

# Immune Dysregulation in Monogenic Inborn Errors of Immunity in Oman: Over A Decade of Experience From a Single Tertiary Center

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Al Farsi T, Ahmed K, Alshekaili J, Al Kindi M, Cook M, Al-Hosni A, Ansari Z, Nasr I and Al Sukaiti N (2022) Immune Dysregulation in Monogenic Inborn Errors of Immunity in Oman: Over A Decade of Experience From a Single Tertiary Center. Front. Immunol. 13:849694. doi: 10.3389/fimmu.2022.849694 **Background:** Inborn errors of immunity (IEIs) are being recognized as an important cause of morbidity and mortality in communities with a high frequency of consanguinity, such as Oman, and thus recessively inherited conditions. Various monogenic causes of IEI have been recently discovered; however, the disease phenotype may be variable and does not always include infection at presentation, leading to a delay in diagnosis and a poor outcome. It is now well recognized that immune dysregulation manifestations are observed in a significant proportion of patients with IEI and occasionally precede infection.

**Methods:** Here, we retrospectively report the epidemiological, clinical, immunological, and molecular findings and outcomes from 239 patients with IEI who were diagnosed and managed at the Royal Hospital, Oman, from January 2010 to October 2021.

**Results:** The estimated annual cumulative mean incidence of IEI was 25.5 per 100,000 Omani live births with a total prevalence of 15.5 per 100,000 Omani population. Both the high incidence and prevalence are attributed to the high rate of consanguinity (78.2%). Defects affecting cellular and humoral immunity including severe combined immunodeficiency (SCID), combined immunodeficiency (CID), and CID with syndromic features were the predominant defects in IEI (36%). Immune dysregulation was a prominent manifestation and occurred in approximately a third of all patients with IEI (32%), with a mean age of onset of 81 months and a mean diagnostic delay of 50.8 months. The largest percentage of patients who showed such clinical signs were in the category of diseases of immune dysregulation (41%), followed by predominantly antibody deficiency (18%). The overall mortality rate in our cohort was 25.1%, with higher death rates seen in CID including SCID and diseases of immune dysregulation.

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**Conclusion:** Immune dysregulation is a frequent manifestation of Omani patients with IEI. Early detection through raising awareness of signs of IEI including those of immune dysregulation and implementation of newborn screening programs will result in early intervention and improved overall outcome.

Keywords: inborn errors of immunity, immunodeficiency, immune dysregulation, phenotype, genotype, children, adults, Omani

# INTRODUCTION

Inborn errors of immunity (IEIs) are a heterogeneous group of more than 400 primary immunodeficiency (PID) disorders, which are classified into 10 groups based on the involved pathophysiology, clinical phenotype, and genotype (1, 2). Prevalence studies based on the given clinical diagnosis have been conducted worldwide. Using disease registries, the prevalence is estimated to range from 1:8,500 to 1:100,000 people (3), according to the ethnic group and method used.

In a historical cohort study performed over a 31-year period using a public administrative healthcare database in the USA, the incidence rate of IEI was approximately 10.3/100,000 personyears, with predominantly antibody deficiency (PAD) accounting for 78% of all cases compared to 10.5% for combined immunodeficiency (CID) including severe combined immunodeficiency (SCID) (4). However, Asian registries especially those of Arabian gulf countries reported an IEI prevalence (per 100,000 children) of 20.2 in Kuwait (5), 4.7 in Qatar (6), and 7.2 in Saudi Arabia (7), with a predominance of CIDs affecting cellular and humoral immunity. In Oman, a previous report on PID among a pediatric cohort described a prevalence of 7/100,000 with an estimated incidence of 5.0/ 100,000. The main encountered IEIs were phagocytic defects (35%), followed by PAD (20.7%) and CID (17.8%) (8). In contrast, a study from our center demonstrated a higher incidence of SCID among an Omani pediatric population (4/ 100,000) compared to the earlier published data (9). Such epidemiological discrepancies in Oman can suggest underreporting of IEI in such retrospective reports.

A previous report from Oman described recurrent and severe infections as the only main clinical presentation of IEI (8). Infection is the cornerstone of the 10 warning signs of PID first proposed by the Jeffrey Modell Foundation in 1993 as a screening tool. However, with the expansion of knowledge on IEI, it is gradually becoming clearer that immune dysregulation is a major manifestation of this disease group. Indeed, later studies have demonstrated inadequate sensitivity of the initial 10 warning signs especially in infant and pediatric populations and have discussed the need for adjustment (10-12). In line with this, Thalhammer et al. (13) recommended adding immune dysregulation and syndromic features to the list of IEI warning signs to avoid diagnostic delay, which is associated with poorer health outcomes.

This study aimed to collect information on the frequency and manifestation of non-infectious phenotypes in the current extended cohort of pediatric and adult patients with IEI in Oman. Additionally, we provide more recent data on the incidence, prevalence, molecular diagnosis, and outcome of IEI in the Omani population.

### **METHODS**

Data were extracted from electronic medical records by International Statistical Classification of Diseases (ICD)-10 codes (D80–D89) and were filled into Google forms and then an Excel sheet. A manual selection of patients was also performed, as some patients were not linked to ICD-10 codes. Further analysis was performed *via* Excel and GraphPad Prism-9 (GraphPad Software, Inc., San Diego, CA, USA). The results are expressed as means and medians with ranges and frequency (%) for continuous and categorical variables, respectively. The study was approved by the Research and Ethics Review and Approval Committee in the Ministry of Health, Sultanate of Oman.

#### **Patients**

We performed an analysis of a cohort of 239 children and adults with IEI, who were seen and managed at the Royal Hospital-the main governmental tertiary hospital in Oman-from January 2010 to October 2021. The epidemiological details included the annual incidence per Omani live birth and the prevalence among the Omani population. The cumulative incidence was calculated by defining the mean of the yearly new diagnoses of IEI from the annual population of Omani live births obtained from local registries for the last 11 years. Given that most of our cohort were from the pediatric age group, the Omani live birth group was considered a reasonable population at risk to extrapolate a relatively true incidence. However, prevalence included all patients with IEI who were diagnosed from the Omani population over the last 11 years. Additionally, other information such as demographics (sex and age), family history, and clinical manifestations of infection, immune dysregulation, and malignancy, as well as molecular diagnosis, long-term events, and outcomes were collected into an electronic database. The adopted diagnostic criteria were based on The European Society for Immunodeficiencies (ESID) Registry Working Definitions for the Clinical Diagnosis of IEI (14). The classification and subclassification of IEI were based on the Human Inborn Errors of Immunity: 2019 Update of the International Union of Immunological Societies (IUIS) Phenotypical Classification (1, 2).

### Age Categories and International Union of Immunological Societies (IUIS) Classification

The age of onset and age of diagnosis were grouped into the following eight categories: 0-2, 3-5, 6-10, 11-15, 16-20, 21-30, 31-40, and >40 years. The phenotypic and genotypic classification was based on the main categories of IEI described in the IUIS (1, 2). Autoinflammatory disorders and syndromes of familial hemophagocytic lymphohistocytosis were excluded from the analysis due to the unavailability of patient's details. Unclassified IEI was defined when the clinical phenotype and genotype did not fit the above classes. Diseases with possible contributions to IEI and those that were yet to be further studied were highlighted.

# Clinical Presentation, Disease Manifestation, and IEI Complications

Clinical presentations were divided into infection, immune dysregulation, malignancy, or asymptomatic. Detailed infectious and non-infectious disease manifestations and complications are listed. We performed a focused analysis on immunodysregulatory disorders to reveal specific characteristics with IEI classification, phenotype, genotype, diagnostic delay, and outcome.

### Laboratory Evaluation

The laboratory evaluation included full blood count (hemoglobin level and total lymphocyte, neutrophil, eosinophil, and platelet count), basic lymphocyte subsets [T, B, and Natural killer (NK) cell count] and total serum immunoglobulin levels (IgG, IgA, and IgM, IgE). Moreover, we also utilized a specific antibody panel for tetanus, diphtheria toxin, *Haemophilus influenzae* type B, pneumococcal antibodies, hepatitis B, measles, mumps, rubella and varicella, and dihydrorhodamine (DHR) assay for neutrophil function, a functional complement assay for classical and alternative hemolytic pathways and a CD11/CD18 expression assay for adhesion defect when clinically indicated.

# Genotype

Molecular diagnosis was obtained through whole-exome sequencing, Sanger sequencing, targeted mutation analysis, fluorescent *in situ* hybridization (FISH), or microarray. Confirmed genetic diagnosis was determined when patient had a positive pathogenic or likely pathogenic genetic change that could explain the clinical phenotype. A note was made on the proportion of positive mutations according to the results of a commercial lab, National Genetic Centre (NGC), in Oman or *via* the help of external expert research laboratories. The novelty of the mutation detected was confirmed by reviewing the query interface on the ClinVar database. Genetic workup for patients with Predominantly Antibody Deficiency (PAD) (IUIS class III) was not frequently requested due to limited resources.

### Long-Term Events and Outcome

The patients' clinical outcomes were determined after reviewing the medical record system, noting long-term infectious and noninfectious manifestations. We also reported on the treatment options received, and information on the recent status was defined as follows: alive and well, alive with complications, need for Intensive Care Unit (ICU) admission, defaulted patients, mortality, and the contributions to mortality.

# RESULTS

The Sultanate of Oman is the second largest territory in the Arabian Peninsula with an area of 120,000 square miles, a total coastal border of 3,165 km, and a total population of 4,471,148 in 2020. The geographical location has led to open access to immigration and trading from various ancient civilizations in Asia and North Africa. Oman has two major tertiary referral centers for IEI, and one bone marrow transplant unit, which is limited to four beds. The Bacillus Calmette–Guerin (BCG) vaccine is a routine immunization at birth for all newborns. There is currently no newborn screening program for T- and B-cell deficiencies, and referrals from primary physician to tertiary units are based on clinical suspicion and previous family history of IEI. Most patients were referred from government primary or secondary hospitals (68.6%). This is the first report to describe our IEI cohort over the last 11 years.

## **Patient Demographics**

Two hundred thirty-nine (n = 239) patients were diagnosed and managed at the Royal Hospital over a period of 11 years (January 2010-October 2021). The estimated annual cumulative mean incidence of IEI was 25.5 (range: 20.0-29.8) per 100,000 Omani live births, and combined with the Middle East and North Africa region (MENA) Omani cohort (15), the total prevalence of IEI was 15.5/100,000 Omani population (Table 1). There were slightly more boys in the registry (n = 139, 58.1%, and M/F: 1.4), and 194 (81.2%) patients were under 18 years of age. More than two-thirds of the cohort (n = 187, 78.2%) were born to consanguineous parents. Among the relatives of patients with IEI, a positive family history of recurrent infections was detected in 100 patients (41.8%) compared to a positive family history immune dysregulation (n = 38, 15.9%) and a positive family history of malignancy (n = 17, 7.1%). Regardless of the age of disease onset, there was a diagnostic delay. The mean and median age differences between the onset of symptoms and diagnosis were 41.7 and 15 months (range: 1-453), respectively. Details of the age of onset and diagnosis for Omani patients with IEI are shown in Table 2.

### **Clinical Phenotype**

Most patients presented with infection (n = 219, 91.6%) at clinical presentation, among whom 40 of them (16.7%) also had symptoms of immune dysregulation. Five patients presented with malignancy (2%), and the remainder were asymptomatic (n = 5, 2%) at clinical presentation as they were familial.

### Infection

The mean age of infection episode onset was 42.6 months (range: 1-480). The documented infectious etiology varied but mainly included Gram-negative (n = 143, 61.6%) and Gram-positive

TABLE 1	Combined data showing	g the prevalence of IEI in Omani	patients according to IUIS classification.
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Type (IUIS)	MENA Omani cohort 2021	Current cohort	Total
Phagocytic defects (V)	59	35	94
SCID/CID (I)	38	55	93
PAD (III)	33	40	73
Syndromic CID (II)	35	31	66
Innate immune defects (VI)	5	35	40
Immune dysregulation (IV)	8	32	40
Complement deficiencies (VIII)	7	6	13
Phenocopies (X)	NR	1	1
Unclassified to IUIS	NR	4	4
Total number	185	239	424
Prevalence/100,000	6.8	8.7	15.5

IEI, Inborn Errors of Immunity; IUIS, International Union of Immunological Societies; MENA, Middle East and North Africa region; SCID, Severe Combined Immunodeficiency; CID, Combined Immunodeficiency; PAD, Predominantly Antibody Deficiency; NR, Not Reported.

(n = 130, 56%) bacterial infections; this was followed by viral infections including the common viruses (n = 114, 49.1%), cytomegalovirus (n = 29, 12.5%), Epstein-Barr virus, (n = 16, (6.9%), and adenovirus (n = 13, 5.6\%); fungal infections, including non-filamentous (n = 37, 15.9%), filamentous (n = 29, 12.5%), and dimorphic fungi (n = 13, 5.6%); and mycobacterial infections with Mycobacterium bovis, including BCG strain (n = 41, 17.7%), Mycobacterium tuberculosis (n = 3, 1.3%), and atypical mycobacterium (n = 3, 1.3%). Of note, most patients (n = 231, 96.7%) received BCG vaccination at birth before diagnosis. The lowest reported infection etiology was protozoal agents (n = 5, 2.2%). In regard to the frequency of infectious etiology among patients with infections (n = 219), approximately half (n = 106, 48.4%) had up to two etiologies, a third (n = 64, 29.2%) had three etiologies, and a fifth have four or more etiologies (n = 49, 22.3%). The most commonly reported infection site was the respiratory tract (41.1%), followed by gastrointestinal (12.2%), cutaneous (8.5%), bacteremia and septicemia (8.4%), and other infections. The frequency of clinical presentations is grouped under infections, and the involved sites are illustrated in Figure 1.

#### Immunodysregulation

Immunodysregulatory manifestations were prominent in 77 patients (32.2%), among whom 27 patients (35%) died and 5 patients received hematopoietic stem cell transplantation (HSCT), as it was clinically indicated for their phenotype and

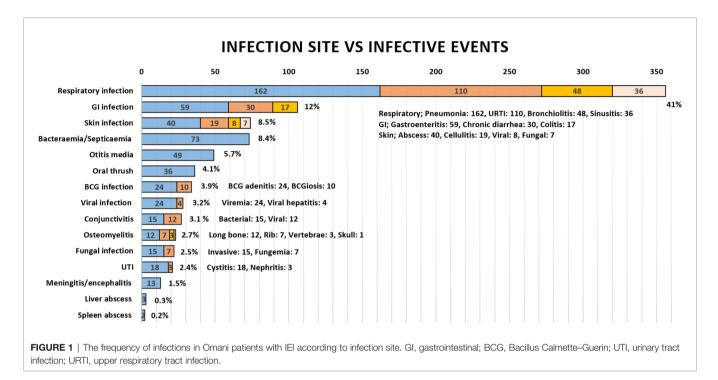
genotype (DCLRE1C, RAB27A, LYST, LRBA, and XIAP). The mean and median age of onset of immune dysregulation was 81 and 25 (range: 1-480) months, respectively. The mean and median diagnostic delay in patients with immunodysregulatory manifestations was 50.8 and 19 months, respectively. Thirty-two patients were categorized as IEI with immunodysregulation (13.4%) according to IUIS classification, among whom the genotype of 21 patients (8.8%) was identified. The recorded immunodysregulatory manifestations included Omenn's syndrome, recurrent oral ulcers, autoimmune cytopenia, lymphoproliferation, autoimmune enteropathy, autoimmune thyroid disease, autoimmune nephropathy, diabetes mellitus type 1, autoimmune arthritis, systemic lupus erythematosus, hemophagocytic lymphohistiocytosis, interstitial lung disease, autoimmune eye disease, and others. The features of the genotype, phenotype, and outcomes of patients with immune dysregulation are detailed in Table 3. Patients with non-infective lymphoproliferation were found to have splenomegaly (n = 32, 13.4%), hepatomegaly (n = 29, 12.1%), generalized (n = 25, 10.5%), and localized lymphadenopathy (n = 13, 5.4%).

#### Malignancy

The mean and median age of malignancy episode onset was 54 and 36 months, respectively (range: 12–114). A malignant process was reported as Hodgkin's lymphoma (n = 3, 1.3%), non-Hodgkin's lymphoma (n = 2, 0.8%).

Age in years Onset		Diagnosis							Total	%
	0–2	3–5	6–10	11–15	16–20	21–30	31–40	>40		
0–2	136	18	23	7	2		1		187	78.2
3–5		5	9	2		2			18	7.8
6–10			2	2	2	1			7	3.0
11–15				2	4	1	1		8	3.4
16–20					2	4	1		7	3.0
21–30						5	1		6	2.6
31–40							5	1	6	2.6
Total	136	23	34	13	10	13	9	1	239	
%	56.9	9.6	14.2	5.6	4.3	5.6	3.9	0.4		100

IEI, Inborn Errors of Immunity.



#### Immunological Evaluation

In more than a third of the patients, the basic immune workup revealed T-cell lymphopenia (n = 88, 37.9%) and B-cell lymphopenia (n = 70, 30.1%). Other observed cell line abnormalities excluding autoimmune cytopenia included anemia (n = 70, 30.1%), neutropenia (n = 45, 19.4%), thrombocytopenia (n = 34, 14.7%), and eosinophilia (n = 5, 2.2%). Various serum immunoglobulin abnormalities were detected including hypogammaglobulinemia (n = 55, 23.7%), hypergammaglobulinemia (n = 30, 12.9%), hyper-IgE (n = 28, 12.1%), dysgammaglobulinemia (n = 26, 11.2%), agammaglobulinemia (n = 18, 7.8%), specific antibody deficiency (n = 7, 3%), IgG subclass deficiency (n = 6, 2.6%), IgA deficiency (n = 2, 0.9%), and hyper-IgM (n = 2, 0.9%). Other reported immunological findings were abnormal DHR123 assay (n = 33, 14.2%), abnormal complement number and function assay (n = 6, 2.6%), and abnormal expression of CD11/CD18 on flow cytometry (n = 1, 0.4%).

### Genotype

Genetic diagnosis was confirmed in 120 patients (50%), with a mean and median age of 59 and 21 months, respectively (range: 0.5-492). However, the median age (in months) of a delay in obtaining a genotype was 69 for class VI, 26.5 for class V, 21.5 for class III, 14 for class IV, 13.5 for class II, and 6 for class I. Homozygosity was paramount, as 90% of all genotypes were autosomal recessive in inheritance (n = 108). In addition to the known mutations associated with the described groups of IEI, we reported three mutations in genes described to cause IEI that are not yet classified into IUIS [LIFR (16), DIAPH1 (17), ZNFX1 (18)]. Additionally, there were two homozygous variants [LAT2 (19) and EBF3

(20)] in genes implicated in immune function in mice that require further immunological functional studies to support a disease phenotype–genotype correlation in humans (**Table 4**). The modalities used for confirming the molecular diagnosis were whole-exome sequencing and next-generation sequencing (n = 70), Sanger sequencing as targeted mutation analysis (n = 38), and FISH and microarray (n = 12). We identified the genotype using a commercial lab (n = 92, 38.5%), the NGC in Oman (n = 20, 8.4%), and through external expert research laboratories (n = 8, 3.3%). The percentage of familial cases among IUIS classes was 67.6% for class V, 61.8% for class I, 46% for class II, 33.3% for class IV, 16.7% for class VI, and 7.5% for class III. No genetic diagnosis was obtained after a patient's death.

### Long-Term Events and Outcome

One hundred thirty-one (54.8%) patients failed to gain adequate weight during their early life. Chronic lung disease constituted a major complication of IEI. Bronchiectasis (n = 62, 25.9%), bronchial asthma (n = 27, 11.3%), and interstitial lung disease (ILD; n = 12, 5%) were the most commonly reported lung complications. End-organ damage (n = 54, 22.6%) was recorded for the brain (n = 14, 5.9%), hearing (n = 12, 5%), liver (n = 8, 3.3%), bone marrow (n = 6, 2.5%), kidney (n = 6, 2.5%), skin (n = 4, 1.5%), and eye (n = 4, 1.5%). In comparison to the overall median age of diagnostic delay (15 months), further delay was noted for patients with the following: bronchiectasis, 60 (2-453); combined endorgan damage, 32.5 (1–204); and bronchial asthma, 28.5 (1–396); and a lesser delay was observed for patients with ILD, 8.5 (2-84) months. Long-term enteropathy (n = 23, 9.6%) was noted as one of the infectious and non-infections complications that contributed to morbidity.

TABLE 3 | Summary describes the immunodysregulatory manifestations of patients with IEI according to IUIS category, genotype, phenotype, and outcome.

Classification	Gene	Immunodysregulation type	Median (months)	Outcome
Immunodeficiencies affecting cellular and	JAK3 (2)	Omenn's syndrome	Immunodysregulation onset: 8 Diagnostic delay: 3.5	Died (2)
humoral immunity (la)	RAG1 (2)	Omenn's syndrome	Immunodysregulation onset: 0.25 Diagnostic delay: 1.5	Died (2)
	CD3E (1)	Omenn's syndrome	Immunodysregulation onset: 2.5 Diagnostic delay: 0.5	Died (1)
	DCLRE1C (1)	Omenn's syndrome	Immunodysregulation onset: 2 Diagnostic delay: 1	Alive (1) HSCT (1)
	NA (1)	Omenn's syndrome	Immunodysregulation onset: 6 Diagnostic delay: 4	Died (1)
Immunodeficiencies affecting cellular and	STK4 (2)	Lymphoproliferation. Autoimmune eye disease. Atopic dermatitis.	Immunodysregulation onset: 78 Diagnostic delay: 99	Alive (2)
humoral immunity (lb)	CD40LG (1)	Recurrent oral ulcers. Autoimmune enteropathy.	Immunodysregulation onset: 16 Diagnostic delay: 1	Alive (1)
Combined immunodeficiencies (II)	TTC7A (2)	Autoimmune enteropathy	Immunodysregulation onset: 1 Diagnostic delay: 3	Died (2)
	CHD7 (2)	Autoimmune thyroid disease. Autoimmune nephropathy. CNS vasculitis.	Immunodysregulation onset: 73 Diagnostic delay: 25.5	Died (2)
	SPINK5 (3)	Lymphoproliferation. Autoimmune nephropathy. Ichthyosis	Immunodysregulation onset: 1 Diagnostic delay: 4	Alive (1) Died (2)
	NA (4)	Lymphoproliferation. Autoimmune cytopenia. Autoimmune thyroid disease. Hemophagocytic lymphohistocytosis. Autoimmune enteropathy. Atopic dermatitis. Vitiligo	Immunodysregulation onset: 25 Diagnostic delay: 13.5	Alive (3) Died (1)
Predominantly antibody deficiencies (III)	NA (14)	Recurrent oral ulcers. Autoimmune cytopenia. Lymphoproliferation. Autoimmune enteropathy. Autoimmune nephropathy. Autoimmune eye disease. Autoimmune thyroid disease. Diabetes mellitus type 1. Autoimmune encephalitis. Autoimmune arthritis. Systemic lupus erythematosus. Serositis.	Immunodysregulation onset: 178 Diagnostic delay: 48	Alive (12) Died (2)
Diseases of immune dysregulation (IVa)	AP3D1 (4)	Lymphoproliferation	Immunodysregulation onset: 2 Diagnostic delay: 35	Died (3) Alive (1)
-)(	RAB27A (3)	Lymphoproliferation. Autoimmune enteropathy. Autoimmune cytopenia. Hemophagocytic lymphohistocytosis.	Immunodysregulation onset: 36 Diagnostic delay: 60	Alive (1) HSCT (1) Died (2)
	AP3B1 (3)	Lymphoproliferation. Autoimmune eye disease.	Immunodysregulation onset: 14 Diagnostic delay: 9.5	Alive (2) Died (1)
	PRKCD (1)	Nil so far	Diagnostic delay: 22	Alive (1)
	LYST (1)	Lymphoproliferation. Hemophagocytic lymphohistocytosis.	Immunodysregulation onset: 20 Diagnostic delay: 3	HSCT (1) Died (1)
Diseases of immune dysregulation (IVb)	LRBA (5)	Lymphoproliferation. Autoimmune cytopenia. Autoimmune thyroid disease. Diabetes mellitus type 1. Interstitial lung disease. Autoimmune eye disease. Alopecia areata. Atopic dermatitis.	Immunodysregulation onset: 2 Diagnostic delay: 7	Alive (5) HSCT (1)
	XIAP (2)	Lymphoproliferation. Hemophagocytic lymphohistocytosis.	Immunodysregulation onset: 120 Diagnostic delay: 12	Alive (2) HSCT (1)
	IL2RA (1)	Lymphoproliferation. Autoimmune cytopenia. Autoimmune thyroid disease. Diabetes mellitus type 1. Autoimmune hepatitis. Interstitial lung disease.	Immunodysregulation onset: 1 Diagnostic delay: 10	Died (1)
	FOXP3 (1)	Recurrent oral ulcers. Lymphoproliferation. Systemic lupus erythematosus.	Immunodysregulation onset: 180 Diagnostic delay: 96	Alive (1)
Diseases of immune dysregulation (IV)	NA (11)	Recurrent oral ulcers. Autoimmune thyroid disease. Autoimmune cytopenia. Hemophagocytic lymphohistocytosis. Lymphoproliferation. Autoimmune hepatitis. Autoimmune nephropathy. Diabetes mellitus type 1. Autoimmune enteropathy. Autoimmune joint disease. Systemic lupus erythematosus. Alopecia areata. Atopic dermatitis.	Immunodysregulation onset: 17 Diagnostic delay: 6	Alive (9) Died (2)
Congenital functional defects of phagocyte (V)	NCF1 (2)	Recurrent oral ulcers. Lymphoproliferation. Autoimmune enteropathy. Autoimmune eye disease.	Immunodysregulation onset: 16.5	Alive (2)
Defects in intrinsic and innate immunity (VI)	STAT1-GOF (2)	Autoimmune thyroid disease	Diagnostic delay: 48.5 Immunodysregulation onset: 66 Diagnostic delay: 261	Alive (2)
	NA (1)	Autoimmune arthritis	Immunodysregulation onset: 468 Diagnostic delay: 12	Alive (1)
Complement deficiencies (VIII)	NA (1)	Lymphoproliferation. Autoimmune cytopenia. Hemophagocytic. Lymphohistocytosis.	Immunodysregulation onset: 144 Diagnostic delay: 28	Alive (1)
Phenocopies of PID (X)	NA (1), [Good syndrome]	Autoimmune cytopenia.	Immunodysregulation onset: 396 Diagnostic delay: 120	Died (1)

(Continued)

TABLE 3 | Continued

Classification	Gene	Immunodysregulation type	Median (months)	Outcome
Unclassified IEI	ZNFX1 (1)	Recurrent oral ulcers. Autoimmune cytopenia. Hemophagocytic. Lymphohistocytosis.	Immunodysregulation onset: 3 Diagnostic delay: 9	Died (1)
Potential IEI	LAT2 (1)	Autoimmune thyroid disease. Autoimmune nephropathy. Autoimmune eye disease. Autoimmune arthritis. Atopic dermatitis. Ichthyosis.	Immunodysregulation onset: 48 Diagnostic delay: 396	Alive (1)
	EBF3 (1)	Autoimmune enteropathy. Atopic dermatitis.	Immunodysregulation onset: 96 Diagnostic delay: 164	Alive (1)

IEI, Inborn Errors of Immunity; IUIS: International Union of Immunological Societies; JAK3, Janus Tyrosine Kinase 3; RAG1, Recombination Activating Gene 1; CD3E, Cluster of Differentiation 3 Epsilon; DCLRE1C, DNA Cross-Link Repair 1C; NA, Not Available; STK4, Serine/Threonine Kinase 4; CD40LG, Cluster of Differentiation 40 Ligand; TTC7A, Tetratricopeptide Repeat Domain 7A; CHD7, Chromodomain Helicase DNA-binding protein 7; SPINK5, Serine Peptidase Inhibitor Kazal Type 5; AP3D1, Adaptor Related Protein Complex 3 Delta 1; RAB27A, Ras-related protein Rab 27A; AP3B1, Adaptor-related Protein complex 3 Beta 1; PRKCD, Protein Kinase C Delta; LYST, Lysosomal Trafficking regulator; LRBA, Lipopolysaccharide-Responsive and Beige-like Anchor; XIAP, X-linked Inhibitor of Apoptosis; IL2RA, Interleukin-2 Receptor subunit Alpha; FOXP3, Forkhead Box P3; NCF1, Neutrophil Cytosolic Factor 1; STAT1, Signal Transducer and Activator of Transcription 1; GOF, Gain Of Function; ZNFX1, Zinc Finger NFX1-type containing 1; LAT2, L-type Amino acid Transporter 2; EBF3, Early B-cell Factor 3. Unclassified IEI: a genetic variant that cause a novel IEI that is not yet classified into the current categories of IUIS. Potential IEI: a genetic variant with possible causality to IEI, and yet to be studied and confirmed on Humans.

Management embraced frequent interaction with patients and their families. Extensive counseling was provided on nutrition, infection prevention, recognition of warning signs, adherence to action plans, and disease-specific treatment options. Proper assessment and follow-up of an individual clinical course for each patient were implemented. Most patients were evaluated by multidisciplinary teams for disease monitoring, complication prevention, and management. Management strategies included prophylactic antimicrobials (n = 142, 59.4%), intravenous immunoglobulin (IVIG) reconstitution therapy (n = 98, 41%), HSCT (n = 24, 10%), targeted immune therapy (n = 14, 5.9%), and biological therapy (n = 9, 3.8%). One patient with complete 22q11.2 deletion syndrome received thymic transplantation. At the time of the study, 92 patients (38.5%) were alive and well, and 66 patients (27.6%) were alive but with complications and morbidity. Seventy-six patients (31.8%) had been admitted to the ICU at least once, and 21 patients defaulted (8.8%). The management of immune dysregulation involved high-dose immunoglobulin therapy and topical and/or systemic immunosuppressive therapy with corticosteroids, interleukin-1, and interleukin-6 receptor antagonists, calcineurin inhibitors, mammalian Target of Rapamycin (mTOR) inhibitors, Janus kinase (JAK) inhibitors, and anti-CD20 monoclonal antibody. All patients with Lipopolysaccharide-Responsive Beige-Like Anchor Protein (LRBA) deficiency received abatacept.

The mean and median age of transplant was 32 and 19 months, respectively (range: 5–144). Among the 24 patients who received HSCT, 14 (58.3%) were reported to be in remission, 3 (12.5%) demonstrated rejection, and 2 (8.3%) had a relapse of original disease. Five patients are currently undergoing HSCT, with no conclusion of outcome at the time of this report. The donor source was a matched sibling in 12 patients (50%), haploidentical in 8 patients (33.3%), and a matched family donor in 4 patients (16.7%). More than half of the patients who received HSCT (n = 14/24, 58.3%) were transplanted in centers abroad, while 10 patients (41.7%) received HSCT in Oman.

The overall mortality rate was 25.1% (n = 60), with a mean and median age of 60 and 14 months, respectively (range: 1–408). The survival curve for patients with IEI is illustrated in **Figure 2**. Immunodeficiencies affecting cellular and humoral immunity (I)

had the worst probability of survival at 44%, followed by syndromic CID (II) and immune dysregulation (IV) at approximately 68%. The causes of death included severe infection (n = 51, 21.3%), endorgan disease (n = 27, 11.3%), immunodysregulation complications (n = 13, 5.4%), do-not-resuscitate (DNR) order (n = 12, 5%), HSCT-related (n = 6, 2.5%), malignancy (n = 3, 1.2%), and others (n = 2, 0.8%). The bulk of the mortality was reported in class I (n = 20, 58.8%), followed by class II (n = 15, 30%), and class IV (n = 10, 37%). The mortality in class I was due to severe infection in 95%, uncontrolled immune dysregulation in 30%, end-organ damage in 30%, HSCT-related in 15%, and DNR order in 15%. The mortality in class II was due to severe infection in 93%, end-organ damage in 53%, HSCT-related in 40%, uncontrolled immune dysregulation in 26.7%, and DNR order in 6.7%. The mortality in class IV was due to uncontrolled immune dysregulation in 100%, severe infection in 60%, end-organ damage in 50%, HSCT-related in 10%, and DNR order in 10%.

#### DISCUSSION

The IUIS PID classification committee classified IEI into 10 major groups based on clinical and laboratory findings along with molecular diagnosis. The current study is the first to characterize 239 pediatric and adult patients with IEI in Oman and provides upto-date detailed clinical and genetic data. The present results support a higher prevalence and incidence of IEI in such highly consanguineous community and poor survival. Early prevention and early management through screening programs for the classical T- and B-cell deficiencies as well as incorporating immunodysregulation as a warning sign for IEI are considered to represent effective approaches to improve survival.

In this study, we analyzed the demographic, clinical, and molecular data and outcomes of 239 patients diagnosed with IEI at the Royal Hospital. In line with the previously reported high prevalence of consanguineous marriage rate in Oman (49%) (21), greater than two-thirds of the cohort had a history of consanguinity. Therefore, one would expect to see more autosomal recessive and almost equal female-to-male distribution. However, this cohort had slightly more boys to girls (male/female: 58.1% vs. 41.9%), which is similar to the ESID

ADA         c.815GS-A         p.(Tmp2/2)         9         Stop-gain         Homozygous         Novel, not report           ADA         c.910dal         p.(Gly/216Arg)         7         Missense         Homozygous         Novel, not report           JAK3         c.1613GS-A         p.(Gly/330Asp)         12         Missense         Homozygous         Novel, not report           JAK3         c.1613GS-A         p.(Arg396His)         12         Missense         Homozygous         Novel, not report           PAG         c.1187GS-A         p.(Arg396His)         2         Missense         Homozygous         VC/00001314.6           PAG1         c.1187GS-A         p.(Arg396His)         2         Missense         Homozygous         VC/00001314.6           PCLETC         c.404GS-A         p.(Arg396His)         6         Missense         Homozygous         Novel, not report           PCLETC         c.404GS-A         p.(Arg396His)         6         Missense         Homozygous         Novel, not report           PCLETC         c.404GS-A         p.(Arg396His)         6         missense         Homozygous         Novel, not report           PCLETC         c.304GS-A         p.(Arg1758r)         6         Subsititition         Homozygous         N	IUIS class	Gene	Mutation	Protein effect	Exon	Туре	Zygosity	Novelty
ADA         c.815G>A         p.(JL)(2)         0         Storg-gain         Homozypus         Noel, not report ADA           ADA         c.645G>A         p.(JQ)(2)(PArg)         7         Misense         Homozypus         Noel, not report ADA           JARG         c.1613G>A         p.(JQ)(388Ag)         1.2         Misense         Homozypus         Noel, not report Participania           JARG         c.2400-1G>A, c.1845D>T         p./49(598Ag)         1.2         Misense         Homozypus         Noel, not report Participania           PAG1         c.118/G>A         p./49(598Ag)         1.2         Misense         Homozypus         Noel, not report Participania           PAG1         c.2494G>C         p./49(595Hb)         2         Misense         Homozypus         Noel, not report Participania           DCLEEIC         c.4045A         p./49(595Hb)         6         Fermeritit         Homozypus         Noel, not report Participania           DCLEEIC         c.4045A         p./49(595Hb)         6         missense         Homozypus         Noel, not report Participania           DCLEEIC         c.4045A         p./49(285Gh)         6         missense         Homozypus         Noel, not report Participania           DCLEEIC         c.4045A         p./49(285Gh)	la	IL7R	c.616c>T	p.(Arg206)	5	Nonsense	Homozygous	Novel, not reported
ADA         c.81(Ool         p.1.4(s)(2)(TrpRr)         1.0         FrameSprit         Homozgous         Novel, not report           JAG         c.4483-A         p.1G/92(16Arg)         7         Missense         Homozgous         Novel, not report           JAG         c.4483-A         c.1810S-A         p.1G/92(36Ke)         12         Missense         Homozgous         Novel, not report           JAG         c.4485-A         c.1875-A         p.1G/92(36Ke)         12         Missense         Homozgous         Pathogonic           JAG         c.1187G-A         p.1Arg39Ha         2         Missense         Homozgous         VCX00001348           DCLREIC         c.4463-A         p.1Arg39Ha         6         Missense         Homozgous         Novel, not report           DCLREIC         c.4463-A         p.1Arg317Ha         6         Missense         Homozgous         Novel, not report           Missense         Locadio-A         p.1Arg317Ha         6         Missense         Homozgous         Novel, not report           L2281         c.4516-A         p.1Arg317Ha         6         missense         Homozgous         Novel, not report           L2876         c.9516-A         p.1Arg324528H1         6         Missense         Homo		ADA	c.815G>A	p.(Trp272)	9	Stop-gain	Homozygous	Novel, not reported
ADA         0.64/GS-A         p.(8/92164rg)         7         Missme         Homogqua         VCV0000188, Pathoganic           JAK3         c.1613G-A         p.(4/93384gp)         12         Missmes         Homogqua         Nowl, not report (VCV000188, Pathoganic           PAG1         c.1187G-A         p.(4/9398/hg)         2         Missmes         Homogqua         VCV0000188, Pathoganic           PAG1         c.1187G-A         p.(4/9398/hg)         2         Missmes         Homogqua         VCV0000188, Pathoganic           DCLEFED         c.40465-A         p.(4/9378/hg)         6         Missmes         Homogqua         VCV00001788, Pathoganic           DCLEFED         c.40465-A         p.(4/9378/hg)         6         Missmes         Homogqua         VCV00001788, Pathoganic           DCLEFED         c.40465-A         p.(4/9378/hg)         6         Missmes         Homogqua         VCV00001788, Pathoganic           DCLEFED         c.40465-A         p.(4/9378/hg)         6         Missmes         Homogqua         VCV00001788, Nowl, not report           DCLEFED         c.43465-C         p.(4/9378/hg)         1         Missmes         Homogqua         VCV0000768, Nowl, not report           DCLAFED         c.434665-A         p.(4/93149/hg)         1		ADA	c.910del	p.(Leu304Trpfs7)	10	Frameshift		Novel, not reported
JAK3         c.16130-A         p.(AyG83Aspi)         12         Misserse         Homospoul         Novel, for teport           JAK3         c.2400-1GsA, c.1646CST         p.(AyG940)         16         Novel, ent report         Heterusgous         pathogenic           FAG1         c.1167GsA         p.(Ayg358His)         2         Misserse         Homospous         Pathogenic           FAG1         c.22024G-C         p.(Ayg175Rv)         2         Misserse         Homospous         Pathogenic           DCLFF10         c.404G5-A         p.(Ayg175Rv)         2         Misserse         Homospous         Novel, not report           ME10         c.501-GsA         p.(Ayg175Rv)         6         Firsmethit         Homospous         Novel, not report           ME10         c.501-GsA         p.(Ayg175Rv)         6         Risserse         Homospous         Novel, not report           ME10         c.501-GSA         p.(Ayg175Rv)         1         Misserse         Homospous         Novel, not report           ME30         CORCK8         c.531-240A-C         p.(Ayg145Gr)         1         Misserse         Homospous         Novel, not report           ME30         CORCK8         c.531-240A-C         p.(Ayg145Gr)         7         Misserse								VCV000001968,
JAK3         c.2460+1G>A, c.1645C>T         p.(Arg549)         18         Nomenne         Compound Hetrozygous         VCX001008636, pathogenic           RAG1         c.1187G>A         p.(Arg530Ha)         2         Maserse         Homozygous         VCX001008636, pathogenic           RAG1         c.2224G>C         p.(Arg530Ha)         2         Maserse         Homozygous         VCX000001346, pathogenic           DCLEFIC         c.444G>A         p.(Arg757br)         2         Maserse         Homozygous         Novel, not report Pathogenic           DCLEFIC         c.444G>A         p.(Arg757br)         6         Maserse         Homozygous         Novel, not report Pathogenic           DCLEFIC         c.444G>A         p.(Arg282Ghi)         6         Maserse         Homozygous         Novel, not report Pathogenic           MB         DOCK8         c.5240A>C         p.(Arg282Ghi)         1         Maserse         Homozygous         Novel, not report Pathogenic           C1TA         c.1546G>A         p.(Arg140Ghi)         7         Maserse         Homozygous         Novel, not report Pathogenic           C1TA         c.1546G>A         p.(Arg140Ghi)         7         Maserse         Homozygous         Novel, not report Pathogenic           C1TA         c.164G>A		JAK3	c.1613G>A	p.(Gly538Asp)	12	Missense	Homozygous	Novel, not reported
Peteriozygous         Peteriozygous         petrogenics (VCV000001324)           RAG1         c.1187Ga-A         p./Arg309His)         2         Missense         Hornoxygous         VCV00001314           RAG1         c.2187Ga         p./Arg375Pro)         2         Missense         Hornoxygous         VCV00001314           DCLRETC         c.404GS-A         p./Arg117Sm)         6         Frameshift         Hornoxygous         Nowl, not report           NHSU         c.539-1GS-A         p./Arg117Sm)         6         Frameshift         Hornoxygous         Nowl, not report           NHSU         c.539-1GS-A         p./Arg117Sm)         6         Frameshift         Hornoxygous         Nowl, not report           LE2RG         c.551/GS-A         p./Arg117Sm)         6         missense         Hornoxygous         Nowl, not report           CITA         c.321/F3-G         p./Arg140Gin         1         Missense         Hornoxygous         Nowl, not report           GUTA         c.321/F3-G         p./Arg140Gin         7         Missense         Hornoxygous         Nowl, not report           GUTA         c.321/F3-G         p./Arg140Gin         7         Missense         Hornoxygous         Nowl, not report           GUTA         c.321/F3-G </td <td></td> <td></td> <td>c.2490+1G&gt;A, c.1645C&gt;T</td> <td></td> <td></td> <td>Nonsense</td> <td></td> <td>VCV001066836, likely</td>			c.2490+1G>A, c.1645C>T			Nonsense		VCV001066836, likely
FAG1         c.1187G>A         p.(Arg3502His)         2         Missense         Homozypus         Verub001314C           RAG1         c.2924G>C         p.(Arg975Pro)         2         Missense         Homozypus         Verub001314C           DCLEFIC         c.404G>A         p.(Arg975Pro)         2         Missense         Homozypus         Novel, not report           DCLEFIC         c.404G>A         p.(Arg1728)         6         Frameshitt         Homozypus         Novel, not report           NHEJ1         c.530-1G>A         p.(Arg255Gin)         6         missense         Hemizypus         VCV00001034G           LIZRG         c.854Q-GA         p.(Myr178e)         1         Missense         Homozypus         Novel, not report           GDCK8         c.531464amCT         p.(Myr1711h)         17         Missense         Homozypus         Novel, not report           GDTA         c.16313464imSCT         p.(Myr142Gr)         1         Missense         Homozypus         Novel, not report           GDTA         c.1763(03766-         234 bp Deletion         11         Frameshitt         Homozypus         Novel, not report           GDTA         c.1784(040771)         p.(Myr142161)         1         Subestituion         Homozypus <td< td=""><td></td><td></td><td>·</td><td></td><td></td><td></td><td>,</td><td>pathogenic. VCV000803542,</td></td<>			·				,	pathogenic. VCV000803542,
RAG1         c.28243-C         p.(Arg375Pro)         2         Mesense         Homozygous         pathogenic           DCLFETC         c.4043-A         p.(Ary1350k)         6         Mesense         Homozygous         Novel, not reportinit           CD2E         c.351-A-C         p.(Ary1173er)         6         Frameshitt         Homozygous         Novel, not reportinit           NLPEL         c.351-A-C         p.(Ary2255Gr)         6         Frameshitt         Homozygous         Novel, not reportinit           NLPEL         c.353-140-C         p.(Ary2255Gr)         1         Mesense         Homozygous         Novel, not reportinit           CITA         c.351-240A-C         p.(Ary12457)         2         Missense         Homozygous         Novel, not reportinit           CITA         c.351-240A-C         p.(Ary1349Cin)         7         Missense         Homozygous         Novel, not reportinit           CITA         c.351-240A-C         p.(Ary149Cin)         7         Missense         Homozygous         Novel, not reportinit           CITA         c.321-250A         p.(Ary149Cin)         7         Missense         Homozygous         Novel, not reportinit           CITA         c.321-25C         p.(Ary149Cin)         7         Nissense		RAG1	c.1187G>A	p.(Arg396His)	2	Missense	Homozygous	VCV000013146,
CO2E         c.351A-C         p.(Arg117Ser)         6         Frameshift         Homoxygous         Novel, not reportsite           IL2RG         c.350-1G-A         Intronic acceptor spile         5         Substitution         Homoxygous         Novel, not reportsite           IL2RG         c.354-GAA         p.(Arg285Grip)         6         missense         Hemixygous         VCV000010026, Pathoganis           ODCK8         c.318_3184/delinsCT         p.(Lys43Arg)         1         Missense         Homoxygous         Novel, not report           CITA         c.183_184/delinsCT         p.(Lys43Arg)         1         Missense         Homoxygous         Novel, not report           CITA         c.183_184/delinsCT         p.(Lys42)         7         Missense         Homoxygous         Novel, not report           CITA         c.116.1090/7590-         24 Missense         Homoxygous         Novel, not report           MAD         c.796-3c-G         Intronic         8         Substitution         Hemixygous         Novel, not report           MAPR14         c.344-5C         p.(Arg149Gin)         7         Missense         Homoxygous         Novel, not report           MaProxini         c.334-5T         p.(Arg2851120         11         Missense         Homoxygous <td></td> <td>RAG1</td> <td>c.2924G&gt;C</td> <td>p.(Arg975Pro)</td> <td>2</td> <td>Missense</td> <td>Homozygous</td> <td>VCV000013146,</td>		RAG1	c.2924G>C	p.(Arg975Pro)	2	Missense	Homozygous	VCV000013146,
NHEUT         c.530-1G>A         Infrom acceptor spice bits         5         Substitution         Homozygous         Novel, not report Participant           IL2RG         c.854G>A         p.(Arg285Gin)         6         missense         Hemizygous         VCV000010026, Participant           ID         DOCK8         c.53+240A>C         p.(Lys452)         2         Missense         Homozygous         Novel, not report VCV0000780001           CITA         c.183,1840alinsGT         p.(Lys452)         2         Missense         Homozygous         Novel, not report VCV00007816,           CITA         c.183,1540alinsGT         p.(Arg149Gin)         7         Missense         Homozygous         Novel, not report VCV0000784,           RFXA         c.4465A         p.(Arg149Gin)         7         Missense         Homozygous         Novel, not report Participant           MSN         c.796-3c>G         infronic         8         Substitution         Hemizygous         Novel, not report Participant           MSN         c.796-3c>G         p.(Pro56ELua)         1         Missense         Homozygous         Novel, not report Participant           MSN         c.796-3c>G         p.(Arg149Gin)         1         Missense         Homozygous         Novel, not report Participant           CD40		DCLRE1C	c. 404G>A	p.(Gly135Glu)	6	Missense	Homozygous	Novel, not reported
iste         iste         iste           IL2RG         c.854G>A         p.(Årg285Gin)         6         missense         Hemizygous         VCV000010026, Pathogenic           Ib         DOCK8         c.53+240A>C         p.(Lys62)         1         Missense         Homozygous         VCV000010026, Pathogenic           CIITA         c.3212T>C         p.(Met1071Thh)         17         Missense         Homozygous         Novel, not report           CIITA         c.3212T>C         p.(Met1071Thh)         17         Missense         Homozygous         Novel, not report           O0078300al         p.(Arg149Gin)         7         Missense         Homozygous         Novel, not report           100078300al         p.(Arg149Gin)         7         Missense         Homozygous         Novel, not report           MAP3K14         c.1694 G>T         p.(Ry656Lu)         11         Missense         Homozygous         Novel, not report           CD40LG         c.360A>G         p.(Ry169Cs)         5         Missense         Hemizygous         Novel, not report           CD40LG         c.360A>G         p.(Ry119Cs/se)         5         Missense         Hemizygous         Novel, not report           MAP3K14         c.1894 G>T         p.(Met12u		CD3E	c.351A>C	p.(Arg117Ser)	6	Frameshift	Homozygous	Novel, not reported
Ib         DCCK8         c.534-240A-C         p.(Lys43Arg)         1         Missense         Homozygous         Novel, not report           GITA         c.132_18/delinsCT         p.(Lys62)         2         Missense         Homozygous         Novel, not report           GITA         c.32127-C         p.(Mat1071Th)         17         Missense         Homozygous         Novel, not report           GITA         c.32127-C         p.(Arg149Gin)         7         Missense         Homozygous         VCV000007F48,           PRXS         c.446GSA         p.(Arg149Gin)         7         Missense         Homozygous         VCV00007F48,           PRXS         c.446GSA         p.(Arg149Gin)         7         Missense         Homozygous         Novel, not report           MSN         c.796-36-G         Intronic         8         SUbstitution         Hemizygous         Novel, not report           CD40LG         c.4300-T         p.(Gly144)         5         Norsense         Hemizygous         Novel, not report           CD40LG         c.4300-T         p.(Gly144)         5         Norsense         Hemizygous         Novel, not report           MATM         c.748-1dup         p.(Am2494Ly86)         50         Frameshift         Homozygous		NHEJ1	c.530-1G>A		5	Substitution	Homozygous	Novel, not reported
CIITA         c.181.84delineCT         p.LysE2         2         Missense         Homozygous         Novel, not report           CIITA         c.3212T>C         p.Met107Tht)         17         Missense         Homozygous         Novel, not report           CIITA         c.3212T>C         p.Met107Tht)         17         Missense         Homozygous         Novel, not report           CIITA         c.3212T>C         p.(Arg149Gin)         7         Missense         Homozygous         VCV000007648,           FRX6         c.44663-A         p.(Arg149Gin)         7         Missense         Homozygous         VCV00007648,           MSN         c.796-3c>G         Intronic         8         Substitution         Hemizygous         Novel, not report           CD40LG         c.6306-5         p.(Tyr199Cys)         5         Missense         Homozygous         Novel, not report           CD40LG         c.1405A-3         p.(Tyr199Cys)         5         Missense         Homozygous         Novel, not report           MI#         c.1410_u         1         Splice         Homozygous         Novel, not report           MI#         c.142149         p.(Re12934Lysf85)         50         Frameshift         Homozygous         Novel, not report <t< td=""><td></td><td>IL2RG</td><td>c.854G&gt;A</td><td>p.(Arg285Gln)</td><td>6</td><td>missense</td><td>Hemizygous</td><td>,</td></t<>		IL2RG	c.854G>A	p.(Arg285Gln)	6	missense	Hemizygous	,
CIITA         c.3212T-C         p.Met1OrTTm/n         17         Mssense         Homozygous         Novel, not report           CIITA         cd+16:10907596- 10907830del         234 bp Deletion         11         Frameshitt         Homozygous         VCV00007643; VCV000174711, Pathogenic           RFXANK         c.634CS-T         p./Ag212Tef)         8         Nonsense         Homozygous         VCV000174711, Pathogenic           MSN         c.796-3c>G         Intronic         8         Substitution         Hemizygous         Novel, not report           CD40LG         c.306A-ST         p./(GN144)         5         Nonsense         Homozygous         Novel, not report           CD40LG         c.506A-G         p.(Tyr16SOys)         5         Nonsense         Hemizygous         Novel, not report           CD40LG         c.506A-G         p.(Tyr16SOys)         5         Nonsense         Hemizygous         Novel, not report           CD40LG         c.306A-G         p./(He1003Set16)         2         Frameshift         Homozygous         Novel, not report           Ifb         C.110-2A-G         p.(Leu2805Val)         38         Mssense         Homozygous         Novel, not report           Ifb         c.550+1C>T         Donor spice site         Intron	lb	DOCK8		p.(Lys43Arg)		Missense	Homozygous	VCV000676901,
CIITA         christion         234 bp Deletion         11         Frameshitt         Homozygous         Novel, not report           RFX5         c.446G-A         p.(Arg149Cin)         7         Missense         Homozygous         VCV000007648, VCV001074711, Pathoogenic           MSN         c.796-3c-G         Intronic         8         Substitution         Hemizygous         Novel, not report           MAP8rt.4         c.1694 C-ST         p.(Pap565Lus)         11         Missense         Hemizygous         Novel, not report           CD40LG         c.430G-ST         p.(Gly144)         5         Nonsense         Hemizygous         Novel, not report           CD40LG         c.430G-ST         p.(Gly144)         5         Nonsense         Hemizygous         Novel, not report           CH01LG         c.430G-ST         p.(Gly144)         5         Nonsense         Hemizygous         Novel, not report           CH01LG         c.4161dup         p.(Ara2494Lysts6)         50         Frameshift         Homozygous         Novel, not report           MIM         c.2132T-G         p.(Ide0385dr516)         22         Frameshift         Homozygous         Novel, not report           MIM         c.32132T-G         p.(Ide1385dr516)         2         Frameshift <td></td> <td>CIITA</td> <td>c.183_184delinsCT</td> <td>p.(Lys62)</td> <td>2</td> <td>Missense</td> <td>Homozygous</td> <td>Novel, not reported</td>		CIITA	c.183_184delinsCT	p.(Lys62)	2	Missense	Homozygous	Novel, not reported
INDUCTSSCIER         PArg149/GIN         7         Missense         Homozygous         VCV00000748, VCV0001074711, Pathogenic           MSN         c.796-3c-G         Intronic         8         Substitution         Hemizygous         Novel, not report Pathogenic           MAP3K14         c.1694 C-T         p./Pro566Lsu)         11         Missense         Homozygous         Novel, not report Pathogenic           C040LG         c.430C>-T         p./Gly144)         5         Nonsense         Hemizygous         Novel, not report Pathogenic           C040LG         c.506A-G         p./Tyr1950ys)         5         Missense         Hemizygous         Novel, not report Pathogenic           STK4         C.1A-T         p./Met1Leu         1         Splice         Homozygous         Novel, not report Pathogenic           ATM         c.7327delA         p./Ide1249Lys56)         50         Frameshift         Homozygous         Novel, not report Homozygous         Novel, not report Pathogenic           IIIb         STAT3         c.1110-2A-G         p./Ag1322Trp)         12         Substitution         Hetrozygous         Novel, not report Pathogenic           STAT3         c.150+1C-T         Donor splice site         Intron         Splicing         Homozygous         Novel, not report Pathogenic		CIITA	c.3212T>C	p.(Met1071Thr)	17	Missense	Homozygous	Novel, not reported
RFXANK         c.634C>T         p.(Arg212Ter)         8         Nonsense         Homozygous         VCV001074711, Pathogenic           MISN         c.796-3c>G         Intronic         8         Substitution         Hemizygous         Novel, not report           MAP3K14         c.1694 C>T         p.(Pro565Leu)         11         Missense         Homozygous         Novel, not report           CD40LG         c.306A>G         p.(Fyr169Cys)         5         Missense         Hemizygous         Novel, not report           IIa         CT41         p.Met1Leu         1         Splice         Homozygous         Novel, not report           IIa         C.1A>T         p.Met1Leu         1         Splice         Homozygous         Novel, not report           IIa         C.1A>T         p.Met1Leu         1         Splice         Homozygous         Novel, not report           IIa         C.1A>T         p.(Her0386716)         22         Frameshit         Homozygous         Novel, not report           IIa         StaTa3         c.510+1C>T         p.(Arg382Trp)         12         Substitution         Heterozygous         Novel, not report           STAT3         c.110+2A>G         p.(Arg853)         27         Stop-gain         Homozygous		CIITA		234 bp Deletion	11	Frameshift	Homozygous	Novel, not reported
MSN     c.796-3c>G     Intronic     8     Substitution     Hemizgous     Novel, not report       CD40LG     c.430Gs-T     p.(Pro565Leu)     11     Missense     Hemizgous     Novel, not report       CD40LG     c.430Gs-T     p.(By(144)     5     Nonsense     Hemizgous     Novel, not report       CD40LG     c.430Gs-T     p.(By(144)     5     Nonsense     Hemizgous     Novel, not report       CD40LG     c.430Gs-T     p.(By(144)     5     Nonsense     Hemizgous     Novel, not report       ATM     c.7481dup     p.(Asr1244Lysts6)     50     Frameshift     Homozygous     Novel, not report       ATM     c.3277delA     p.(Ile11093Serfs16)     22     Frameshift     Homozygous     Novel, not report       UIb     STAT3     c.1110-2A>G     p.(Arg382Trp)     12     Substitution     Heterozygous     Novel, not report       SPINK5     c.1887+1G>A     hg19:Chr5:147492498     Intron     Splicing     Homozygous     Novel, not report       SPINK5     c.1887+1G>A     hg19:Chr5:147492498     1     Frameshift     Homozygous     Novel, not report       SPINK5     c.1887+1G>A     hg19:Chr5:147492498     1     Frameshift     Homozygous     Novel, not report       TTC7A     c.122del </td <td></td> <td>RFX5</td> <td>c.446G&gt;A</td> <td>p.(Arg149Gln)</td> <td>7</td> <td>Missense</td> <td>Homozygous</td> <td>VCV000007648, VUS</td>		RFX5	c.446G>A	p.(Arg149Gln)	7	Missense	Homozygous	VCV000007648, VUS
MAP3K14c.1694 C.5Tp.(Pro565Leu)11MissenseHomozygousNovel, not reportCD40LGc.303Q-5Tp.(Gy)144)5NonsenseHemizygousNovel, not reportCD40LGc.506A-Gp.(Tyr169Cys)5MissenseHemizygousNovel, not reportTG4ATMc.7481dupp.(Asr2494Lysfs6)50FrameshiftHomozygousNovel, not reportATMc.3277delAp.(Ile1033Sefs16)22FrameshiftHomozygousNovel, not reportCH07c.8416C-Gp.(Ile206Val)38MissenseHomozygousNovel, not reportMbSTAT3c.2132T>Gp.(Ile206Val)38MissenseHomozygousNovel, not reportSTAT3c.1110-2A>Gp.(Ile206Val)38MissenseHomozygousNovel, not reportSTAT3c.1110-2A>Gp.(Arg382Trp)12SubstitutionHeterozygousNovel, not reportSTAT3c.150+1C>TDonor splice siteIntronSplicingHomozygousNovel, not reportSPINK5c.2557C>Tp.(Arg853)27Stop-gainHomozygousNovel, not report1TC37c.2124lp.(Ile17Tyrfs15)9FrameshiftHomozygousNovel, not report1TBCH1445G>AIntronSplicingHomozygousNovel, not report1TC37c.2124lp.(Ile17Tyrfs15)9FrameshiftHomozygousNovel, not report1TC37c.111-25840380-2NissenseHomozygousNovel, no		RFXANK	c.634C>T	p.(Arg212Ter)		Nonsense		
CD40LGc.430G>Tp.(Gly144)5NonsenseHemizygousNovel, not reportCD40LGc.506A>Gp.(Tyr169Cys)5MissenseHemizygousVCV000191254, pathogenicIIaATMc.7481dupp.(Asr2494Lysfs6)50FrameshiftHomozygousNovel, not reportATMc.3277dalAp.(Ile10935erfs16)50FrameshiftHomozygousNovel, not report(IIbSTAT3c.2132T>Gp.(Ile10935erfs16)22FrameshiftHomozygousNovel, not report(IIbSTAT3c.2132T>Gp.(Ile20806Val)38MissenseHeterozygousNovel, not reportSTAT3c.2132T>Gp.(Arg382Trp)12SubstitutionHeterozygousNovel, not reportSTAT3c.550+1C>Tp.(Arg382Trp)12SubstitutionHeterozygousNovel, not reportSPINK5c.2557C>Tp.(Arg3853)27Stop-gainHomozygousNovel, not reportTTC7Ac.122delp.(Mel41Serfs38)1FrameshiftHomozygousNovel, not reportTTC37c.2114+5G>AIntron20SplicingHomozygousNovel, not reportTTC37c.122delp.(Mel41Serfs38)1FrameshiftHomozygousNovel, not reportTTC37c.124elp.(Mel41Serfs38)1FrameshiftHomozygousNovel, not reportTTC37c.124elp.(Mel41Serfs38)1FrameshiftHomozygousNovel, not reportTTC37c.124elp.(Mel41Serfs			c.796-3c>G	Intronic		Substitution	Hemizygous	Novel, not reported
CD40LGc.506A>Gp.(Tyr169Cys)5MissenseHemizygousVCV000191254, pathogenicIIaATMC.1A>Tp.Met1Leu1SpliceHomozygousNovel, not reportATMc.3277delAp.(Ile1093Ser1s16)22FrameshiftHomozygousNovel, not reportCH07c.8416C>Gp.(Ile20260Val)38MissenseHetrozygousNovel, not report(HbSTAT3c.2132T>Gp.(Ile1200Val)38MissenseHetrozygousNovel, not reportSTAT3c.1110-2A>Gp.(Ile1200Val)38MissenseHetrozygousNovel, not reportSTAT3c.1110-2A>Gp.(Ile71Thr)23MissenseHetrozygousNovel, not reportSTAT3c.550+1C>TDonor splice siteIntronSplicingHetrozygousNovel, not reportSPINK5c.1887+1G>Ahg19:Chr5:147492498IntronSplicingHomozygousNovel, not reportTTG7Ac.122delp.(Met41Serfs38)1FrameshiftHomozygousNovel, not reportTTG7Ac.122delp.(Ile17Tyrfs15)9FrameshiftHemizygousNovel, not reportIIIaETKc.828dupp.(Ile17Tyrfs15)9FrameshiftHemizygousNovel, not reportUT9LYSTChr1:23640380-p.(Ile114Val)1_5MissenseHomozygousNovel, not reportUT9Chr2:32640919p.(Ile114Val)1_5MissenseHomozygousNovel, not reportAB21Chr1:2364038				, ,				Novel, not reported
Bit Note         Strike         C.1A>T         p.Met1Leu         1         Splice         Homozygous         Novel, not report           ATM         c.7481dup         p.(Asn2494Lysfs6)         50         Frameshift         Homozygous         Novel, not report           ATM         c.3277delA         p.(Ile1093Serfs16)         22         Frameshift         Homozygous         Novel, not report           CHD7         c.8416C>G         p.(Ile20280Eval)         38         Missense         Homozygous         VCV0000803390, pathogenic           IIb         STAT3         c.1110-2A>G         p.(Ile711Thr)         23         Missense         Heterozygous         Novel, not report           STAT3         c.1110-2A>G         p.(Arg382Trp)         12         Substitution         Heterozygous         Novel, not report           STAT3         c.550+1C>T         Donor splice site         Intron         Splicing         Heterozygous         Novel, not report           SPINK5         c.1887+1G>A         hg19:Ch5:147492498         Intron         Splicing         Homozygous         Novel, not report           TTC7A         c.122del         p.(Met11Serfs38)         1         Frameshift         Homozygous         Novel, not report           TTC37         c.21144-5G>A				,				Novel, not reported
Ifa       ATM       c.7481dup       p.(Asn2494Lysfs6)       50       Frameshift       Homozygous       Novel, not reports         ATM       c.3277deIA       p.(Ile1093Serfs16)       22       Frameshift       Homozygous       Novel, not reports         (HD       STAT3       c.2132T>G       p.(Ile1290Serfs16)       22       Frameshift       Homozygous       VCV000803390, pathogenic         STAT3       c.2132T>G       p.(Ile711Thr)       23       Missense       Heterozygous       Novel, not reports         STAT3       c.1110-2A>G       p.(Arg382Trp)       12       Substitution       Heterozygous       Novel, not reports         STAT3       c.550+1C>T       Donor splice site       Intron       Splicing       Heterozygous       Novel, not reports         SPINK5       c.1887+1G>A       hg19:Chr5:147492498       Intron       Splicing       Homozygous       Novel, not reports         20       SPINK5       c.2557C>T       p.(Arg853)       27       Stop-gain       Homozygous       Novel, not reports         1TC7A       c.122del       p.(Met41Serfs38)       1       Frameshift       Homozygous       Novel, not reports         1TC7A       c.212del       p.(Ile1277Tyrfs15)       9       Frameshift       Homozygous <td></td> <td></td> <td></td> <td>p.(Tyr169Cys)</td> <td></td> <td>Missense</td> <td>Hemizygous</td> <td></td>				p.(Tyr169Cys)		Missense	Hemizygous	
ATMc.3277delAp.(lle1093Serfs16)22FrameshiftHomozygousNovel, not reportsI/bCHD7c.8416C>Gp.(Leu2806Val)38MissenseHomozygousVCV00098814I/bSTAT3c.2132T>Gp.(lle711Thr)23MissenseHeterozygousVCV00080390, pathogenicSTAT3c.1110-2A>Gp.(Arg382Tp)12SubstitutionHeterozygousNovel, not reportsSTAT3c.550+1C>TDonor splice siteIntronSplicingHeterozygousNovel, not reportsSPINK5c.1887+1G>Ahg19:Chr5:147492498IntronSplicingHomozygousNovel, not reportsSPINK5c.2557C>Tp.(Arg853)27Stop-gainHomozygousNovel, not reportsTTC7Ac.122delp.(Met41Serfs38)1FrameshiftHomozygousNovel, not reportsIIIaBTKchrX:100601487-10061436711_19DeletionHemizygousNovel, not reportsIIIaETKchrX:100601487-10061436711_19DeletionHemizygousNovel, not reportsIIIaETKchrX:100601487-10061436711_19DeletionHomozygousNovel, not reportsIIIaETKchr3:25840380-29-50DeletionHomozygousNovel, not reportsIIIaETKchr3:25840380-49-50DeletionHomozygousNovel, not reportsIIIaCD79Ac.91C <t< td="">p.(Ile114Val)1_5MissenseHomozygousNovel, not reportsIIIaCLYST</t<>								Novel, not reported
CHD7c.8416C>Gp.(Leu2806Va)38MissenseHomozygousVCV00095814IIbSTAT3c.2132T>Gp.(Ile711Thr)23MissenseHeterozygousVCV000980390, pathogenicSTAT3c.1110-2A>Gp.(Arg382Trp)12SubstitutionHeterozygousNovel, not reportsSTAT3c.550+1C>TDonor splice siteIntronSplicingHeterozygousNovel, not reportsSPINK5c.1887+1G>Ahg19:Chr5:147492498IntronSplicingHomozygousVCV00082372, pathogenicSPINK5c.2557C>Tp.(Met41Serfs38)1FrameshiftHomozygousVCV00082372, pathogenicTTC7Ac.122delp.(Met41Serfs38)1FrameshiftHomozygousNovel, not reportsIIIaBTKchrX:100601487-10061436711_19DeletionHemizygousNovel, not reportsIVaCD79Ac.91C <t< td="">p.(Gin31)2NonsenseHomozygousNovel, not reportsVMaLYSTChr1:235840380- 235840391949-50DeletionHomozygousNovel, not reportsIVaLYSTChr1:235840380- 235840919LYSTChr1:235840380- 2358403919VSNel, not reportsIVaLYSTChr1:235840380- 2358403919LYSTChr6:CAcceptor splice site3SplicingHomozygousNovel, not reportsIVaLYSTChr1:235840380- 2358403919LYSTChr6:CAcceptor splice site3SplicingHomozygousNovel, not reportsIVa&lt;</t<>	lla							Novel, not reported
IIIb     STAT3     c.2132T>G     p.(Ile711Thr)     23     Missense     Heterozygous     VCV000803390, pathogenic       STAT3     c.1110-2A>G     p.(Arg382Trp)     12     Substitution     Heterozygous     Novel, not reports       STAT3     c.550+1C>T     Donor splice site     Intron     Splicing     Heterozygous     Novel, not reports       SPINK5     c.1887+1G>A     hg19:Chr5:147492498     Intron     Splicing     Homozygous     Novel, not reports       SPINK5     c.2557C>T     p.(Arg853)     27     Stop-gain     Homozygous     Novel, not reports       TTC7A     c.122del     p.(Met41Serfs38)     1     Frameshift     Homozygous     Novel, not reports       IIIa     BTK     c.21487-100614367     11_19     Deletion     Hemizygous     Novel, not reports       IIIa     BTK     c.828dup     p.(Ile171Tyrfs15)     9     Frameshift     Hemizygous     Novel, not reports       IIIa     BTK     c.828du380-     p.(Ile114Val)     1_5     Missense     Homozygous     Novel, not reports       IIIa     BTK     c.828du380-     p.(Ile114Val)     1_5     Missense     Homozygous     Novel, not reports       IIIa     BTK     c.12_13delTA     p.(Arg1271)     2     Nonsense     Homozygo								Novel, not reported
STAT3 STAT3c.1110-2A>G c.150+1C>Tp.(Arg382Trp) Donor splice site12 Intron Intron SplicingHeterozygous HeterozygousNovel, not reports Novel, not reportsSPINK5c.1887+1G>Ahg19:Chr5:147492498Intron 20SplicingHomozygousNovel, not reports 20SPINK5c.1887+1G>Ahg19:Chr5:147492498Intron 20SplicingHomozygousNovel, not reports 20TTC7Ac.2557C>Tp.(Arg853)27Stop-gainHomozygousNovel, not reports 20TTC7Ac.122delp.(Met41Serfs38)1FrameshiftHomozygousNovel, not reports pathogenicIIIaETKc.828dupp.(Ile27TTyrfs15)9FrameshiftHemizygousNovel, not reportsIVaLYSTChr1:235840380- 2584091915MisenseHomozygousNovel, not reports vorel, not reportsIVaLYSTChr1:235840380- 25840919p.(Ile114Val)1_5MisenseHomozygousNovel, not reports vorel, not reportsIVaLYSTChr1:235840380- 25840919p.(Ile114Val)1_5MisenseHomozygousNovel, not reports vorel, not reportsIVaLYSTC.25-1G>CAcceptor splice site1FrameshiftHomozygousNovel, not reports vorel, not reportsIVaLYSTChr3:25840380- 258409191FrameshiftHomozygousNovel, not reports vorel, not reportsIVaLYSTChr3:257G>CAcceptor splice site3SplicingHom				, ,				
STAT3       c.550+1C>T       Donor splice site       Intron       Splicing       Heterozygous       Novel, not reports         SPINK5       c. 1887+1G>A       hg19:Chr5:147492498       Intron       Splicing       Homozygous       Novel, not reports         SPINK5       c. 2557C>T       p.(Arg853)       27       Stop-gain       Homozygous       VCV000623372, pathogenic         TTC7A       c.122del       p.(Met41Serfs38)       1       Frameshift       Homozygous       Novel, not reports         IIIa       BTK       c.htx:100601487-100614367       11_19       Deletion       Hemizygous       Novel, not reports         IIIa       BTK       c.s282dup       p.(Ile27TTyrfs15)       9       Frameshift       Hemizygous       Novel, not reports         IIIa       BTK       c.32040       p.(Ile114Val)       1       2       Nonsense       Homozygous       Novel, not reports         IIIa       BTK       c.340 A>G       p.(Ile114Val)       1       5       Missense       Homozygous       Novel, not reports         IVa       LYST       Chr1:235840380-       49-50       Deletion       Homozygous       Novel, not reports         AP3B1       c.12_13delTA       p.(Asri4LysfsStop6)       1       Frameshift	llb							
18     18     18     18     18     10     10       SPINK5     c. 1887+1G>A     hg19:Chr5:147492498     Intron     Splicing     Homozygous     Novel, not reporte       20     SPINK5     c.2557C>T     p.(Arg853)     27     Stop-gain     Homozygous     Novel, not reporte       20     TTC7A     c.122del     p.(Met41Serfs38)     1     Frameshift     Homozygous     Novel, not reporte       20     TTC37     c.2114+5G>A     Intronic     20     Splicing     Homozygous     Novel, not reporte       21     TTC37     c.2114+5G>A     Intronic     20     Splicing     Homozygous     Novel, not reporte       21     TTC37     c.2114+5G>A     Intronic     20     Splicing     Homozygous     Novel, not reporte       21     BTK     chrX:100601487-100614367     11_19     Deletion     Hemizygous     Novel, not reporte       23     BTK     c.828dup     p.(Ile177Tyrfs15)     9     Frameshift     Homozygous     Novel, not reporte       23     Chr1:235840380-     23     Noleinon     Homozygous     Novel, not reporte       23     Chr1:235840380-     249-50     Deletion     Homozygous     Novel, not reporte       23     RAB27A     c.153+2T>C				1 ( )			,0	
20     20       SPINK5     c.2557C>T     p.(Arg853)     27     Stop-gain     Homozygous     VCV000623372, pathogenic       TTC7A     c.122del     p.(Met41Serfs38)     1     Frameshift     Homozygous     Novel, not reporte       IIIa     BTK     chrX:100601487-100614367     11_19     Deletion     Hemizygous     Novel, not reporte       BTK     chrX:100601487-100614367     11_19     Deletion     Hemizygous     Novel, not reporte       CD79A     c.91C <t< td="">     p.(Gin31)     2     Nonsense     Homozygous     Novel, not reporte       Va     LYST     Chr1:235840380-     49-50     Deletion     Homozygous     Novel, not reporte       RAB27A     c.340 A&gt;G     p.(Ile114Val)     1_5     Missense     Homozygous     Novel, not reporte       AP3B1     c.12_13delTA     p.(Asn4LysfsStop6)     1     Frameshift     Homozygous     Novel, not reporte       AP3B1     c.205-1G&gt;C     Acceptor splice site     3     Splicing     Homozygous     Novel, not reporte       AP3B1     c.205-1G&gt;C     Acceptor splice site     3     Splicing     Homozygous     Novel, not reporte       AP3B1     c.205-1G&gt;C     Acceptor splice site     3     Splicing     Homozygous     Novel, not reporte       <t< td=""><td></td><td></td><td></td><td></td><td>18</td><td></td><td></td><td></td></t<></t<>					18			
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#### TABLE 4 | Summary of the identified genotype of IEI cohort shown in categories of IUIS, unclassified IEI, and potentially disease-causing variants.

(Continued)

#### TABLE 4 | Continued

IUIS class	Gene	Mutation	Protein effect	Exon	Туре	Zygosity	Novelty
	FOXP3	c.1186G>C	P.(Val396Leu)	10	Missense		Novel, not reported
	XIAP	c.990_991del	p.(Leu331Argfs18)	4	Frameshift	Hemizygous	Novel, not reported
Va	SBDS	c.258+2T>C,	Donor splice site	Intron 2	Splicing,	Compound Heterozygous	VCV000003196, pathogenic
		c.183_184delinsCT	p.(Lys62)	Exon 2	Nonsense		VCV000003195, pathogenic
Vb	NCF1	c.579G>A	P.(Trp193)	7	Stop-gain	Homozygous	VCV00042699, Pathogenic
	CYBA	c.314T>G	p.(Leu105Arg)	165	Missense	Homozygous	Novel, not reported
Vla	MYD88	c.814C>T	p.(Arg272Ter)	5	Nonsense	Homozygous	Novel, not reported
	IFNGR2	c175+102del	Intronic	1	Deletion	Homozygous	Novel, not reported
	STAT1	c.820C>T	p.(Arg274Trp) GOF	8	Missense	Heterozygous	VCV000030083, Pathogenic
	STAT1	c.800C>T	p.(Ala267Val) GOF	8	Missense	Heterozygous	VCV000030084, likely pathogenic
	IL17RC	c.1414C>T	p.(Arg472)	17	Nonsense	Homozygous	Novel, not reported
VIb	STAT1	c.778C>T	p.(Q260X)	8	Nonsense	Homozygous	Novel, not reported
	IL12RB1	Chr19:18186575: c.804_805insT	p.(Val269fs)	9	Frameshift	Homozygous	Novel, not reported
	TYK2	c.1969G>A	p.(E657K)	14	Missense	Homozygous	Novel, not reported
Unclassified IEI	LIFR	c.653dup	p.(Glu219fs)	6	Duplication frameshift	Homozygous	VCV000281444, Pathogenic
	DIAPH1	c.2769del	p.(Phe923Leufs4)	21	Frameshift	Homozygous	VCV000217753, Pathogenic
	ZNFX1	c.1405G>C	p.(Val469Leu)	1_12	Missense	Homozygous	Novel, not reported
Potential IEI	LAT2	c.95G>T	p.(Gly32Val)	3	Missense	Homozygous	Novel, not reported
	EBF3	c.509G>T	p.(Cys170Phe)	6	Missense	Heterozygous	Novel, not reported

Immunodeficiencies affecting cellular and humoral immunity (I). Combined immunodeficiencies (II). Predominantly antibody deficiencies (III). Diseases of immune dysregulation (IV). Congenital functional defects of phagocyte (V). Defects in intrinsic and innate immunity (VI).

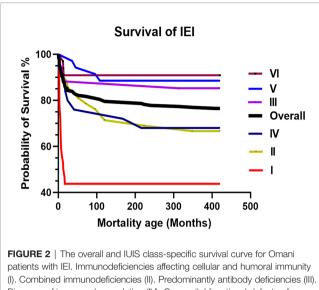
IEI, Inborn Errors of Immunity; IUIS: International Union of Immunological Societies; IL7R, Interleukin 7 Receptor; ADA, Adenosine Deaminase; JAK3, Janus Tyrosine Kinase 3; RAG1, Recombination Activating Gene 1; DCLRE1C, DNA Cross-Link Repair 1C; CD3E, Cluster of Differentiation 3 Epsilon; NHEJ1, Non-Homologous End-Joining factor 1; IL2RG, Interleukin-2 Receptor subunit Gamma; DOCK8, Dedicator of Cytokinesis 8; CIITA, Class II major histocompatibility complex Transactivator; RFX5, Regulatory Factor X5; RFXANK, Regulatory Factor X-associated Ankyrin-containing; MSN, Moesin; MAP3K14, Mitogen-Activated Protein 3 Kinase 14; CD40LG, Cluster of Differentiation 40 Ligand; STK4, Serine/Threonine Kinase 4; ATM, Ataxia Telangiectasia Mutated; CHD7, Chromodomain Helicase DNA-binding protein 7; STAT3, Signal Transducer and Activator of Transcription 3; SPINK5, Serine Peptidase Inhibitor Kazal Type 5; TTC7A, Tetratricopeptide Repeat Domain 7A; TTC37, Tetratricopeptide repeat domain 37; BTK, Bruton's Tyrosine kinase; CD79A, Cluster of Differentiation 79A; LYST, Lysosomal Trafficking regulator; RAB27A, Ras-related protein Rab 27A; AP3B1, Adaptor-related Protein complex 3 Beta 1; AP3D1, Adaptor Related Protein Complex 3 Delta 1; PRKCD, Protein Kinase C Delta; LRBA, Lipopolysaccharide-Responsive and Beige-like Anchor; L2RA, Interleukin-2 Receptor subunit Alpha; FOXP3, Forkhead Box P3; XIAP, X-linked Inhibitor of Apoptosis; SBDS, Shwachman-Bodian-Diamond Syndrome; NCF1, Neutrophil Cytosolic Factor 1; CYBA, Cytochrome B-245 Alpha chain; MYD88, Myeloid Differentiation primary response 88; IFNGR2, Interferon Gamma Receptor 2; EBF3, Early B-Cell Factor 3; Arg, Arginine; Trp, Trypophan; del, deletion; ins, insertion; dup, dublication; Leu, Leucine; Gly, Glycine; Lys, Lysine; Met, Methionine; Thr, Threonine; bp, base pair, Gln, Glutamine; Val, Valine; Pro, Proline; Trp, Trypophan; del, deletion; ins, insertion; dup, dublication; Leu, Leucine; Gly, Glycine; Lys, Lysine; Met, Methionine; Thr, Threonine; bp, base pair, Gln, Glutamine; Va

registry (56% vs. 44%) (15). This finding may be because males are more commonly affected with X-linked diseases in addition to the autosomal recessive disease that affect both sexes in a similar proportion.

According to a previous Omani study, Al-Tamemi et al. (8) described an IEI prevalence of 7/100,000, while the current cohort reports a prevalence of 8.7/100,000. The overall calculated combined prevalence of this cohort and the Omani cohort included in the recent MENA report in 2021 (15) was 15.5 per 100,000 Omani population (**Table 1**). This emphasizes the importance of establishing a detailed national IEI registry in Oman.

Similar to previously published literature, infection was found to be the predominant clinical presentation, followed by immune dysregulation and then malignancy. We also observed that symptomatic recurrent bacterial infections were the most common clinical presentation with the respiratory tract being the predominant site of infection. Failure to thrive, chronic lung diseases, infective lymphadenopathy, and enteropathy were major complications of IEI in our group. This is in agreement with previous studies conducted in Qatar, Kuwait, and Egypt (5, 6, 22).

Interestingly, we found that immune dysregulation was prominent and occurred in approximately one-third of the patients (32%), which was a higher rate than that reported by previous studies from France (26%), Kuwait (20%), and ESID registries (18%) (23, 24). During the last 25 years, immune dysregulation was frequently reported in patients who suffer from IEI, and this association prompted further studies that led to discovery of new monogenic disorders, improvement in the knowledge of the pathogenesis of autoimmunity, and introduction of targeted treatments. The largest percentage of patients who showed clinical signs of immune dysregulation was in the category of diseases of immune dysregulation (41%), followed by PAD



patients with IEI. Immunodeficiencies affecting cellular and humoral immunity (I). Combined immunodeficiencies (II). Predominantly antibody deficiencies (III). Diseases of immune dysregulation (IV). Congenital functional defects of phagocyte (V). Defects in intrinsic and innate immunity (VI). IEI, Inborn Errors of Immunity; IUIS, International Union of Immunological Societies.

(18%) (**Table 3**). As depicted by Costagliola et al. (25), failure to eliminate self-reactive B cells, T-cell dysfunction, and reduced number and function of regulatory T cells (Tregs) are the main contributing factors in the development of immune dysregulation in such patients. A previous literature review showed that, regardless of what aspect of PID has been studied, early diagnosis reduces healthcare consumption and leads to better health outcomes in nearly all cases (26). Unfortunately, 35% of those who manifested with immune dysregulation died at a mean age of 50.8 months compared to the overall mean age of 41.7 months for the entire cohort. However, a mean difference of 9 months of delay is not statistically significant, highlighting the possibility of other factors such as uncontrolled immune dysregulation, ongoing end-organ damage, and/or treatment-related immunosuppression and effect of toxicity.

Another relevant finding was that the prevalence of both CID and SCID exceeded the frequency of congenital functional phagocyte defects in this cohort. A similar pattern was observed by Barbouche et al. (27) in Egypt, but was in contrast to other studies from the ESID registry (13), Iran (28), Kuwait (5), Tunisia (27), and Turkey (29), where other types of IEI were dominant. One possibility of the higher prevalence of these groups of immunodeficiencies in the current study compared to previous reported findings in the country (8) is related to the direct access and referral of different healthcare facilities to the Royal Hospital, which is considered the largest tertiary hospital in Oman. However, late recognition and referral hamper the appropriate care needed and often increase morbidity and mortality at peripheral hospitals.

We also found that 77% (n = 184) of this cohort had an attempt made toward obtaining molecular confirmation of their underlying IEI, with 50% (n = 120/239) having their genetic defect identified. Compared to the global molecular diagnosis rate of 13.2% (3) this higher percentage could be attributed to the

higher rate of consanguinity in our cohort. The method of detection varies, but almost 90% were identified using wholeexome sequencing/next-generation sequencing and Sanger sequencing/targeted mutation analysis. The establishment of a molecular diagnosis has enabled the support of the suspected diagnosis and its expected spectrum of different IEIs. Moreover, molecular characterization guides the treating physician to establish a proper targeted and personalized clinical management, minimizing complications and allowing the provision of evidence-based genetic counseling.

Long-term follow-up of patients revealed that IVIG replacement therapy was conducted in 41% of patients, which is concordant with other cohorts from Germany (47%) (30) and Kuwait (58%) (5). HSCT was achieved in 10% of patients with IEI, among whom more than 56% underwent remission. The mortality rate in our cohort was 25.1% (n = 60), with a mean age of 60 months (range: 1-408). This is comparable to other reports of 26% in Kuwait (5) and 18.7% in Iran (28). A higher mortality rate was seen in patients with SCID/CID due to the delayed diagnosis. Similarly, patients with immune dysregulation had a mortality rate that was comparable to CID probably due to delayed diagnosis. Overall, the mean delayed diagnosis for all patients was 41.7 months, while it was 50 months for those with immune dysregulation. The lack of awareness that such patients is among the spectrum of IEI that has also contributed to the delay in diagnosis. As most of patients with IEI (SCID, CID and patients with immune dysregulation) are relatively asymptomatic at birth, in the absence of a proactive screening program such as a newborn screen program for T- and B-cell deficiencies, the presence of disease can easily be missed until manifestation. Indeed, the newborn screen program has been shown to be sensitive in detection by the new finding that Saudi Arabia has a SCID incidence of 1/2,906 live births (31) compared to the previous retrospectively reported 5.39/100,000 (7). The lack of adequate HSCT units in Oman that can urgently accommodate a sufficient number of patients also contributed in management delay, as most patients were transplanted abroad (58.3%). To overcome the aforementioned obstacles, our prospective proposition is to implement a national newborn screening program, recommend expanding the HSCT service in the country, establish a national IEI registry, and increase the awareness toward the phenotype and genotype of IEI in Oman.

#### CONCLUSION

This study is the largest in the country and addresses important factors that lead to poor outcome in patients with IEI. Our findings acknowledge the need to include immune dysregulation as one of the warning signs of primary immunodeficiency to avoid delayed diagnosis of patients with non-infectious manifestations. The higher mortality rate seen in patients with SCID/CID highlights the urgent need for proactive detection through the establishment of a national IEI newborn screening program. Finally, the development of a national IEI registry is a priority, as it will help to unify the national efforts and develop effective short- and long-term strategies. Addressing the above issues will pave the way for better disease ascertainment, phenotype characterization, early diagnosis, and early intervention, thereby improving the likelihood of positive health outcomes for Omani patients with IEI.

#### DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/supplementary material. Further inquiries can be directed to the corresponding author.

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# **AUTHOR CONTRIBUTIONS**

TF: Conception of idea, research design, data collection, data management, analysis, report writing, and intellectual input. KA: Data collection and data management. JA: Critical reviewing and report writing. MK: Critical reviewing and report writing. MC: Critical reviewing. AH: Reviewing genotype. ZA: Data collection and data management. IN: Data collection and data management. NS: Conception of idea, research design, data collection, data management, analysis, report writing, and intellectual input. All authors contributed to the article and approved the submitted version.

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