CASE REPORT

Case Report: Whole exome sequencing identifies variation c.2308G>A p.E770K in RAG1 associated with B- T- NK+ severe combined immunodeficiency [version 1; peer review: 2 approved with reservations, 1 not approved]

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Abstract
Severe combined immunodeficiency is a large clinically heterogeneous group of disorders caused by a defect in the development of humoral or cellular immune responses. At least 13 genes are known to be involved in the pathophysiology of the disease and the mutation spectrum in SCID have been well documented. The widespread application of whole-exome sequencing based on next-generation sequencing has offered a new opportunity to systematically screen these genes in clinical scales. In this report, we describe the application of whole exome sequencing for arriving at a molecular diagnosis in a child suffering from B- T- NK+ severe combined immunodeficiency. Apart from making the accurate molecular diagnosis, we also add a genetic variation c.2308G>A p.E770K to the compendium of variations associated with the disease.

Keywords
Severe Combined Immunodeficiency, B- T- NK+ SCID, Whole Exome Sequencing, RAG1

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1
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3

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Competing interests: No competing interests were disclosed.

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Introduction
Severe combined immunodeficiency (SCID) encompasses a constellation of clinically and genetically heterogeneous diseases resulting in defects of the humoral and/or cellular immune defence mechanism\(^1\). Accurate molecular diagnosis of the disease is of prime importance, not only in offering appropriate genetic counselling, but also in understanding the exact molecular defect and would potentially enable prenatal screening\(^2\). The accurate molecular diagnosis would provide a fresh opportunity to enable cost-effective screening of family members and offer appropriate genetic counselling especially for populations where there is a high degree of consanguinity\(^3\),\(^4\). So far, arriving at a precise molecular diagnosis has been quite cumbersome, technically challenging and expensive as over a dozen genes are known to be implicated in the disease, which would require systematic targeted sequencing of each of the gene\(^5\),\(^6\). The advent of next generation sequencing, especially whole exome and sometime whole genome sequencing has significantly enabled the rapid identification of the causative genetic variations in clinical settings\(^6\).

In the present report, we describe the application of whole exome sequencing for the accurate molecular diagnosis of a case of B-T-NK+ SCID. Our report also adds a genetic variation c.2308G>A p.E770K to the compendium of variations associated with the disease.

Case report
Here we report a case of a seven-month-old boy, born out of a third degree consanguineous marriage, with a history of recurrent episodes of pneumonia, acute otitis media, diarrhea and oral thrush since two months of age. The child was pale, emaciated, febrile, and had respiratory distress with lower chest retractions. He was in compensated shock. There was no clubbing, cyanosis or lymphadenopathy. There was no facial dysmorphism and skin and hair were normal. He weighed 5.4 kg; measured 64 cm in length and head circumference was 39.5 cm. Examination of the chest showed evidence of bronchopneumonia while there was no evidence of congenital heart disease or neurological deficits. There was mild hepatomegaly with a liver span of 6.5 cm.

On investigation, the child was found to have hypochromic microcytic anemia, lymphocytopenia with absolute lymphocyte counts less than 1000/cu.mm and a normal platelet count. Liver and renal function tests were normal. The ionized calcium was 1.1 mg%. Blood culture was positive for Enterobacter species. The baby was negative for HIV infection and there was no evidence of tuberculosis. His chest X-Ray showed absence of the thymus shadow apart from evidence of bronchopneumonia.

Figure 1. [Pedigree of the family][1] (b) domain mapping of the RAG1 p.E770K on RAG1 protein showing the variation lies on RAG1 domain highlighted with red triangle and (c) capillary sequencing of the locus in the proband and family members. The homozygous variation c.2308G>A in the proband is marked with an asterisk.

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\(^1\) Accurat et al., 2001
\(^2\) Dearden et al., 2002
\(^3\) Deaver et al., 2003
\(^4\) Deaver et al., 2004
\(^5\) Deaver et al., 2005
\(^6\) Deaver et al., 2006

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A close workup of the immunoglobulin profile revealed hypogammaglobulinemia-IgA 23 mg%, IgG 44 mg% and IgM 26 mg%. IgE was 1 IU/L. The absolute CD3 count was 464 cells/ul (normal range 1,460–5,440 cells/ul), absolute CD19 lymphocyte count was 12 cells/ul (normal 430–3,300 cells/ul) and absolute NK cell count was 1,328 cells/ul (normal 80–340 cells/ul). Flow cytometry suggested absent B and markedly reduced T cell populations suggestive of B- T- NK+ SCID.

The child was treated with piperacillin (80mg/kg/dose Q8H), vancomycin (15 mg/kg/dose Q6H), dopamine (10 mic/kg/min), IVIG and other supportive measures and was put on cotrimoxazole (6 mg/kg/day OD) prophylaxis. He was treated with ganciclovir for CMV infection and for staphylococcal pneumonia.

The clinical diagnosis of SCID and family history of sibling death prompted us to investigate the molecular genetic correlates of the disease. Since over 13 genes are implicated in SCID and regular molecular testing was not readily available for the genes, we resorted to whole exome sequencing. After obtaining informed consent from the parents, blood was drawn after venipuncture under aseptic precautions. DNA was isolated from whole blood using salting out method. Exome capture was performed on DNA using the Illumina Nextera rapid capture expanded exome kit using standard protocols (Illumina Inc USA). We generated 47.95 million paired end reads and an average on target coverage of over 25x on Illumina HiSeq 2500 (Illumina Inc. USA). Alignment was performed using BWA (v0.7.12-r1039) and Stampy (v1.0.20) and variants were called using Platypus (v0.8.1)10. For the prioritisation of variants, we filtered all homozygous variants, further filtered by an allele frequency of <1% in the 1000 Genome and Exac. Variants in the 13 genes were prioritised and annotated for their deleteriousness using SIFT, Polyphen and Mutation Taster annotations obtained from annovar11.

Analysis revealed a homozygous missense variation (c.2308G>A) in exon number 2 of Recombination activating gene 1 (RAG1). The variant was predicted to be highly deleterious by SIFT (score 0.000), PolyPhen2 (0.991) and Mutation Taster (1.00). The variation causes an amino acid change p.E770K, which lies on RAG1 domain of the protein (Figure 1b). The present variation was not found in the 1000 Genome (http://browser.1000genomes.org/index.html), Exac (http://exac.broadinstitute.org/) or internal control database of over 150 exomes from South East Asian ancestry. Incidentally the mutation was previously reported and analysis suggested a significantly reduced recombination activity11.

The variation was further confirmed using targeted PCR amplification around the locus and confirmed by capillary sequencing. The variant was found to be heterozygous in both the parents as well as the surviving siblings (Figure 1c). The status of the variation could not be ascertained in the sibling who died because no sample was archived and primary immune deficiency was not suspected at the time.

Discussion

Mutations in RAG1 gene cause various degrees of severe combined immunodeficiency syndrome. RAG1 is involved in the V(D)J recombination12,13. The child was suspected to have a primary immune deficiency disorder since he had unusually frequent and severe infections and in addition had lost a male sibling due to similar illness. Further, he was born to third degree consanguineous parents. The early onset of symptoms by 2 months of life with increased susceptibility to both bacterial and fungal infections was a pointer to a T cell defect or a phagocytic defect rather than to an antibody deficiency like X linked agammaglobulinemia, which usually presents by 5 to 6 months of age, when maternal antibodies are on the wane14. The immunoglobulin profile showed that there was also a B cell defect. The low absolute lymphocyte counts coupled with radiological evidence of an absent thymus shadow was proof of a T cell defect as well. Thus, a provisional diagnosis of a severe combined immunodeficiency was made even before the flow cytometry results became available and helped confirm the diagnosis.

The possibility of Omenn syndrome was not considered since there was no history of a rash and there was no lymphadenopathy or hepatosplenomegaly, nor was there eosinophilia in the peripheral smear. XR SCID is characterized by an elevated percentage of B cells and in the absence of B cells in the child ruled this out. Jak3 deficiency was also not thought of for the same reason. ADA deficient SCID is characterized by bony abnormalities including rib cage defects, which were absent.

RAG 1 or RAG 2 deficiencies are associated with a lack of both B cells and T cells and NK cells are predominant in the circulation13. With this possibility in mind, and with a view to offer genetic counselling to the family, whole exome sequencing was considered. The child was referred for a bone marrow transplant, since SCID is not compatible with life beyond infancy. The patient underwent a matched sibling donor bone marrow transplant at the age of 1 year and 3 months. Post-transplant, he developed hypertension and later developed septic shock, which were managed successfully. He is now one year three months post-transplant and off all medications including immunosuppressive therapy.

Ethics approval

The whole exome sequencing was approved by the Institutional Ethical Committee of CSIR - Institute of Genomics and Integrative Biology (IHECC proposal number 8).

Consent

Written informed consent for publication of the patients’ details and/or their images was obtained from the patients/parents of the patient.

Data availability

All the raw sequencing data are available at the NCBI Sequence Read Archive (http://www.ncbi.nlm.nih.gov/sra), accession number SRR4088561.
Author contributions
GG, CK, MPJ, RA and RR clinically evaluated and characterised the patient. SKV, RJ, RR and AV performed the whole exome sequencing, computational analysis, data interpretation and validation experiments. SS and VS oversaw all the experiments and data interpretation. VS, SKV, GG and SS contributed towards writing the manuscript.

Competing interests
No competing interests were disclosed.

Grant information
SS and VS acknowledge funding from the Council of Scientific and Industrial Research (CSIR) India through Grant BSC0212.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgment
Authors acknowledge support from the GUaRDIAN consortium.

References
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Version 1

Reviewer Report 20 February 2017

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Lennart Hammarström
Department of Laboratory Medicine, Karolinska Institutet, Stockholm, Sweden

Govindaraj et al. report a typical SCID patient with a known mutation in Rag1 (p.E770K) with a previously known defective recombination activity and thus, there is very little novel information in this manuscript. In fact, the manuscript is already in itself published in F1000 (October 18th, 2016) and available on the web. The mutation should simply be added to existing databases.

Additional comments:
• The figure should be improved – providing the different domains.
• The pedigree (inheritance pattern is incomplete) - or simply state that the missing individuals were not sampled.
• Introduction should be more focussed on Rag1.
• Immunization schedule (if any) for live vaccines could be of interest for the readers (but not necessary).
• In the methods section, uniformity should apply (cc, mm ul etc). The number of NK cells appear to be too high (higher than the total lymphocyte count).
• Gene names should be in italics and transcript IDs should be given.
• Abbreviations should be correctly used and introduced at the first time of presentation.

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Reviewer Report 31 January 2017

https://doi.org/10.5256/f1000research.10202.r19588
David K. Buchbinder
Division of Hematology, Department of Pediatrics, Children's Hospital of Orange County, Orange, CA, USA

The authors provide a case report of a patient with severe combined immunodeficiency secondary to RAG deficiency. Whole exome sequencing was utilized to ensure a rapid and accurate diagnosis. Overall, the report is well written. Despite this there are some minor changes that should be considered. I also do not appreciate the novelty of this report and what it adds to the existing literature. The clinical diagnosis of severe combined immunodeficiency is clear. The routine use of next generation sequencing approaches are widely used to provide accurate and rapid diagnoses.

Introduction
- Page 3: I would consider focusing the introduction on the topic of RAG deficiency.
- Page 3: I would also note that an accurate and timely diagnosis is vital to the provision of life-saving therapy.
- Page 3: At the end of the first paragraph the word “sometime” is missing an “s”.
- Page 3: In the last paragraph of the introduction you talk about a genetic variation E770K. A genetic variation in what gene? Please state RAG1.

Case Report
- Page 3: When talking about the patient weight, height, and head circumference I would add in percentiles.
- Page 3: Please define the abbreviation “PICU”.
- Page 3: I would review the units on measurements. I would consider using SI units. For example, please review the use of “mg%”. I would address this issue throughout the manuscript.
- Page 3: How was HIV and tuberculosis excluded?
- Page 3: Is chest X-Ray correct?
- Page 3: Was there any evidence of eosinophilia?
- Page 4: For the immunological evaluation - were antibody responses assessed? Were RA/RO populations assessed? Were T cell responses to mitogens assessed? Was TCR diversity assessed? Was maternal engraftment assessed?
- Page 4: Please define the abbreviation “IVIG”.

© 2017 Buchbinder D. This is an open access peer review report distributed under the terms of the Creative Commons Attribution Licence, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
• Page 4: How was the CMV infection identified? Where was the “infection”? How was staph pneumonia identified?

• Page 4: I would consider adding a “Methods” section where you talk about the whole exome techniques used and confirmatory sequencing. I don’t really like how it is right in the middle of the case report.

• Page 4: In the 4th paragraph I would italicize “RAG1”. This should be addressed throughout the manuscript.

• Page 4: You mention that the mutation was previously reported. This detracts a bit from the novelty. I would also consider noting the RAG activity that was assessed in-vitro from the citation.

Discussion
• Page 4: You fail to use the abbreviation “SCID” in the first paragraph of the discussion which you defined earlier.

• Page 4: Please define the abbreviations “XR, Jak3, and ADA”.

• Page 4: I would include the portion about the transplant course in the case report section and not at the end of the discussion. I would add in additional details as well - what type of conditioning was used? Graft-versus-host-disease prophylaxis? What was the etiology of the hypertension? PRES? What was the organism isolated during sepsis? Any other post-transplant issues such as GVHD, VOD, etc.? Was engraftment assessed (i.e. lineage specific chimerism)?

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 26 Jul 2017
Vinod Scaria, CSIR Institute of Genomics and Integrative Biology, Delhi, India

The authors provide a case report of a patient with severe combined immunodeficiency secondary to RAG deficiency. Whole exome sequencing was utilized to ensure a rapid and accurate diagnosis. Overall, the report is well written. Despite this there are some minor changes that should be considered. I also do not appreciate the novelty of this report and what it adds to the existing literature. The clinical diagnosis of severe combined immunodeficiency is clear. The routine use of next generation sequencing approaches are widely used to provide accurate and rapid diagnoses.

Introduction
• Page 3: I would consider focusing the introduction on the topic of RAG deficiency. Clarification: Suggestions have been incorporated. Introduction is added with focus on RAG1 deficiency.

• Page 3: I would also note that an accurate and timely diagnosis is vital to the provision of life-saving therapy. Clarification: Suggestions have been incorporated.
Case Report

Page 3: At the end of the first paragraph the word “sometime” is missing an “s”.
Clarification: Corrections has been incorporated.

Page 3: In the last paragraph of the introduction you talk about a genetic variation E770K. A genetic variation in what gene? Please state RAG1.
Clarification: Suggestions have been incorporated.

Page 3: When talking about the patient weight, height, and head circumference I would add in percentiles.
Clarification: His weight, length and head circumference were below the 3rd centile as per WHO Child Growth Standards. This is updated in the manuscript.

Page 3: Please define the abbreviation “PICU”.
Clarification: Suggestions have been incorporated.

Page 3: I would review the units on measurements. I would consider using SI units. For example, please review the use of “mg%”. I would address this issue throughout the manuscript.
Clarification: Ionized calcium was 0.28 mmol/L.

Page 3: How was HIV and tuberculosis excluded?
Clarification: The child’s mother was HIV ELISA negative and the child had a negative Mantoux test and negative gastric acid AFB stain.

Page 3: Is chest X-Ray correct?
Clarification: Lateral view of the Chest X Ray.

Page 3: Was there any evidence of eosinophilia?
Clarification: There was no evidence of eosinophilia.

Page 4: For the immunological evaluation - were antibody responses assessed? Were RA/RO populations assessed? Were T cell responses to mitogens assessed? Was TCR diversity assessed? Was maternal engraftment assessed?
Clarification: Antibody responses, RA/RO populations, responses to mitogens, TCR diversity and maternal engraftment were not assessed.

Page 4: Please define the abbreviation “IVIG”.
Clarification: Suggestions have been incorporated.

Page 4: How was the CMV infection identified? Where was the “infection”? How was staph pneumonia identified?
Clarification: CMV infection was identified by DNA PCR. The child had disseminated CMV infection. Staph. pneumonia was identified by characteristic radiological findings and positive blood culture.

Page 4: I would consider adding a “Methods” section where you talk about the whole exome techniques used and confirmatory sequencing. I don’t really like how it is right in the middle of the case report.
Clarification: Suggestions have been incorporated.

Page 4: In the 4th paragraph I would italicize “RAG1”. This should be addressed throughout the manuscript.
Clarification: Suggestions have been incorporated.

Page 4: You mention that the mutation was previously reported. This detracts a bit from the novelty. I would also consider noting the RAG activity that was assessed in-vitro from the citation.
Clarification: We are not claiming that the mutation is novel. We are pointing that the variation is so rare that it is reported only once. In-vitro assay for RAG activity from citation is noted down in manuscript.

Discussion
The manuscript “Whole exome sequencing identifies variation c.2308G>A p.E770K in RAG1 associated with B- T- NK+ severe combined immunodeficiency” is the description of a case report, that is a child as a supposed case of SCID. Exactly, the authors found a homozygous variation c.2308G>A by whole exome sequencing and they hypothesized that this variant is associated with the disease. All the sections of the manuscript are well presented and written (title, abstract, content and discussion).

However, there are two points that I would like to comment:

1. In the introduction the authors wrote that there are over a dozen genes known to be implicated in the disease. So, what about these genes in this case report? By performing a whole exome sequencing, did they also observed the variants of these genes? if yes or not, please comment!

2. In order to explain the functional consequences of the mutated protein, the authors write “The variation causes an amino acid change p.E770K, which lies on RAG1 domain of the protein……Incidentally the mutation was previously reported and analysis suggested a significantly reduced recombination activity” referring to work of Asai E et al. Clin Immunol. 2011. In Asai’s work the nucleotide mutation is referred as 2420 G>A with a E770K effect. The position of nucleotide between the two works is different, but the authors of the manuscript declare the same position for amino acid change and the same reduced recombination activity. Please, specify/insert the RS ID number of the homozygous variation.
**Competing Interests:** No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

**Author Response 26 Jul 2017**

**Vinod Scaria, CSIR Institute of Genomics and Integrative Biology, Delhi, India**

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1. In the introduction the authors wrote that there are over a dozen genes known to be implicated in the disease. So, what about these genes in this case report? By performing a whole exome sequencing, did they also observed the variants of these genes? if yes or not, please comment

Clarification 1: We have observed the variations in the genes, which are previously reported with primary immunodeficiency. The prioritized variations are shown in table uploaded in answer to reviewer’s comments. (Sent to editor while uploading revised version). Among the variations, the RAG1:c.2308G>A:p.E770K variation was prioritised due to pathogenic and rarity of variation.

2. In order to explain the functional consequences of the mutated protein, the authors write “The variation causes an amino acid change p.E770K, which lies on RAG1 domain of the protein……Incidentally the mutation was previously reported and analysis suggested a significantly reduced recombination activity” referring to work of Asai E et al. Clin Immunol. 2011. In Asai’s work the nucleotide mutation is referred as 2420 G>A with a E770K effect. The position of nucleotide between the two works is different, but the authors of the manuscript declare the same position for amino acid change and the same reduced recombination activity. Please, specify/insert the RS ID number of the homozygous variation.

Clarification 2: In the original publication by Asai et al. 2011, the nucleotide position is mentioned as c.2420G>A. While the position of amino acid is clear from the publication, we are not sure if nucleotide position denotes the position in cDNA or other. In our case, we mentioned the cDNA change as c.2308G>A and amino acid change as p.E770K. We clearly indicated the change in cDNA and it is also the reported nomenclature from database. For reference, Cosmic mutation ID: COSM3447065. The rsID for mutation is rs768260595.

**Competing Interests:** No competing interests were disclosed.
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