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PEER-REVIEW REPORT

Name of journal: World Journal of Clinical Cases

Manuscript NO: 60876

Title: Study on pathogenic genes of dwarfism disease by next-generation sequencing

Reviewer's code: 02857964
Position: Peer Reviewer
Academic degree: FRCS (Gen Surg), MD, PhD
Professional title: Associate Professor
Reviewer's Country/Territory: United Kingdom
Author's Country/Territory: China

Manuscript submission date: 2020-11-23
Reviewer chosen by: AI Technique
Reviewer accepted review: 2020-11-24 02:42
Reviewer performed review: 2020-11-26 01:56
Review time: 1 Day and 23 Hours

Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish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

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SPECIFIC COMMENTS TO AUTHORS

Human height is a related to a combination of genetics, hormones, nutrition, environment and other factors. It is a complex process involving multiple genes and multiple factors. Genetic factors are the main factors affecting individual height differences. Genetic, nutritional, environmental, mental and mental diseases, intrauterine growth retardation, hypothalamic-pituitary-insulin-like growth factor growth axis dysfunction, chromosomal aberrations, systemic chronic diseases, genetic metabolic diseases and endocrine hormones and other factors are related to the incidence of dwarfism. However, the mechanism has not yet been clarified. Efficient and highly sensitive diagnosis methods have become the focus of dwarfness research in recent years. In this study, the authors analyzed the genetic variation by using a constructed panel related to dwarfism through next-generation sequencing platform sequencing analysis and screened candidate-related gene mutations. In my opinion, the manuscript is very well written. The title reflect the main subject of the manuscript, and the methods are described in adequate detail. Results are very interesting, and well discussed. Comments: 1. Some very minor language polishing should be revised. 2. The data analysis section, please state, when it consider as significant difference? $P < 0.05$? Please make it clear. 3. What's the article highlights? Should it be deleted? If this is required by the journal, please ignore my words.