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Is there any difference in clinical outcome according to the tumor subsite location within the colon when performing laparoscopic complete mesocolic excision?

Jun-Gi Kim, Min Ki Kim, Dae Youn Won, In Kyu Lee, Hyeon-Min Cho and **Bong-Hyeon Kye**
Catholic University of Korea, South Korea

Aim: Procedures of laparoscopic colectomy are different from each other according to the tumor subsite within the colon, and short-and long-term outcomes of laparoscopic complete mesocolic excision (CME) and central vascular ligation (CVL) for colon cancer have never been compared based on the tumor location.

Method: Clinical data of patients who received laparoscopic colectomy for primary colon cancer between April 1995 and December 2010 from single surgeon were retrospectively reviewed. Data were analyzed and compared among three groups; patients whose tumor location was between ascending and proximal transverse colon (A, n=142), mid transverse and descending colon (TD, n=55), and sigmoid and rectosigmoid colon (S, n=214).

Results: Female patients were more common in group A (53.5% vs. 38.2% vs. 39.3%, p=0.020). Other baseline characteristics were comparable. Operative time was shorter in group S than another groups [245(145-855) vs. 279(150-485) vs. 295(145-455) min, p=0.000]. There were no differences among the groups in perioperative complication and patient recovery. Local recurrence rate was comparable among the groups (4.2% vs. 5.5% vs. 3.3%, p=0.594) for the median follow up period of 73(0-120) months.

Conclusion: Laparoscopic CME and CVL for colon cancer can be performed with comparable short- and long-term outcomes regardless of tumor subsite except for the operative time.

edemiel@cmcnu.or.kr

Computational analysis to detect resistance mutations to direct acting antivirals in hepatitis C virus

Karina Salvatierra
National University of Misiones, Argentina

Hepatitis C virus (HCV) infection is considered as a major public health problem, with an estimate of 200 million people infected worldwide. HCV infection is the major cause of chronic liver disease, with severe outcomes including cirrhosis and hepatocellular carcinoma and it is the main cause of liver transplantation. The treatment for HCV chronic infection with pegylated interferon alpha plus ribavirin inhibitors is unspecific; consequently, the treatment is effective in only 50% of patients infected. This has prompted the development of direct-acting antivirals agents (DAA's) that target virus proteins. Unfortunately, since the virus has a high replication rate and its RNA polymerase lacks proofreading activity, genetic variations might produce resistance against the DAA's. These DAA's have demonstrated a potent effect in vitro and in vivo; however, virus mutations associated with the development of resistance have been described. The objective of this work is to detect mutations in known aminoacids to be implicated in resistance to DAA's in sequences obtained of conventional Sanger and cloning sequencing. We have designed and developed an online information system named Biomedical Mutation Analysis (BMA), which allows users to calculate changes in nucleotide and amino acid sequences for each selected sequence from conventional Sanger and cloning sequencing. BMA allows the computational analysis quickly, easily and effectively. Furthermore, the development of different visualization techniques allows a proper interpretation and understanding of the results. The data obtained from BMA will be useful for HCV resistance surveillance, for the design of broad-range inhibitors and rationale therapeutic regimen.

kariales@gmail.com