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PEER-REVIEW REPORT

Name of journal: *World Journal of Clinical Cases*

Manuscript NO: 80226

Title: Clinical manifestations of adult hereditary spherocytosis with novel SPTB gene mutations and hyperjaundice: A case report

Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 05393679
Position: Peer Reviewer
Academic degree: MD

Professional title: Doctor

Reviewer's Country/Territory: India

Author's Country/Territory: China

Manuscript submission date: 2022-10-05

Reviewer chosen by: AI Technique

Reviewer accepted review: 2022-10-19 00:52

Reviewer performed review: 2022-10-30 14:26

Review time: 11 Days and 13 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Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish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

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Peer-reviewer statements	Peer-Review: [ ] Anonymous [Y] Onymous
	Conflicts-of-Interest: [ ] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

Is a good study of identification of a new mutation on chromosome 14 resulting in a variant of heriditary spherocytosis resulting in appropriate management of the clinical problem. My concern is why cholecystectomy was not done during splenectomy which is commonly carried out in Heriditary spherocytosis with gallstones.Eventhough there was no anaemia hemolysis was certainly present. Otherwise this is a good research .

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Reviewer's code: 03730113
Position: Peer Reviewer
Academic degree: PhD

Professional title: Academic Research

Reviewer's Country/Territory: India

Author's Country/Territory: China

Manuscript submission date: 2022-10-05

Reviewer chosen by: AI Technique

Reviewer accepted review: 2022-11-08 05:17

Reviewer performed review: 2022-11-17 03:44

Review time: 8 Days and 22 Hours

Scientific quality	[ ] Grade A: Excellent [ ] Grade B: Very good [Y] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish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
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	Conflicts-of-Interest: [ ] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

The case report by Ni Jiang et al., is a good read. Few suggestions to improve the work are given below: Comments • In the case summary (Page 2) it is advised to add the source of DNA i.e., either blood or tissue. Also, the genotype of the variant (heterozygous or homozygous) needs to be given. • It is surprising that the variant was not seen in the parents. The authors should clarify whether they are the biological parents. Has adoption been ruled out? If so that needs to be mentioned. Have the authors confirmed the variant by drawing an independent blood sample? • The authors in the introduction mention that HS is an autosomal recessive hereditary disease. However, they have identified a heterozygous variant in the SPTB gene (c.1801C>T). How do they justify the causal role of the variant? • In personal and family History (Page 4), although the personal history of the patient is given no mention as to any other family members being affected is not mentioned. • Under Physical examination, have the authors collected the Waist circumference and Hip circumference? • Although the authors mention that "High-throughput sequencing of a liver panel" on Page 5, there is no mention of the panel they have used, the genes they have screened. It would be beneficial to mention the liver panel genes and the platform for the high through-put sequencing that was used (Illumina/Ion torrent). • Were any other variants identified in the patient? Any VUS variants identified? • The rsID for the identified variant should be given. • It is preferable to call the changes in DNA as variants rather than mutation. • The authors mention that high-through put sequencing was used to identify the variant. However, electropherogram (Sanger's sequencing) is given. This is leading to confusion. In case they have validated the variant that was identified in the high through put

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sequencing by Sanger's sequencing they need to mention this. Was high through put sequencing done in all the family members or only the identified variant was screened?