Genetics of inflammatory bowel disease in Japan

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To the Editor,

I read with great interest the recent review article by Ishihara et al. [1]. In a very sophisticated approach, these authors have reviewed recent topics in the genetics of inflammatory bowel disease, focusing on human genetics and murine immunogenetics. In the section on human genetics, they give an outline of the latest insights in the candidate gene approach and genome-wide association screening. As they also note, the most striking event in this particular field can be considered to be the identification of *Nod2* as the first susceptibility gene for Crohn's disease, with the carriage rate of risk alleles estimated to be as high as 17.1-fold. The authors also point out that the degree of contribution of *Nod2* varies from race to race, with a higher incidence of risk alleles of *Nod2* among East Asian populations, including Chinese and Japanese. In doing so, they cite a paper by Yamazaki et al. [2], apparently overlooking a paper which our group had published slightly earlier in which we identify the absence of risk alleles in 350 Japanese patients with Crohn's disease [3]. Yamazaki et al.'s study was carried out by the research group of a leading geneticist in Japan, Professor Y. Nakamura. Our study was

published in *Gastroenterology* and had a clinical impact in Japan because it was organized by the Study Group for Intractable Inflammatory Bowel Disease (chief investigator: Professor T. Shimoyama) and supported by the Japanese Ministry of Health, Labor and Welfare. In view of the clinical relevance of our published study, I like to suggest that Ishihara et al. strongly consider not only citing our publication in their review article but also bestowing it the attention it deserves.

References

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