

PEER-REVIEW REPORT

Name of journal: *World Journal of Gastroenterology*

Manuscript NO: 67926

Title: Autosomal recessive 333 base pair interleukin 10 receptor alpha subunit deletion in very early-onset inflammatory bowel disease

Reviewer's code: 03764458

Position: Editorial Board

Academic degree: FACG, FACP, MBBS, MD

Professional title: Assistant Professor

Reviewer's Country/Territory: United States

Author's Country/Territory: China

Manuscript submission date: 2021-05-31

Reviewer chosen by: AI Technique

Reviewer accepted review: 2021-06-11 11:23

Reviewer performed review: 2021-06-14 22:42

Review time: 3 Days and 11 Hours

Scientific quality	<input checked="" type="checkbox"/> Grade A: Excellent <input type="checkbox"/> Grade B: Very good <input type="checkbox"/> Grade C: Good <input type="checkbox"/> Grade D: Fair <input type="checkbox"/> Grade E: Do not publish
Language quality	<input type="checkbox"/> Grade A: Priority publishing <input checked="" type="checkbox"/> Grade B: Minor language polishing <input type="checkbox"/> Grade C: A great deal of language polishing <input type="checkbox"/> Grade D: Rejection
Conclusion	<input type="checkbox"/> Accept (High priority) <input checked="" type="checkbox"/> Accept (General priority) <input type="checkbox"/> Minor revision <input type="checkbox"/> Major revision <input type="checkbox"/> Rejection
Re-review	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No
Peer-reviewer statements	Peer-Review: <input checked="" type="checkbox"/> Anonymous <input type="checkbox"/> Onymous Conflicts-of-Interest: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No



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SPECIFIC COMMENTS TO AUTHORS

VEO-IBD has been linked to several monogenic variations. Its very difficult to diagnose and manage VEO-IBD compared to adult iBD. I would like to appreciate authors for focussing their resources on this complex clinical entity. All the four patients had elevated IL-10 activity which is an indirect indicator of IL10RA dysfunction. Even though whole exon sequencing was not conclusive, whole genome sequencing identified a novel 333bp deletion in IL10RA. I felt the only limitation of this study is cost effectiveness and feasibility of whole genome sequencing compared to whole exon sequencing which needs less resources compared to WGS