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45P Deep learning model identifies lynch syndrome versus sporadic MSI-H from adenoma histology

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Background: Lynch syndrome (LS) is the most common hereditary colorectal cancer (CRC), affecting up to 1 in 300 individuals with lifetime CRC risks >60% and high rates of metachronous cancers. Early recognition is essential for surveillance and preventive care, ideally before manifest cancer develops, yet germline testing is costly and not universally accessible. While both LS and sporadic microsatellite instability-high (MSI-H) cancers share molecular features, they arise from distinct precursors, conventional adenomas versus serrated polyps, suggesting that adenoma morphology may provide clinically useful, though not definitive, signals for differentiation. We hypothesised that such features can be detected by deep learning (DL) models on routine histology slides.

Methods: We trained a transformer-based deep learning (DL) model on Haematoxylin and Eosin (H&E)-stained whole slide image (WSI) features (using VIRCHOW-2) to distinguish LS from sporadic cases. The training cohort comprised 298 WSIs from 297 adenoma patients (120 LS, 177 sporadic) from Bonn, Germany. Generalisability was tested on an external MSI-H CRC cohort from the Hellenic Cooperative Oncology Group (HeCOG), Greece (n = 164; 27 LS, 137 sporadic; 176 WSIs).

Results: In 3-fold cross-validation, the model achieved a mean area under the receiver operating characteristic curve (AUROC) of 0.92 [0.91–0.94] and mean area under the precision-recall curve (AUPRC) of 0.95 [0.95–0.95] for classifying sporadic cases (p < 0.001). Despite being trained only on adenomas, the model achieved a mean AUROC of 0.73 [0.66–0.79] and mean AUPRC of 0.92 [0.89–0.95] for sporadic classification (p < 0.001) on the external MSI-H CRC cohort, suggesting morphological signals persist in carcinomas. Explainability analysis using heatmaps, top tiles, and pathology review suggests the model may detect subtle patterns like lymphocyte-rich mucosa in LS adenomas. Though subtle features remain hard to interpret, the DL model's ability to identify them indicates they warrant deeper analysis.

Conclusions: Our findings demonstrate that an H&E-based DL model trained on adenomas can effectively differentiate LS from sporadic MSI-H CRC, supporting a scalable and affordable histopathology-based approach to LS screening.

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