatment has been revolutionized by the introduction of immune checkpoint inhibitors (CPIs) that, in combination with platinum-based chemotherapy as first line, have improved both