

DISCOVERY OF GENETIC FACTORS THROUGH GENOME-WIDE ASSOCIATION STUDY IN NON-HEREDITARY COLORECTAL POLYPOSIS

Jae Jun Park

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Poster

Colorectal

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A genome-wide association study identified 71 novel genetic risk variants for non-hereditary colorectal polyposis in 638 patients compared to 7087 controls.

KEY POINTS

- The study included patients with 10 or more biopsy-proven cumulative polyps but no genetic mutations or family history of colorectal polyposis, compared to controls with normal colonoscopy results.
- Seven SNPs overlapping or nearest to five genes previously linked to colorectal cancer (UPF3A, BICRA, CBWD6, PDE4DIP, ABCC4) were confirmed as risk variants for non-hereditary colorectal polyposis.
- Two novel genes (CNTN4, CNTNAP3B) not previously associated with colorectal cancer or polyps were identified.
- The SNP rs149368557 was significantly associated with increased risk of polyp recurrence (odds ratio 2.991, 95% CI 1.006–8.899, $p=0.049$).
- The authors suggest these risk variants and genes might serve as novel targets for future colorectal cancer prevention.

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