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PEER-REVIEW REPORT

Name of journal: *World Journal of Clinical Cases*

Manuscript NO: 77881

Title: Eczema herpeticum vs dermatitis herpetiformis as a clue of dedicator of cytokinesis 8 deficiency diagnosis: A case report

Provenance and peer review: Unsolicited manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 02936529
Position: Editorial Board
Academic degree: FRCS (Hon), MD, PhD
Professional title: Professor, Surgical Oncologist
Reviewer's Country/Territory: Brazil
Author's Country/Territory: Saudi Arabia

Manuscript submission date: 2022-05-27

Reviewer chosen by: AI Technique

Reviewer accepted review: 2022-05-27 18:22

Reviewer performed review: 2022-05-27 18:28

Review time: 1 Hour

Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish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) [Y] Accept (General priority) [ ] Minor revision [ ] 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

This very well conducted case report reflects the challenges of PID diagnosis, and the role of targeted gene testing with CNV analysis that ultimately might detect deletions that can be missed by WES. The manuscript is very concise, and for enriching the report, some figures illustrating the genetic tests would be valuable.

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Reviewer's code: 05234825
Position: Peer Reviewer
Academic degree: MD

Professional title: Staff Physician

Reviewer's Country/Territory: Taiwan

Author's Country/Territory: Saudi Arabia

Manuscript submission date: 2022-05-27

Reviewer chosen by: AI Technique

Reviewer accepted review: 2022-06-17 03:14

Reviewer performed review: 2022-06-17 08:43

Review time: 5 Hours

Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish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) [Y] Accept (General priority) [ ] 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

The author described a case of DOCK8 immunodeficiency syndrome with large deletion. The author claimed initial WES did not detect the deletion. The DOCK8 deletion was finally confirmed by MLPA. This case highlighted the important of using the right method to detect the clinically meaningful mutation. However, some revision is required. Major issue: 1. The author stated they detected the large deletion of DOCK8 by "copy number variation (CNV) analysis of NGS data". However, the kit they used is actually Multiplex Ligation Probe Amplification (MLPA) not NGS. MLPA is generally not classified as NGS. Therefore, I recommended the author to use the term "MLPA" in the whole manuscript. 2. To see is to believe. Please provide the MLAP result that indicated the DOCK8 deletion. Minor issue: 1. The author only described they use "Agilent SureSelect Human All Exon platform" for WES. This is a exome capture kit for WES library. It will be better to provide more detail information about the analysis pipeline (mapping, annotation, variant calling and variant filtration). Actually it is possible to detect large deletion in WES using specific CNV analysis software. But the MLPA remains the gold standard for DNA copy number determination.