On "diagnostic value of aberrant gene methylation in stool samples for colorectal cancer or adenomas"

On ñDiagnostic value of aberrant gene methylation in stool samples for colorectal cancer or adenomas: a meta-analysisò

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Dear Editor,

Colorectal cancer (CRC) is the third most frequent cancer in humans and more than 90% of cases originate from colorectal adenoma.[1] The malignant evolution into CRC is characterized by a sequential process of genetic and epigenetic alterations in colocytes. Recently, the growing interest towards epigenetic regulation of gene expression, led to the identification of different potential epigenetic biomarkers of CRC. In particular, DNA methylation represent one of the most investigated biological event involved CRC development bearing potential clinical implications for CRC diagnosis, prognosis and response to treatment.[2]

In a recent interesting paper, Yuan and colleagues evaluated the diagnostic accuracy of stool DNA methylation detection for CRC and adenoma performing a meta-analysis.[3] According to selection criteria adopted, authors included 13 studies for a total of 716 patients with CRC, 220 with adenoma and 414 healthy subjects. Seven studies assessed the methylation status of a single gene whereas 6 studies evaluated a panel of various genes. Moreover, different methylation detection techniques were used including methylation-specific PCR, methylation-sensitive high-resolution melting and microarray DNA methylation assay followed by pyrosequencing. Finally, area under the summary receiver operator characteristic curve values of 0.9385 and 0.9438 for adenoma and CRC detection were estimated, respectively, indicating a high diagnostic accuracy for fecal gene methylation testing.[3]

Although the authors performed a meta-regression analysis that showed no effect of heterogeneity on diagnostic accuracy, in our opinion both underlying differences in biomarkers tested and in assay methods inevitably led to unreliable results. In fact, included studies were carried out by using 3 different techniques as many several target genes (alone or combined into panels) not allowing a proper results comparison.

Considering that hundreds of genes are aberrantly methylated in the setting of CRC and standardized testing protocols are still required, we suggest that further meta-analysis should be performed with a more precise study selection criteria.

References

1. Mill J, Lawrance IC. Prevention of cancer in IBD - a balancing act. Minerva Gastroenterol Dietol 2013;59:261-72.
2. Coppedè F, Lopomo A, Spisni R, Migliore L. Genetic and epigenetic biomarkers for diagnosis, prognosis and treatment of colorectal cancer. World J Gastroenterol 2014;20:943-56.
3. Yuan Y, Qu B, Yan J, Wang H, Yin L, Han Q. Diagnostic value of aberrant gene methylation in stool samples for colorectal cancer or adenomas: a meta-analysis. Panminerva Med 2015;57:55-64.