have been recently described. We report herein five cases of a unique and rare subtype of GI indolent T-cell lymphoma that has not been recognized in the current WHO classification.

Methods: Hematoxylin and eosin-stained sections of the five cases were reviewed. Immunohistochemical studies as well as *in situ* hybridization for Epstein-Barr virus-encoded small RNAs (EBER) were performed on formalin-fixed, paraffin-embedded tissue sections using a BechMark XT automated immunostainer. In four cases with available tissue, PCR-based analysis for the rearrangement of the T-cell receptor (*TCR*) genes was also performed.

Results: There were one female and four male patients, with a median age of 52 years (range, 29 to 66 years). The most common presenting symptoms included abdominal pain or distention, diarrhoea, dyspepsia, and weight loss. Gastric body was the most commonly involved site, followed by colorectum and small intestine. Three patients had involvement of only one site, whereas an extensive whole-bowel involvement or disseminated disease was noted in the other two patients. Endoscopically, the lesions presented with multiple or solitary polyps or nodules, diffuse finely nodular lesions throughout the bowels, and alternatively, giant ulcerating masses. Staging work-up revealed the lesions were restricted to the GI tract in most cases at diagnosis. Histologically, the lesions were characterized by either non-destructive infiltration of the lamina propria, or sometimes, transmural massive infiltration of the entire wall, by small to medium-sized atypical T-cells with a similar phenotype of CD3+, CD4+, CD5+, CD8-, CD30-, CD56-, TIA1+, EBER-. All lesions featured an extremely low proliferation activity reflected by the Ki-67 index. The molecular studies for the *TCR* gene rearrangement confirmed a clonal lymphoproliferative disorder in all four cases examined. Except for one patient was managed by a 'watch and wait' approach, four of the five patients were treated with CHOP-based chemotherapy due to an initial diagnosis of peripheral T-cell lymphoma, among whom two patients with giant ulcerating lesions also received a prior total or subtotal gastrectomy to reduce the risk that might caused potentially by chemotherapy. The two patients treated merely with chemotherapy showed little response and were both alive with persistent disease at last follow-up, whereas the other two patients received combined surgery and chemotherapy kept well without disease during follow-up.

Conclusions: We suppose the currently reported lesions might represent a novel subtype of peripheral T-cell lymphomas featuring a peculiar indolent clinical course. These lesions display clinicopathological features similar to but not identical to those described recently by Jaffe and Chan. Awareness of these indolent T-cell lymphoproliferative disorders of the GI tract is important for the correct diagnosis and optimal management.

66. THE EXPRESSION AND ROLE OF CDK4 IN RHABDOMYOSARCOMA

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Background: Rhabdomyosarcoma (RMS) is the most common soft tissue sarcoma among children and adolescents, which

includes two major subtypes, embryonal RMS (ERMS) and alveolar RMS (ARMS). Previous research has shown that CDK4 gene shows amplification and gain in RMS.

Aims: We detected CDK4 protein and mRNA expression in RMS, and analyzed its clinicopathological variable in RMS.

Methods: We investigated the expression of CDK4 in 45 cases of RMS and 36 cases of normal muscle controls by immunohistochemistry (IHC) using tissue microarrays and quantitative real-time polymerase chain reaction (QRT-PCR), respectively.

Results: The mean mRNA level of CDK4 in RMS samples was 4.53-fold of those in normal muscle tissues, indicating that the expression of CDK4 mRNA in RMS were significantly higher than those in normal control group. In addition, the rates of CDK4 protein expression in RMS, ARMS, and ERMS was 48.89%, 65%, and 34.78%, suggesting that difference in CDK4 protein expression exists among different RMS types ($p=0.048$). Moreover, CDK4 protein expression was significantly associated with lymph node metastasis ($p=0.026$).

Conclusions: These data suggest that CDK4 may be associated with the progression and metastasis of RMS.

67. A RETROSPECTIVE STUDY TO CLASSIFY BREAST CARCINOMAS ACCORDING TO MOLECULAR CLASSIFICATION AND TO CORRELATE THE ER, PR, HER2 RESULTS WITH THE NOTTINGHAM GRADE AND THE AXILLARY LYMPH NODE STATUS AND TO COMPARE THE NOTTINGHAM GRADE WITH AXILLARY LYMPH NODE STATUS IN BREAST CARCINOMAS

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Background: Breast carcinoma (BC) is a heterogeneous disease. Gene expression analyses identify several subtypes which are of prognostic and predictive importance.

Aims: (1) to determine the prevalence of BC subtypes from SSWPS area patients according to molecular classification using immunohistochemistry (IHC) as surrogate markers and (2) to determine the relationship between certain pathological characteristics.

Methods: We reviewed 312 cases of BC diagnosed in 2013 in our department. Molecular classification of BC was based on Estrogen Receptor (ER), Progesterone Receptor (PR), HER2/neu (HER2), HER2 CISH and Ki-67 results. Triple negative cases were subdivided into Basal-like and Unclassified groups using CK5/6, CK14 and EGFR. The ER, PR and HER2 results were correlated with Nottingham grade (NG) and axillary lymph node (ALN) status.

Results: The commonest molecular subtype was Luminal A subtype (45%) followed by Luminal B (38%) [Luminal B HER2 negative (32%) and Luminal B HER2 positive (6%)], HER2 positive (7%), Basal-like (9%) and Unclassified subtype (2%). Positive ER and PR findings were inversely correlated with higher NG ($p\leq 0.0001$) whereas high NG was positively correlated with positive HER2 status ($p\leq 0.0001$). There was no correlation between ALN status and ER, PR and HER2 results. A statistically significant correlation was found between higher NG and number of ALN metastasis. Majority of Luminal A subtype BCs were either of NG 1 or 2 (135 cases, 96.4%). Amongst the