Unmasking of a Recessive SCARF2 Mutation by a 22q11.12 de novo Deletion in a Patient with Van den Ende-Gupta Syndrome

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Key Words
Arachnocamptodactyly • Blepharophimosis • Congenital contractures • SCARF2 • Van den Ende-Gupta syndrome

Abstract
Van den Ende-Gupta syndrome (VDEGS) is a congenital condition characterized by craniofacial and skeletal manifestations, specifically blepharophimosis, malar and maxillary hypoplasia, distinctive nose, arachnocamptodactyly, and long slender bones of the hands and feet. To date, only 24 patients have been described. It is generally thought that the syndrome is transmitted by an autosomal recessive mode of inheritance, although evidence for genetic heterogeneity has recently been presented. We report on a girl followed from birth up to 3 years of life with a set of peculiar minor anomalies, arachnocamptodactyly of hands and feet, characteristic of VDEGS in association with a 22q11.12 deletion. Recently, the VDEGS gene was mapped to the DiGeorge syndrome region on 22q11.2, and homozygous mutations in the SCARF2 gene were identified. We now report the first patient with VDEGS due to compound heterozygosity for the common 22q11.2 microdeletion and a hemizygous SCARF2 splice site mutation.
tively long fibulae. The bones of the hands and feet were relatively long, with the exception of the terminal phalanges which were shortened.

Following these initial observations, Phadke et al. [1998] reported 2 unrelated Indian girls with some features of the condition. Bistritzer et al. [1993] reported 2 double second cousins from an inbred pedigree suspected to have VDEGS. Cardiac examination and general development were normal. One female infant had a prominent clitoris and fused labia. Schweitzer et al. [2003] reported 2 Hispanic brothers born to unrelated parents, who both had distinctive cerebellar enlargement, a new finding for this disorder. Ali et al. [2010] observed cutaneous syndactyly of toes 2 and 3 as a consistent feature in their patients. Further patients with this constellation of anomalies have been reported, reinforcing the hypothesis of an autosomal recessive mode of inheritance [Bistritzer et al., 1993; Schweitzer et al., 2003; Carr et al., 2007; Ali et al., 2010]. Only one report by Leal and Silva [2009] suggested genetic heterogeneity and an autosomal dominant trait based on the observation of 3 affected individuals, 2 brothers and their half-sister, assuming gonadal mosaicism.

The patients affected by VDEGS had a normal karyotype, and FISH for specific 22q11.12 abnormalities performed in 3 cases was normal [Gupta et al., 1995; Schweitzer et al., 2003; Carr et al., 2007; Ali et al., 2010]. Recently, Anastasio et al. [2010] mapped VDEGS to the DiGeorge syndrome region on 22q11.2 and identified homozygous mutations in the SCARF2 gene as the underlying cause in 4 patients from 3 highly inbred Bedouin families. We now report the first patient with VDEGS due to compound heterozygosity for the common 22q11.2 microdeletion and a hemizygous SCARF2 splice site mutation.

Clinical Report

The female proband is the first child born to a 30-year-old mother and a 32-year-old father. Both parents were healthy and non-consanguineous, and no drugs had been taken during the gestational period. Pregnancy was uneventful except for bilateral clubfeet, mild bilateral pyelectasis, and lack of visualization of opening-closing hand movements observed at 21+6 weeks of gestation by prenatal ultrasound scan. Growth parameters were: biparietal diameter 52 mm (25th–50th centile), head circumference 193 mm (25th–50th centile), abdominal circumference 160 mm (25th–50th centile), femur length 38 mm (50th centile). Cytogenetic analysis performed on chorionic villous sample was normal: height 87 cm (10th centile), weight 11.9 kg (10th centile), and head circumference 48.3 cm (10th centile).

The same minor facial anomalies were evident, as was arachnodactyly of hands and feet, but camptodactyly and bilateral clubfeet had improved (fig. 3, 4). A cardiac ultrasound scan was performed and showed an ostium secundum atrial septal defect. The child had a mild motor developmental delay that improved progressively with physiotherapy. The major motor milestones were sitting at 8 months and walking at 22 months. Speech development was normal.

Molecular Analysis

Array-comparative genomic hybridization (array-CGH) analysis was performed using commercially available oligonucleotide microarrays containing about 99,000 60-mer probes with an estimated median spatial resolution of nearly 10 kb and a functional resolution close to 35 kb (Human Genome CGH Microarray 105A Kit, Agilent Technologies). Labeling and hybridization were performed following the protocols provided by the manufacturer (Agilent Technologies according to the Agilent protocol Oligonucleotide Array-Based CGH for Genomic DNA Analysis v 2.0). Slides were dried and then scanned using an Agilent G2565BA DNA microarray scanner.

Image analysis was performed by CGH Analytics software v. 3.4.40 with default settings. The software automatically determines the fluorescence intensities of the spots for both fluorochromes, performs background subtraction and data normalization, and compiles the data into a spreadsheet that links the fluorescence signal of every oligo on the array to the oligo name, its position on the array, and its position in the genome. The linear order of the oligos is reconstituted in the ratio plots consistent with an ideogram. The ratio plot is arbitrarily assigned such that gains and losses in DNA copy number at a particular locus are
observed as a deviation of the ratio plot from a modal value of 1.0. DNA sequence information is taken from the public UCSC database (Human Genome Browser, http://genome.ucsc.edu, March 2006 assembly).

Mutational analysis of the SCARF2 gene in the patient was performed by Sanger sequencing using an ABI 3730 capillary sequencer after PCR amplification with intronic primers for the 11 coding exons. In addition, both parents were sequenced for exon 4 and flanking intronic regions.

Results

A 22q11.1–q11.21 microdeletion was identified with the proximal breakpoint in 22q11.1 located between 17.08 and 17.27 Mb (last oligonucleotide present and first deleted, respectively) and the distal breakpoint between 19.83 and 19.89 Mb in 22q11.21 (last oligonucleotide de-
Thus the deletion corresponds to the common DiGeorge/VCFS ‘3-Mb’ deletion between low copy repeats LCR-A (LCR22–2) and LCR-D (LCR22–4) [Rauch et al., 2005; Guo et al., 2011]. To confirm the array data, a second array-CGH experiment was performed in the patient and parents. The deletion was confirmed in the patient, while the parents showed a normal result. Analysis of the deleted region suggested the absence of at least 39 known genes (fig. 5).

Sanger sequencing of the \textit{SCARF2} gene revealed the c.854 + 1G>T (intron 4) splice acceptor mutation hemizygous in the patient and heterozygous in the healthy mother, while the father showed the wild-type sequence (fig. 6). Online bioinformatics tools such as ‘Mutation taster’ and ‘Human splicing finder’ both indicated loss of the splicing site.

\textbf{Discussion}

The facial phenotype of our case and the pattern of congenital anomalies are similar to that of patients previously reported by van den Ende et al. [1992] and Gupta et al. [1995]. Since the VDEGS was considered an autosomal recessive condition, detection of a heterozygous 22q11.2 deletion in the proband and first present, respectively, referring to hg18).
deletion in our patient was surprising. The recent identification of homozygous mutations in the SCARF2 gene in inbred families with VDEGS [Anastasio et al., 2010] suggested unmasking of a recessive mutation of SCARF2, which is located within the 22q11.2 common deletion region. Subsequent sequencing of SCARF2 in our patient revealed indeed a maternally inherited splice site mutation in addition to the 22q11.2 microdeletion and hence absence of a functional SCARF2 gene. SCARF2 contains putative epidermal growth factor-like domains in its extracellular domain, along with a number of positively charged residues in its intracellular domain, indicating that it may be involved in intracellular signaling. Scarf2 is expressed in mouse branchial or pharyngeal arches and mandibular maxillary and urogenital ridge tissues [Anastasio et al., 2010].

Comparison of the clinical findings of our case with clinical characteristics of 24 patients described with this condition (table 1) [van den Ende et al., 1992; Bistritzer et al., 1993; Gupta et al., 1995; Phadke et al., 1998; Schweitzer et al., 2003; Guerra et al., 2005; Carr et al., 2007; Leal and Silva 2009; Ali et al., 2010; Anastasio et al., 2010] confirms considerable overlap of our case with the published patients with VDEGS, particularly the facial appearance and the arachnocamptodactyly. The most common anomalies are indeed arachnodactyly, camptodactyly, an unusual facial appearance with blepharophimosis, beaked nose, malar hypoplasia, everted lips, and prominent ears. Growth and intelligence are normal in all cases. The finger contractures usually gradually improve and do not cause functional limitations. In all cases, radiographic features showed slender long bones, metacarpals, metatarsals, and phalanges. Further investigation is warranted concerning the relevance of cerebellar enlargement and learning difficulties reported by Schweitzer et al. [2003].

In addition, the patient reported here had sclerocornea and cataracts never described previously in VDEGS. Instead, ocular findings such as sclerocornea, microptalmia, and cataract have been described in the 22q11 deletion syndrome [Binenbaum et al., 2008; Casteels et al., 2008]. The patient here reported presented with a 2.56–2.8 Mb deletion that represents the typical 3-Mb deletion at 22q11.2 that is usually observed. In addition to the ocular anomalies, she showed some typical clinical features of the 22q deletion phenotype such as ostium secundum atrial septal defect and transient neonatal hypocalcemia [McDonald-McGinn and Sullivan, 2011]. The facial features such as small mouth, prominent nose, hypertelorism, and narrow palpebral fissures, although overlapping with the 22q11 deletion syndrome, were clearly dominated by the characteristics of VDEGS. She had no other 22q11.2 deletion features, in particular no velopharyngeal insufficiency, no thymic hypoplasia, and no evidence of immunodeficiency.

Limb anomalies are uncommon in 22q11.2 deletion patients. A few studies reported patients with a 22q11.2 deletion and polydactyly, ectrodactyly, thumb anomalies, minor upper/lower limb skeletal anomalies, synostosis, and contractures, but neither arachnodactyly nor hypo-extensibility of fingers are described so far [Kokitsu-Nakata et al., 2008]. On the contrary, arachnocampodactyly is the most characteristic clinical feature of VDEGS.

To our knowledge, no published patient with a 22q11.2 deletion showed clinical features similar to a VDEGS phenotype. On the other hand, cases with VDEGS had a normal karyotype, and FISH for specific 22q11.2 abnormalities performed in 3 cases was normal [Gupta et al., 1995; Schweitzer et al., 2003; Carr et al., 2007].

VDEGS has been generally considered to be an autosomal recessive entity, given that 3 affected individuals...
from different families were born to normal and consanguineous parents [van den Ende et al., 1992; Bistritzer et al., 1993; Gupta et al., 1995]. The identification of homozygous mutations in the SCARF2 gene as the underlying cause reported by Anastasio et al. [2010] in VDEGS patients from 3 consanguineous families further supports the conclusion that VDEGS is an autosomal recessive entity. Our case, though, demonstrates that sequencing alone might falsely indicate a homozygous mutation and that the recurrence risk is not necessarily 25% in all cases. After exclusion of a compensating deletion/duplication event by FISH in the parents [Alkalay et al., 2011], we would assume an approximately 1% recurrence risk for the 22q11 deletion with reference to the possibility of a germ line mosaicism. Accordingly, recurrence risk for VDEGS would be approximately 0.5%.

Recently, because 3 affected individuals, 2 brothers and their half-sister, were reported, Leal and Silva [2009]
hypothesized an autosomal dominant transmission and gonadal mosaicism, suggesting genetic heterogeneity. However, we consider it more likely, that all 3 half-siblings are by change carriers of recessive mutations, a hypothesis that could now be proven.

Acknowledgments

The authors would like to gratefully thank the patient and her family for their consent to publish this data. We thank Dr. Filomena Papa, UOD Medical Genetic Unit, University of Siena, for her molecular contribution.

References


