Conclusion Our cohort of decompensated cirrhotic patients displayed an overall hypercoagulable TEG profile, despite co-existing thrombocytopenia and a prolonged INR, PT and APTT, demonstrating poor representation of the global haemostatic profile by standard coagulation tests. TEG in peripheral venous blood accurately reflected the haemostatic profile of portal venous blood. TEG parameters correlated with liver disease severity scores in spite of poor representation by INR within these scores, thus the potential benefit of utilising TEG for liver disease severity assessment in routine clinical practice warrants further evaluation.

Oesophagus

Orals

OTU-16 A MACHINE LEARNING-BASED MODEL TO PREDICT THE PRESENCE OF BARRETT'S OESOPHAGUS

¹Laurence Lovat*, ¹Sarmed Sami, ¹David Graham, ²Jose Ariza, ¹Daryl Hagan, ¹Frelyn Ocampo, ¹Marco Novelli, ¹Manuel Rodriguez-Justo, ¹Alison Winstanley, ²Eliyahu Heifetz, ²Mordehy Ben-Zecharia, ²Uria Noiman, ¹Samuel Lovat, ³Rebecca Fitzgerald, ⁴Peter Sasieni, ²Avi Rosenfeld. ¹University College London, London, UK; ²Jerusalem College of Technology, Jerusalem, Israel; ³University of Cambridge, Cambridge, UK; ⁴Kings College London, London, UK

10.1136/gutjnl-2019-BSGAbstracts.251

Introduction Barrett's oesophagus (BO) is the only known precursor of esophageal adenocarcinoma. The current gold-standard test for diagnosing BO is endoscopy which is expensive and impractical as a population screening tool. We aimed to develop a robust questionnaire that could be used in routine clinical practice to identify patients with different likelihoods of having BO.

Methods We retrospectively analyzed data from two independent prospective datasets: BEST2 and BOOST case-control studies with 1299 and 398 patients, respectively. The BEST2 dataset was split into testing (n=776) and independent validation (n=523) cohorts. Using machine learning techniques (information gain and correlation-based feature selection followed by logistic regression); we identified panels of markers which predicted the presence of BO and then cross validated them between the datasets in order to create a robust set of markers that could be used for future studies.

Results Panels comprising the same thirteen demographic and patient symptom features predicted the occurrence of BO in both datasets. These included three demographic features (age,

gender and ethnicity), three general patient characteristics (weight, waist circumference, quantity of cigarettes smoked), and six symptoms (years since heartburn and acid taste developed, frequency of heartburn, acid taste symptoms, chest pain and taking stomach medicines). Although there were minor variations in logistic weights for each feature between the panels, they yielded accuracies with areas under the curve (AUC) of 0.91 in the BEST2 and 0.84 in the BOOST cohorts. Furthermore, despite differences in population composition, the panels validated across datasets. Validating the BEST2 model with BOOST yielded a ROC curve of 0.83 and validating the BOOST model against BEST2 yielded a ROC curve of 0.91. The final panel was also validated with the external BEST2 validation cohort (n=523) with AUC = 0.91 (table 1).

Conclusions This study identifies thirteen markers as a potential method for non-invasive screening for BO. These markers are consistent across different patient study groups. The panel needs to be validated in a prospective study.

OTU-17 METHYLATION PANEL IN THE ASSESSMENT OF CLINICAL RESPONSE TO THE RADIO-FREQUENCY ABLATION FOR BARRETT'S OESOPHAGUS

^{1,2}Wladyslaw Januszewicz, ¹William Waddock*, ¹Vinod Vijay Subhash, ¹Daniel Fernando, ¹Giorgio Bartalucci, ¹Emma Leeman, ¹Hamza Chettouh, ³Ahmad Miremedi, ³Maria O'Donovan, ¹Rebecca C Fitzgerald, ¹Massimiliano di Pietro. ¹Mrc Cancer Unit, Cambridge, UK; ²Medical Centre for Postgraduate Education, Warsaw, Poland; ³Department of Histopathology, Addenbrooke's Hospital, Cambridge, UK

10.1136/gutjnl-2019-BSGAbstracts.252

Introduction After radiofrequency ablation (RFA) for Barrett's oesophagus (BE) random biopsies at the gastro-oesophageal junction (GOJ) are taken to detect residual intestinal metaplasia (IM). It's debatable whether IM at the GOJ is a reliable marker of residual disease since it is subjective and patchy in nature. We have previously shown that methylation panel is accurate in identifying IM within the oesophageal tissue. We aimed to investigate whether a methylation panel in oesophageal and GOJ biopsies can be used to risk-stratify patients after RFA.

Methods We analyzed paraffin-embedded 4-quadrant BE and GOJ biopsies from patients undergoing RFA treatment with at least 2 post-RFA follow-up endoscopies. The IM extent was classified using a 4-tier system (IM-Score) based on number of glands with goblet cells (1, 2-5 or >5 glands) and number of biopsies with IM (0=no IM, 1=focal, 2=moderate and 3=extensive). Promoter methylation at 3 genes (ZNF345, TFP12, ZNF569) was assessed by MethyLight and a mean value was generated (Meth-Score). Methylation levels were compared using one-way ANOVA and Wilcoxon test, where appropriate.

Results We included 45 patients, who achieved endoscopic remission after RFA. The pre-RFA grades included: non-dysplastic BE (NDBE) (24.4%), low-grade dysplasia (LGD) (31.1%), high-grade dysplasia/intramucosal carcinoma (HGD/IMC) (44.4%). Overall, the methylation levels correlated with the degree of dysplasia, with a Meth-Score of 40.5%, 63.0% and 80.6% in NDBE, LGD, HGD/IMC, respectively ($P<0.001$). Hundred-and-five post-RFA GOJ biopsy sets were analysed of which 87(82.9%) had IM-score of 0-1 and 18

Abstract OTU-16 Table 1 Training and validating the BEST2 and BOOST datasets with the full 13 feature panel

Dataset training/testing name	AUC	Specificity at 0.9 sensitivity
Best2 train/Best2 train	0.91	0.78
Boost/Boost	0.84	0.63
Best2 train/Boost	0.83	0.61
Boost/Best2 train	0.91	0.72
BOOST/Validation cohort	0.91	0.7