Baishideng Publishing Group

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PEER-REVIEW REPORT

Name of journal: *World Journal of Clinical Cases*

Manuscript NO: 72702

Title: Clinical features and genetic variations of severe neonatal hyperbilirubinemia: a case report of five patients

Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 03795498
Position: Peer Reviewer
Academic degree: MD
Professional title: Doctor
Reviewer's Country/Territory: Taiwan
Author's Country/Territory: China

Manuscript submission date: 2021-11-01

Reviewer chosen by: AI Technique

Reviewer accepted review: 2021-11-08 02:49

Reviewer performed review: 2021-11-09 01:54

Review time: 23 Hours

Scientific quality	[ ] Grade A: Excellent [ ] Grade B: Very good [Y] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish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

SPECIFIC COMMENTS TO AUTHORS

By retrospectively studying five neonates with severe hyperbilirubinemia, the authors conclude that genetic variants may play an important role in an increased risk of neonatal hyperbilirubinemia, and severe jaundice in neonates may be related to a cumulative effect of genetic variants. This manuscript is a good example for that genetic detection should be considered for the early diagnosis of severe hyperbilirubinemia in neonates. I have three suggestions. 1. Articles of the references were published in or before 2018, excepted for reference 16 (in 2020). It will be better if more articles published in recent three years are mentioned. 2. Line 272: Please insert “16” before the authors’ name. 3. For patient 5: Born at 35+4 weeks of gestation plus heterozygous for the UGT1A1 c.G211A (p.G71R) mutation seems not sufficient to manifest severe hyperbilirubinemia (total bilirubin value = 584.40 μmol/L) at age of 7 d. Because seven variants, c.211G>A, g.-3279T>G, the number of CAT and TA repeats in UGT1A1 gene promoter, c.686C>A, c.1091C>T and c.1456T>G have been determined for the patient, other UGT1A1 gene variants should be concerned. The best way is to determine full-length UGT1A1 gene.

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Reviewer's code: 05226306
Position: Editorial Board
Academic degree: FACS, MBBS, MCh, MD, MNAMS
Professional title: Additional Professor
Reviewer's Country/Territory: India
Author's Country/Territory: China

Manuscript submission date: 2021-11-01

Reviewer chosen by: Fei-Yan Lin (Online Science Editor)

Reviewer accepted review: 2022-03-02 15:34

Reviewer performed review: 2022-03-02 17:08

Review time: 1 Hour

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) [ ] Minor revision [Y] Major revision [ ] Rejection
Re-review	[ ] Yes [Y] No

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

SPECIFIC COMMENTS TO AUTHORS

1. How many cases of jaundice were seen during the period? 2. What was the time line during which the cases were selected for analysis? 3. Were the cases chosen based on the associated conditions? 4. How was the cost of the genetic sequencing met? 5. How did the next generation sequencing influence further management in the cases? 6. Can the randomly chosen 5 cases be representative of all cases of jaundice for association of genetic factors? 7. Based on the manuscript can a routine genetic testing be carried out for all cases of 'severe jaundice'?