INTRODUCTION

Oculodentodigital dysplasia (ODDD) (OMIM#164200) is a rare disorder characterized by various ophthalmic, dental, skeletal, and craniofacial anomalies. It has a high penetrance but its phenotypic expression is variable (Judisch, Martin-Casals, Hanson, & Olin, 1979). ODDD is primarily an autosomal dominant disorder caused by mutations in the gap junction protein alpha 1 (GJA1) gene. GJA1 gene encodes a polytopic connexin membrane protein, Cx43, that is a component of connexon membrane channels.

The phenotypic features characteristic of ODDD are well described (Hennekam, Allanson, & Krantz, 2010). Typical ophthalmologic abnormalities include microphthalmia, microcornea, and various anomalies that involve the iris, which can lead to glaucoma, cataracts, and optic neuropathy. Dental features involve both the primary and secondary dentition and include enamel hypoplasia, microdontia, hypodontia, and premature loss of teeth. Typical skeletal anomalies include bilateral syndactyly of the 2nd to 4th toes and/or of the 4th and 5th fingers, camptodactyly and clinodactyly. Affected individuals also exhibit craniofacial dysmorphic features, including a thin nose, narrow anteverted nares, short palpebral fissures, and microcephaly. A variety of neurological manifestations have been reported, including lower limb spastic paraparesis, ataxic gait, seizures, neurogenic bladder, and uncommonly, psychomotor retardation. These neurological features of ODDD involve 30%
of cases (De Bock, Kerrebrouck, Wang, & Leybaert, 2013). ODDD exhibits extensive phenotypic pleiotropy, and abnormalities involving the heart, lymphatics, and skin have also been reported (Brice et al., 2013; Kogame et al., 2014; Paznekas et al., 2003).

Connexin 43 (Cx43) is a ubiquitously expressed protein that forms hexameric connexin hemichannels, which interact with connexin hemichannels on apposed membranes to form gap junctions. Gap junctions play critical physiological roles, allowing intercellular exchange of ions, metabolites and second messengers (Laird, 2006). The human genome encodes 21 connexin genes, which are co-expressed in diverse combinations to form different channels. Each connexin protein is composed of four transmembrane domains, two extracellular loops and cytoplasmic amino- and carboxyl termini (Yeager & Gilula, 1992). The transmembrane and extracellular domains are highly conserved. Cx43 is the most widely studied connexin, in view of its widespread expression in most body tissues and its extensive interactions with other proteins.

A wide array of human pathologies are caused by mutations in connexin genes, including peripheral neuropathies, skin disorders, non-syndromic hearing loss and congenital cataract (Abrams & Scherer, 2012; Krutovskikh & Yamasaki, 2000; Lee & White, 2009). Mutations in GJA1 lead to an array of developmental abnormalities in ODDD. The mutational spectrum in GJA1 has been extensively reviewed (Laird, 2014). Most changes are dominant missense mutations that alter the sequence of the first two-thirds of the Cx43 protein. Additionally, dominant frameshift, deletion, and duplication variants have also been described, as well as two autosomal recessive variants. The functional effect of a number of GJA1 variants has been evaluated using in vitro cell models, and these studies have shown that even slight sequence changes in Cx43 can compromise gap junction function (Shao et al., 2012).

In this report, we describe two unrelated patients with clinical features of ODDD. Sanger sequencing of GJA1 gene in the probands and family members identified two novel variants that segregate with the phenotype, suggestive of causality.

1.1 Ethical compliance

This study was approved by the local institutional ethics review board and written informed consent was obtained.

1.2 Clinical presentation

The undiagnosed probands were referred to the genetics clinic for review in view of multiple dysmorphic features that had presented at birth. Both probands are female, the offspring of healthy Maltese Caucasian non-consanguineous parents. The respective clinical phenotypes are listed in Table 1 and selected clinical features from proband 1 are shown in Figure 1. Proband 2 was lost to clinical follow-up.

Proband 1 presented at the age of 22 years with facial dysmorphism, hair and weight loss, bone pain, and recent onset of unsteady gait and spastic paraparesis. Clinical features included the absence of subcutaneous fat, mild psychomotor delay, absence of pubic hair and hypoplastic carious teeth which required the use of dentures. She was also being investigated for amenorrhea. Proband 2 presented at the age of 8 years. Her clinical phenotype included various abnormal craniofacial and skeletal features; these included microphthalmia, a bilateral convergent squint, nystagmus, micrognathia, and bilateral fifth finger clinodactyly. She was intellectually normal and showed no neurological signs. Palmoplantar keratosis was absent in proband 1, while proband 2 had palmar keratosis at presentation. Both probands were born at term with birth weights of 2,800 grams (proband 1) and 2,520 grams (proband 2). G-banded chromosome analyses carried out at birth had shown normal 46, XX female karyotypes.

1.3 Genetic analysis

In view of the characteristic clinical features of ODDD, the probands were screened for GJA1 mutations by Sanger sequencing of PCR amplicons (Reference sequence NM_000165.5). GJA1 consists of two exons, the first of which is untranslated, separated by an 11kb intron. The coding exon (exon 2) of GJA1 was amplified in two overlapping fragments of 925 bp and 1,079 bp according to published protocol (Paznekas et al., 2003). The detected variants were analyzed for pathogenicity according to established guidelines from the American College of Medical Genetics/Association for Molecular Pathology (ACMG/AMP). A detailed description of the methodology is provided in the supplementary file Data S1.

2 RESULTS

Nonsense mutations, frameshift mutations, in-frame indels and variants affecting splice sites were not detected in the two probands. Two different novel missense mutations, each in the heterozygous state were detected—NM_000165.5: c.287T>G p.Val96Gly mutation in proband 1 and NM_000165.5:c.77T>C p.Leu26Pro mutation in proband 2 (Figure 2). In-silico analysis of pathogenicity using various bioinformatics approaches is shown on Table 2 Evolutionary conservation analysis indicates that both the p.Val96Gly and p.Leu26Pro GJA1 mutations occur at highly conserved positions within the protein, and that these residues are conserved across multiple species. Additionally, multiple lines of computational evidence provide support for deleterious effects of these missense mutations. Both mutations are absent from the
|                      | Proband 1 p.Val96Gly | Proband 2 p.Leu26Pro |
|----------------------|----------------------|----------------------|
| **Craniofacial features** |                      |                      |
| General              |                      |                      |
| Microcephaly         | Present              | Present              |
| Hair                 | Thin, sparse, widow’s peak | Thin, sparse, widow’s peak |
| Ocular Features      |                      |                      |
| Microphthalmos       | Present bilaterally  | Present bilaterally  |
| Bilateral convergent strabismus | Present          | Present              |
| Nystagmus            | Absent               | Present              |
| Epiblepharon         | Absent               | Present              |
| Telecanthus          | Present              | Absent               |
| Hypertrophic mucosal membrane under eyelids | Present | Absent |
| Short palpebral fissures | Present bilaterally | Present bilaterally |
| Epicanthic folds     | Present bilaterally  | Present bilaterally  |
| Oro‐dental features  |                      |                      |
| Enamel hypoplasia, hypodontia, abnormal 1° and 2° dentitions | Present | Present |
| Auricular features   |                      |                      |
| Low set and prominent pinnae | Present | Present |
| Nasal features       |                      |                      |
| Nasal bridge         | Prominent            | Normal               |
| Thin nose with hypoplastic alae nasi | Present | Present |
| Columella            | Prominent            | Prominent            |
| Other                |                      |                      |
| Hypoplastic maxilla  | Present              | Absent               |
| Micrognathia         | Present              | Present              |
| Skeletal features    |                      |                      |
| Hands and fingers    |                      |                      |
| Camptodactyly of 5th finger | Present bilaterally | Present bilaterally |
| Skin syndactyly of 4th and 5th fingers | Present bilaterally | Absent |
| Single digital crease on 5th finger | Present on left | Present on right |
| Hypoplastic middle phalanx of 5th finger | Present bilaterally | Normal |
| Finger clubbing      | Present bilaterally  | Absent               |
| Transverse palmar crease | Absent            | Present on right     |
| Palmar keratosis     | Absent               | Present bilaterally  |
| Toes and feet        |                      |                      |
| Syndactyly of 4th and 5th toes | Bilaterally present | Absent               |
| Overriding 5th toe   | Present on left      | Absent               |
| Foot length          | Normal               | Long bilaterally     |
| Plantar keratosis    | Absent               | Absent               |
| General features     |                      |                      |
| Thin skin            | Present              | Present              |
| Pallor               | Present              | Present              |
| Build                | Slim                 | Normal               |
| Body hair            | Sparse axillary and pubic hair | Not applicable |
| Neurological manifestations |                  |                      |

(Continues)
gnomAD dataset and are not reported in ClinVar, Varsome and HGMD databases (Kopanos et al., 2019; Landrum et al., 2018; Stenson et al., 2017). No GJA1 mutations were discovered in the parents of probands 1 and 2, indicating that both cases of ODDD are a product of two de-novo and novel mutations. Furthermore, the mutations described here also lie in a well-established functional domain of the Cx43 protein that lacks benign variation. Based on the above findings, both mutations can be considered causal for ODDD.

3 | DISCUSSION

The two novel pathogenic missense mutations described in this report result in transmembrane defects of connexin 43, with the p.Leu26Pro substitution altering the first transmembrane domain and p.Val96Gly the second transmembrane domain of Cx43. Both variants segregated with the disease phenotype and were not present in the unaffected parents. Furthermore, the presence of two different mutations in the unrelated cases suggests the absence of a founder effect at this locus in the Maltese population.

Mutations in each of the four transmembrane domains of Cx43 have been described. The missense variant at position 26 (p.Leu26Pro) has not been reported previously, although a serine to proline substitution at neighboring position 27, p.Ser27Pro has been identified (Richardson, Donnai, Meire, & Dixon, 2004). Mutations that introduce proline into protein sequences are functionally unique, because the cyclical structure of its side chain confers conformational rigidity. Consequently, non-native proline residues can disrupt secondary structures of alpha helices and beta sheets, lead to “kinks” in the protein backbone and have a destabilizing effect due to steric clash with other residues (MacArthur & Thornton, 1991). Additionally, proline lacks the capacity to form hydrogen bonds, which can effect secondary structure formation and stability (Betts & Russell, 2003).

The p.Val96Gly missense mutation identified in proband 1 has not been reported previously, although three other missense variants at this position have been described—p.Val96Ala, p.Val96Glu and p.Val96Met (Paznekas et al., 2009), (Wiest et al., 2006),(Kjaer et al., 2004). The introduction of glycine residues has functional consequences that contrast with those of proline, as its small side chain allows it to adopt a wide range of conformations compared to other residues. Consequently, mutations introducing glycine can lead to loss of stability in the hydrophobic domains of a protein.

Both missense mutations lie in highly-conserved transmembrane domains, and in silico analysis supports their pathogenicity. Analysis using MPEx predicts that both substitutions alter the hydrophobicity of the transmembrane domain relative to the wild-type sequence, but do not shift the residues predicted to span the cell membrane (Snider, Jayasinghe, Hristova, & White, 2009).

The mechanisms linking GJA1 mutations to disease are complex and have been reviewed extensively (Laird, 2014). Functional studies have shown that mutations in GJA1 can attenuate or abolish channel function, disrupt protein trafficking and modulate gap junction assembly. Critically, Cx43 transmembrane domains establish the gap junction pore and are essential for connexin localization to the plasma membrane. Furthermore, in addition to compromising channel

### TABLE 1 (Continued)

|                        | Proband 1 p.Val96Gly | Proband 2 p.Leu26Pro |
|------------------------|----------------------|----------------------|
| Spastic paraparesis and ataxia | Present              | Absent               |
| Psychomotor delay      | Mild                 | Normal               |

**FIGURE 1** Clinical features in proband 1 with the GJA1 NM_000165.5: c.287T>G p.Val96Gly mutation. (a) shows sparse fine lusterless hair (b) front view of face showing distinctive nose and hypoplastic alae nasi. (c) Orthopantogram showing narrow maxilla, microdontia, hypodontia, and widely spaced teeth with irregular roots (d) both hands showing fifth digit camptodactyly and syndactyly of the fourth and fifth digits.
activity, Cx43 mutations exert dominant negative effects on co-expressed wild-type channels, leading to a significant reduction of Cx43-dependent gap junction intercellular transport (Roscoe et al., 2005). The diverse functional effects of \textit{GJA1} variants are thus consistent with the pleiotropic features of ODDD. The genetic heterogeneity of the disease is similarly extensive, and several novel mutations in different ethnic groups have been recently described (Choi et al., 2018; Jamsheer et al., 2014; Porntaveetus, Srichomthong, Ohazama, Suphapeetiporn, & Shotelersuk, 2017; Tumminelli et al., 2016). Most causative mutations are missense, although nonsense and frameshift mutations have also been reported.

The phenotypic heterogeneity in ODDD is further highlighted by the varying hyperkeratotic symptoms reported here. Palmoplantar keratosis (PPK) is regarded as a minor symptom of ODDD that has been associated with C-terminal frameshift and truncation mutations (Pfenniger, Wohlwend, & Kwak, 2011). However, PPK has also been reported in ODDD patients with \textit{GJA1} mutations outside of the C-terminal region (Kelly et al., 2006; Kogame et al., 2014). The presence of palmar keratosis in proband 2 harboring an N-terminus missense mutation is thus significant as it further expands on the genotype-phenotype associations for ODDD. Furthermore, hyperkeratosis of the palms or soles might be easily overlooked, especially if the clinical presentation is subtle. Clinicians should, therefore, be vigilant for minor cutaneous changes that are an important part of the phenotypic spectrum in ODDD.

In conclusion, this report broadens our understanding of \textit{GJA1} variants associated with ODDD and provides the first description of this rare syndrome in individuals of Maltese ethnicity. Further in vitro studies should characterize the functional impact of these variants on connexon activity, which would lead to an improved understanding of the mechanisms leading to congenital anomalies in ODDD.

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**CONFICT OF INTEREST**

The authors declare that they have no conflict of interest.

**DATA AVAILABILITY STATEMENT**

The data that support the findings of this study are available from the corresponding author upon reasonable request.
### TABLE 2  
**GJA1 mutations detected in the two probands, with in-silico pathogenicity prediction scores and ACMG classification criteria**

|                  | Proband 1 p.Val96Gly | Proband 2 p.Leu26Pro |
|------------------|-----------------------|----------------------|
| **General prediction scores** |                       |                      |
| Position^a        | 6-121768280            | 6-121768070          |
| HGVS              | NM_000165.5:c.287T>G   | NM_000165.5:c.77T>C   |
| Amino acid change | p.Val96Gly             | p.Leu26Pro           |
| DANN              | 0.9931                 | 0.9991               |
| Mutation Taster   | Disease causing        | Disease causing      |
| FATHMM            | Damaging               | Damaging             |
| FATHMM-MKL        | Damaging               | Damaging             |
| MetaSVM           | Damaging               | Damaging             |
| MetaLR            | Damaging               | Damaging             |
| SIFT              | Damaging               | Damaging             |
| Provean           | Damaging               | Damaging             |
| PHRED-Scaled CADD | 26.1                   | 29.7                 |
| PolyPhen-2^b      | Possibly damaging      | Probably damaging    |
| **Evolutionary conservation scores** |                       |                      |
| GERP              | 5.67                   | 6.16                 |
| LRT               | Deleterious            | Deleterious          |
| Mutation Assessor | Medium                 | High                 |
| ACMG classification| Pathogenic according to PS2, PM1, PM2, PM5, PP2 and PP3 criteria. | Pathogenic according to PS2, PM1, PM2, PP2 and PP3 criteria. |

^aPosition according to hg19/GRCh37 human reference genome assembly.  
^bPolyPhen-2 predictions using HumVar-trained model.

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