in 15/16 (93.7%) cases, including CK20, mostly 'dot-like' (12/13, 92.3%); CK (6/7, 85.7%), AE1/AE3 (3/3, 100%) and CK7 (1/6, 16.6%), along with neuroendocrine markers (16/16, 100%), including synaptophysin (11/13, 84.6%), chromogranin (12/15, 80%) and CD56 (4/4, 100%). Other positive IHC marker was CKIT/CD117 (3/3). Surgical resection was performed in 11/11 (100%) cases, with adjuvant chemotherapy offered in a single case. On follow-up ($n=4$ cases), two cases with large-sized tumours developed lymph node metastasis, including 1 who also developed pulmonary metastasis. Two patients were free-of-disease (16 months, 21 months) and 2 were alive-with-disease.

Conclusions: MCCs exhibit a wide histopathological spectrum, including co-existing Bowen's and rhabdomyoblastic de-differentiation. Careful analysis of key histopathological features and optimal IHC results with CK20, synaptophysin, chromogranin and CD56 are helpful in a timely diagnosis, as these are aggressive. MCCs also express CKIT.

107. EARLY MARKER OF DNA DAMAGE RESPONSE, ATM, AS A PREDICTOR OF CLINICAL OUTCOME FOLLOWING RADIOTHERAPY IN RECTAL CANCER PATIENTS

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Background: Ataxia telangiectasia mutated (ATM) is a key protein involved in DNA damage repair following double strand breaks and is important in maintaining genomic stability. Altered expression in rectal cancer cells may affect the ability of tumour cells to recover following exposure to ionizing radiation. Thus, we aimed to ascertain the relationship between ATM expression patterns in rectal cancer cells with radiosensitivity and survival outcomes.

Methods: 263 rectal cancer specimens, including 54 patients who received preoperative radiotherapy, were immunohistochemically stained for ATM. Expression patterns were scored separately in cancer cells retrieved from the centre and periphery of the tumour, and compared with clinicohistopathological data, tumour regression grade (TRG) and disease-free and overall survival.

Results: Negative ATM expression in tumour periphery cells correlated with older age ($p=0.013$) and lower grade ($p=0.044$), and predicted greater radiotherapy response as measured by TRG ($p=0.036$). Negative ATM expression in tumour periphery cells was also associated with longer disease-free survival [HR=2.951 (1.128–7.723), $p=0.028$]. Subset analysis in patients who received preoperative radiotherapy showed a similar trend towards longer disease-free survival [HR=7.206 (0.959–54.123), $p=0.055$]. Negative ATM expression in tumour centre cells was associated with longer overall survival [HR=2.117 (1.070–4.188), $p=0.031$].

Conclusions: ATM is a potential predictive and prognostic biomarker for radiosensitivity, disease-free and overall survival in patients with rectal cancer. Furthermore, it may facilitate the identification of patients who would benefit from preoperative radiotherapy.

108. ARE CLINICOPATHOLOGICAL FEATURES OF COLORECTAL CANCERS WITH METHYLATION IN HALF OF CPG ISLAND METHYLATOR PHENOTYPE PANEL MARKERS DIFFERENT FROM THOSE OF CPG ISLAND METHYLATOR PHENOTYPE-HIGH COLORECTAL CANCERS?

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Background: CpG island methylator phenotype (CIMP)-high colorectal cancer (CRC) is defined when a tumor shows methylation at $\geq 60\%$ of CIMP panel markers. Although CRCs with methylation at 50% of panel markers are classified into CIMP-low/CIMP-0 tumors, little is known regarding clinicopathological and molecular features and whether they are akin to CIMP-high or CIMP-low/CIMP-0 CRCs.

Methods: 1,164 cases of surgically resected CRC were analyzed for their methylation status and the frequencies of various clinicopathological and molecular features were compared between CRCs with 0/8, 1/8 to 3/8, 4/8, and 5/8–8/8 methylated markers.

Results: CRCs with 0/8, 1/8 to 3/8, 4/8, 5/8–8/8 methylated markers were found in 62.2%, 31.6%, 1.5%, and 4.7% of CRCs. CRCs with 4/8 methylated markers were closer to CRCs with 5/8–8/8 methylated markers in terms of female, mucin production, serration, nodal metastasis, CK7 expression, CK20 loss, and CDX2 loss frequencies and overall survival rate. CRCs with methylation at 4/8 markers were closer to CRCs with 1/8–3/8 methylated markers in terms of less frequent right colon location and poor differentiation. CRCs with 4/8 methylated markers showed the shortest overall survival time.

Conclusions: In terms of clinicopathological and molecular features, CRCs with 4/8 methylated markers appeared to be closer to CIMP-high than to CIMP-low/CIMP-0 and thus would be better to be classified into CIMP-high if CRCs have to be classified into either CIMP-high or CIMP-low/CIMP-0.

109. EXPRESSION OF IMMUNE CHECKPOINT MOLECULE VSIG4 IS CORRELATED WITH POOR PROGNOSIS IN MULTIPLE MYELOMA

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Background: Multiple myeloma (MM) is an indolent but eventually fatal disease with high heterogeneity. Despite many improvements in treatment, there is an increasing need for novel biomarkers for better risk stratification and treatment. Immune checkpoints that negatively regulate T cell immunity play a crucial role in inducing and maintaining immune tolerance under physiological conditions. Many studies have shown that dysregulated