for neoplastic progression. If true, the presence of one or more TSAs should be associated with synchronous advanced neoplasms.

**METHODS:** Data was extracted from UCCQ2D—a prospectively collected database (2012–2019) inclusive of locations, sizes and pathology of all polyps and masses. A “neoplasm” was defined as carcinoma, adenoma, SSP, or TSAs regardless of size. Cases with advanced neoplasms were defined if any neoplasm was malignant, ≥1 cm, contained villous features or high grade dysplasia, or if ≥3 neoplasms of any size were found. TSAs cases were compared to cases of other lesions for rates and odds ratios of synchronous and advanced neoplasms.

**RESULTS:** A total of 6023 procedures with at least one HP, adenoma, SSP or TSA were included, of which 70 had one or more TSAs (TSA cases). No significant differences in age, body mass index, or gender were seen between TSA and non-TSA cases. TSA cases had a mean of 2.44 neoplasms compared to 1.72 in non-TSA cases (IRR = 1.42 [CI 1.05–1.92] P = 0.022) and were associated with increased numbers of SSPP (IRR = 1.83 [CI 1.34–3.21] P = 0.038) (Table 1). The fraction of cases with synchronous advanced neoplasia was significantly higher in TSA cases (0.79% ± 0.13%) compared to cases with one or more adenomas (0.47% ± 0.01%) or SSPs (0.59% ± 0.034), P = 0.002. Relative to cases with one or more HPs, odds ratios for advanced neoplasia were 1.95 (1.75–2.17), 2.98 (2.54–3.5) and 7.54 (4.23–13.44) for cases with adenoma, SSP and TSA, respectively (Table 2).

**CONCLUSION:** Prior studies have shown that one or more index TSA(s) predict later risk for metachronous advanced neoplasms, more so than an index colorectal carcinoma. We show that the presence of one or more TSAs is also associated with higher risk for synchronous neoplasms and advanced neoplasms, especially SSPP. This suggests that TSA presence may reflect an unknown genetic predisposition and/or intestinal field defect that promotes tumor initiation and malignant progression. Regardless of underlying mechanisms, our data support an aggressive surveillance strategy for patients with one or more TSAs.

### Table 1
<table>
<thead>
<tr>
<th>Polyp Types</th>
<th>Overall</th>
<th>No TSA present</th>
<th>TSA present</th>
<th>95% CI for Mean</th>
<th>95% CI for Mean</th>
<th>95% CI for Mean</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>95% CI</td>
<td>Mean</td>
<td>95% CI</td>
<td>Mean</td>
<td>95% CI</td>
<td></td>
</tr>
<tr>
<td>Total # polyps adjusted for TSA present*</td>
<td>2.05</td>
<td>1.65–2.48</td>
<td>1.72</td>
<td>1.31–2.22</td>
<td>2.46</td>
<td>1.97–3.04</td>
<td>0.02</td>
</tr>
<tr>
<td>Total # true adenomas (%)</td>
<td>1.59</td>
<td>1.30–1.99</td>
<td>1.40</td>
<td>1.09–1.70</td>
<td>1.69</td>
<td>1.34–2.10</td>
<td>2.05</td>
</tr>
<tr>
<td>Total # ESA**</td>
<td>0.76</td>
<td>0.64–0.90</td>
<td>0.72</td>
<td>0.59–0.85</td>
<td>0.83</td>
<td>0.70–0.96</td>
<td>0.71</td>
</tr>
<tr>
<td>Total # nonpolypic polyps</td>
<td>0.62</td>
<td>0.49–0.77</td>
<td>0.76</td>
<td>0.62–0.90</td>
<td>0.90</td>
<td>0.74–1.08</td>
<td>1.65</td>
</tr>
<tr>
<td>Total # other polyps</td>
<td>0.41</td>
<td>0.33–0.50</td>
<td>0.43</td>
<td>0.30–0.57</td>
<td>0.50</td>
<td>0.38–0.64</td>
<td>0.56</td>
</tr>
<tr>
<td>Total # nonmetachronous polyps</td>
<td>1.24</td>
<td>1.00–1.50</td>
<td>1.17</td>
<td>0.92–1.42</td>
<td>1.31</td>
<td>1.04–1.61</td>
<td>1.54</td>
</tr>
</tbody>
</table>

### Table 2
<table>
<thead>
<tr>
<th>Case</th>
<th>Rates ± 95% CI</th>
<th>Rate ± 95% CI</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Baseline</td>
<td>0.13 ± 0.01</td>
<td>0.03 ± 0.01</td>
<td>NS</td>
</tr>
<tr>
<td>ES unknown</td>
<td>0.11 ± 0.01</td>
<td>0.03 ± 0.01</td>
<td>NS</td>
</tr>
<tr>
<td>ES unknown</td>
<td>0.10 ± 0.03</td>
<td>0.03 ± 0.01</td>
<td>NS</td>
</tr>
<tr>
<td>TRA unknown</td>
<td>0.26 ± 0.10</td>
<td>0.03 ± 0.01</td>
<td>NS</td>
</tr>
</tbody>
</table>

ABSTRACTS

**Changes in Antibiotic Usage Patterns for Treatment of Colon Ischemia Since ACG Guideline Recommendations**

Shweta V. Amin, MD; Olga Arevadikid, MD, MSc; Paul Feuerstadt, MD, FACG; JoAnn Kwah, MD, FACG

1Albert Einstein College of Medicine, Beverly Hills, CA; 2Montefiore Medical Center, Bronx, NY; 3Yale New Haven Hospital, Hamden, CT.

**INTRODUCTION:** In 2015, the ACG introduced a clinical guideline defining colon ischemia (CI) severity (mild, moderate, or severe) and recommending administration of antibiotics in those with moderate and severe CI. The goal of our study was to assess for differences in guideline-adherent antimicrobial use pre- and post-guideline publication.

**METHODS:** A database of consecutive patients diagnosed with hypoperfused CI at Montefiore Medical Center and Yale New Haven Hospital was utilized. Patients admitted from 2012–2014 (CI 12–14) and 2015–2017 (CI 15–17) composed the pre- and post-guideline cohorts, respectively. Our primary outcome was the frequency of guideline-recommended antibiotic use, defined as: (i) metronidazole+ (ciprofloxacin or cephalosporin) or (ii) piperacillin-tazobactam in patients with moderate or severe CI. Patients with CI classified as moderate and severe included overall antibiotic use for CI, individual antibiotic type and clinical outcomes (ICU requirement, length of stay, readmission, recurrence, mortality, and colectomy rates).

**RESULTS:** The CI 12–14 (n = 169) and CI 15–17 (n = 84) cohorts were similar in background characteristics: mean age (68.2 ± 18.9 years; P = 0.47), female sex (65.1% ± 76.2%; P = 0.07), and Charlson comorbidity score (3.5 ± 3.1; P = 0.65). CI severity was similar between cohorts: mild (1.3% ± 0.0%; P = 0.15), moderate (41.4% ± 47.6%; P = 0.35) and severe (37.4% ± 52.4%; P = 0.65). A trend for increased guideline-recommended antibiotic use was observed from CI 12–14 to CI 15–17 (50.3% ± 58.3% vs. 53.6% ± 56.1% CI 12–14 vs. CI 15–17, P = 0.23). A non-significant increase was observed in overall antibiotic use (69.4% ± 77.4% vs. 70.2% ± 64.4%; P = 0.03), but no significant differences were observed for other antibiotic types (Figure 2). The 30-day mortality (1.3% ± 8.0%; P = 0.01) and 30-day mortality and/or colectomy rates (6.0% ± 16.0%; P = 0.01) increased from CI 12–14 to CI 15–17. Non-significant differences were observed for other clinical outcomes (Figure 3).

**CONCLUSION:** The trend of increased antibiotic use post-guideline publication may have been a result of the new recommendations or the treatment of acutely sicker patients experiencing worse clinical outcomes. The decrease in ciprofloxacin use follows a nationwide trend and may be due to antimicrobial stewardship efforts to minimize the risk of C. difficile infection. Further research is needed to better understand the indications for antimicrobial use in the post-guideline era and worsened outcomes.

**Targeting MLH-1 Gene of Colorectal Cancer Cell Line Derivat From Patient of Cipto Mangunkusumo National Hospital To CBRISP SAVF for Genome Editing**

Muradhi Abdulrah, MD1, Art Fibril Surya, MD, FACG2, Marcelius Siadmabride, MD, PhD, FACG3, Sofi Melani4, Firda Anna, MD5, Dimas Ramadhan2, Dadang Makmun, MD, FACG1, Abdul Aziz Rani, MD1,2

1Universitas Indonesia, Jakarta Pusat, Jakarta Baya, Indonesia; 2Virology and Cancer Pathobiology Research Center, Universitas Indonesia, Jakarta Pusat, Jakarta Baya, Indonesia; 3Virology and Cancer Pathobiology Research Center, Universitas Indonesia, Jakarta Pusat, Jakarta Baya, Indonesia.

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INTRODUCTION: The mismatch repair genes as MLH-1 facilitate the cells to detect and repair bases mismatch that oftenly occur during replications process. Mutations of MLH-1 gene may be inherited and increase the risk for the related person to develop several tumors including colorectal cancer. The development of gene therapy in the recent decades arise ideas in developing experimental gene editing using CRISPR-Cas9 to the hereditary colorectal cancer patients primary cells. The objective of this study is to apply the CRISPR-Cas9 MLH-1 editing technology to primary cells of colorectal cancer primary cells from hereditary colorectal cancer patient stage 4.

METHODS: The cells from patient biopsy with diagnosis colorectal cancer with mucinous type, the cells were extracted using Collagenase Type I and cultured in Fibroblast Growth Medium for several passages. The cells were then plated on 96-well culture plate. For genome editing we use ribonucleaseprotein (RNP) consisting of Alt-R Sp. Caraf nucleasere in complex with Alt-R CRISPR-Cas9 guide RNA. We design this sg RNA targeted MLH-1 sequence using USCG genome browser. The cells then transfected with MLH-1 CRISPR-Cas9 using DEAE DFC reagent according to the manufacture protocols for 48 hours. After incubations, the cells were harvested. The DNA were isolated using Trizol reagent. Analysis of mutation MLH-1 were using T7E1 enzyme and primers were checked afterwards.

RESULTS: From our study we found that efficiency of introduction of complex Alt-R Sp. Caraf nucleasere in complex with Alt-R CRISPR-Cas9 guide RNA only 40% from total cells, the analysis was performed using Taki Cytometers. For amplification and analysis of Nickase gene was using T7E1 for primary cells of colorectal cancer primary cellswe found that this gene was amplified. From this finding this methods might be alternative therapy for colorectal cancer.

CONCLUSION: Colorectal cancer result from progressive accumulation of multiple genetic and epigenetic aberrations within cells. The progression from colorectal adenoma to carcinoma is caused by three major pathways: microsatellite instability, chromosomal instability and CpG island methylation phenotype: Until now in Indonesia we still cannot define which pathway are the most common. This study we try to find out response of MLH 1 gene editing using CRISPR-Cas 9. From our result we found that MLH 1 gene were able to mutated by using T7E1 assay and it was confirmed using Sanger sequencing.

143 Presidential Poster Award

ATLAS Scores Are Better Than CDSS in Predicting Any ICU Requirement and 30-Day Mortality in Patients With C. difficile Infection (CDI) >65 Years Old

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1 Yale New Haven Hospital, New Haven, CT; 2 Yale New Haven Health Bridgeport Hospital, Bridgeport, CT; 3 Albany Medical Center, Albany, NY; 4 Yale New Haven Hospital, Hamden, CT.

INTRODUCTION: CDI is the most common healthcare-associated infection with significant morbidity, mortality and cost. Various scoring systems have been formulated to aide disease prognosis. Our goal was to compare the ATLAS and CDSS predictive scores, initially to validate them and subsequently establishing which score was more accurately associated with short-term mortality and colorectal cancer. The development of gene therapy in the recent decades arise ideas in developing experimental gene editing using CRISPR-Cas9 to the hereditary colorectal cancer patients primary cells. The objective of this study is to apply the CRISPR-Cas9 MLH-1 editing technology to primary cells of colorectal cancer primary cells from hereditary colorectal cancer patient stage 4.

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144 Efficacy and Safety of NER1006 Versus Standard Bowel Preparations: A Meta-Analysis of Randomized Phase 3 Clinical Trials

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1 S. Elia-Raimondi Hospital, Caltanissetta, Sicilia, Italy; 2 Villa Sofia-Cerroli Hospital, Palermo, Sicilia, Italy; 3 Fondazione Istituto San Raffaele Gigi, Cefalà, Sicilia, Italy.

INTRODUCTION: The efficacy of bowel cleansing is essential for a quality colonoscopy, especially in the setting of colorectal cancer screening. Unfortunately, suboptimal bowel preparation is still observed in 25% of procedures. Recently, a very low-volume 1L PEG solution (NER1006) has been introduced on the evidence of three phase 3 randomized controlled trials. We conducted a meta-analysis to explore cleansing success, adenoma detection rate (ADR), and safety profile of NER1006 versus standard bowel preparations.

METHODS: PubMed/Medline and Embase were systematically searched through April 2019 by two independent reviewers (M.M. and F.S.M.) for randomized phase 3 clinical trials comparing the effectiveness of NER1006 versus standard bowel preparations.

RESULTS: Three RCTs (four arms, 2151 participants) met the inclusion criteria and were included in the meta-analysis (Table 1). The analysis showed a significant higher overall cleansing success for patients receiving NER1006 compared with standard preparations both using the Hare Fieldfel Cleansing Scale (HCS) (OR 1.29; 95% CI 1.02–1.61; P = 0.031, I2 = 0%; 2151 participants) and the Boston Bowel Preparation Scale (BBPS) (OR 1.43; 95% CI 1.15–1.78; P = 0.001, I2 = 0%; 2151 participants) (Figure 1a), as well as a significant greater high-quality cleansing of the right colon both when compared with the HCS (OR 2.26; 95% CI 1.44–3.54; P < 0.001, I2 = 70%; 2151 participants) and with the BBPS (OR 1.74; 95% CI 1.09–2.70; P = 0.021, I2 = 66%; 2151 participants) (Figure 1c). The pooled estimate of the NER1006 effect on ADR showed no significant difference in terms of overall ADR (OR 1.03; 95% CI 0.85–1.24; P = 0.773, I2 = 0%; 2151 participants), and a higher, although not significant, ADR of the right colon (OR 1.24; 95% CI 0.85–1.79; P = 0.262, I2 = 38%; 2151 participants) (Figure 2a). When considering the impact of NER1006 on mild to moderate treatment-emergent adverse events (TEAEs), we observed a significant pooled estimate of number of TEAEs (OR 2.25; 95% CI 1.81–2.80; P < 0.001, I2 = 0%; 2060 participants) and of patients with TEAEs (OR 1.80; 95% CI 1.50–2.16; P < 0.001, I2 = 0%; 2060 participants) (Figure 2b). No serious adverse events occurred.

CONCLUSION: Compared with standard bowel preparations, NER1006 showed a higher overall cleansing success, a greater high-quality cleansing of the right colon and a higher, although not significant, ADR of the right colon. NER1006 showed a higher incidence of mild to moderate TEAEs, in the absence of serious adverse events.