

# First Report of X-Linked Hypohidrotic Ectodermal Dysplasia with a Hemizygous c.1142G >C in the EDA Gene: Variant of Uncertain Significance or New Pathogenic Variant?

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## Case report

**Keywords:** Hypohidrotic Ectodermal Dysplasia, X-linked, EDA gene, variants of uncertain significance (VUS)

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2 in the EDA gene: Variant of Uncertain Significance or new pathogenic variant?

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11 significance (VUS)

12

### 13 **ABSTRACT**

#### 14 ***Background***

15 *Hypohidrotic Ectodermal Dysplasia (HED) is a genetic disorder which affects structures of*  
16 *ectodermal origin. X-linked hypohidrotic ectodermal dysplasia (XLHED) is the most common form*  
17 *of disease. XLHED is characterized by hypotrichosis, hypohydrosis and hypodontia. The cardinal*  
18 *features of classic HED become obvious during childhood.*

19 *Identification of a hemizygous EDA pathogenic variant in an affected male confirms the diagnosis.*

#### 20 ***Case presentation***

21 *We report on a male newborn with the main clinical characteristics of the X-linked HED including*  
22 *hypotrichosis, hypodontia and hypohydrosis. Gene panel sequencing identified a new hemizygous*  
23 *missense variant of uncertain significance (VUS) c.1142G>C (p.Gly318A1a) in the EDA gene,*  
24 *located on the X chromosome and inherited from the healthy mother.*

#### 25 ***Conclusion***

26 *Despite the potential functional impact of VUS remains uncharacterized, our goal is to evaluate the*  
27 *clinical potential consequences of missense VUS on EDA gene. Given the proband's phenotype*  
28 *compatibility with classic HED, it is reasonable to attribute a causative role to the variant found in*  
29 *hemizygosis in the gene EDA. The present case demonstrates that this novel VUS could broaden the*  
30 *spectrum of genes mutations involved in the HED phenotype.*

31

## 32 **Background**

33

34 Ectodermal dysplasia (ED) includes a large and heterogeneous group of rare congenital conditions  
35 with structural and functional abnormalities in various tissues originating from the ectodermal layer  
36 of the developing embryo. Pinheiro and Freire-Maia defined as ED any condition with lack or  
37 dysgenesis of at least two of the ectodermal derivatives: hair, nails, teeth or eccrine sweat glands [1,  
38 2]. The term ED has been used to describe around 200 different clinical conditions. The birth  
39 prevalence is estimated around 7 cases in 10,000 live births [1, 3].

40 The two most common forms of the disease are hypohidrotic/anhidrotic ED (Christ–Siemens–  
41 Touraine Syndrome) in which the sweat glands are either absent or significantly reduced in number  
42 and hidrotic ED (Clouston syndrome) in which the sweat glands are normal. [4, 5]. Hypohidrotic  
43 ectodermal dysplasia (HED) is characterized by a triad of signs comprising sparse hair  
44 (hypotrichosis), abnormal or missing teeth (anodontia or hypodontia), and inability to sweat  
45 (anhidrosis or hypohidrosis). [6, 7]

46 Typical clinical manifestations also include dryness of the skin, eyes, airways, and mucous  
47 membranes presumably due to the defective development of several exocrine glands. HED can be  
48 associated with dysmorphic features (forehead bumps, rings under the eyes, everted nose and  
49 prominent lips) and occasionally with absent nipples [8, 9].

50 Hypohidrotic ED may be inherited as X-linked, autosomal dominant, and autosomal recessive  
51 patterns. Four genes (EDA, EDAR, EDARADD, WNT10A) account for 90% of

52 hypohidrotic/anhidrotic ectodermal dysplasia cases [10, 11]. X-linked hypohidrotic ectodermal  
53 dysplasia (XLHED) is the most common form of disease. The EDA gene, located at Xq12-q13.1 and  
54 encoding the transmembrane type II ectodysplasin-A (EDA) protein, which belongs to the tumor  
55 necrosis factor superfamily, is responsible for XLHED through EDA-EDAR (EDA receptor)-  
56 EDARADD (EDAR-associated death domain) pathway. [12, 13].

57 The function of EDA protein in pathways regulating ectodermal development, is a key regulator of  
58 hair follicle and sweat gland initiation. Normally EDA is expressed in ectodermal tissues; it is  
59 implicated in epithelial-mesenchymal interactions during ectodermal morphogenesis and  
60 odontogenesis [13, 14]. Various mutations in EDA account for vast majority of XLHED cases. The  
61 most frequent mutation type is the missense/nonsense which consists of single base-pair substitutions  
62 in coding regions [12, 15].

63 We report on a three month-old boy with XLHED showing a novel hemizygous missense variant of  
64 uncertain significance (VUS) in the EDA gene, detected by Next Generation Sequencing (NGS).

65

## 66 **Case report**

67

68 A three-month-old, caucasian boy infant was referred to our observation due to decreased sweating,  
69 dry skin and absence of hair on the scalp. Family history for inherited diseases was unremarkable.

70 He was the second child of healthy non-consanguineous parents. He was born by spontaneous  
71 delivery after normal pregnancy, with no birth-related and perinatal complications. APGAR scores  
72 were 8 and 9 at 1 and 5 minutes, respectively. Birth weight was 2390 g (4th centile), length 47 cm  
73 (12th centile), and head circumference 33 cm (19th centile).

74 Physical examination showed scaphocephaly, prominent forehead, forehead bumps, rings under the  
75 eyes, hypertelorism, epicanthic fold, everted nose, depressed nasal bridge and prominent lips. Both  
76 the upper and lower eyelids showed sparse eyelashes. The hair on the scalp and the eyebrows were  
77 absent. The skin was thin, pale, dry and exfoliating with eczematous dermatitis widespread,

78 especially in the scalp. The skin from around the eyes and mouth showed linear wrinkled and was  
79 hyperpigmented. (Fig. 1) The parents reported dryness of eyes. Neuromotor and mental development  
80 index score of Bayley II scale were normal.

81 Ultrasound screening did not detect anomalies and routine ECG and echocardiogram evaluation were  
82 normal.

83 Molecular genetic studies were performed on genomic DNA extracted from peripheral blood,  
84 through Next Generation Sequencing (NGS). A multigene Ectodermal dysplasia panel, that included  
85 EDA, EDAR, EDARADD, EDA2R, TRAF6, NFKBIA, CDH3, WNT10A, was performed. The  
86 analysis revealed the hemizygous variant, NM\_001399.4: c.1142G>C (p.Gly318A1a) in EDA gene  
87 located on the X chromosome. The variant was tested for familial segregation showing heterozygous  
88 maternal state.

89 We established a multidisciplinary follow-up: ophtalmologic evaluation, hearing screen and visual  
90 evoked potentials were normal at five months.

91 The following physical examinations showed delayed teeth eruption: only two small, conical canines  
92 were present at fifteen months.

93 The last clinically evaluation was performed at twenty-four months of age, with persisting poor  
94 weight gain (3<sup>th</sup> centile), reduced ability to sweat, heat intolerance, chronic eczematous rash  
95 especially on the face, wrinkled periorbital skin with Dennie-Morgan infraorbital fold.

96 Intraoral examination revealed severe oligodontia with only two conical anterior teeth eruption  
97 previously described and a wide midline diastema. (Fig. 2)

98 Orthodontic management was planned in order to improve the limited chewing function ability.

99 Neuropsychomotor follow-up and mental development index score of Bayley II scale were in the  
100 normal range for the age.

101

102 **Discussion and conclusions**

103

104 The molecular pathogenesis of HED is not yet fully understood. *EDA* is the gene responsible for X-  
105 linked HED [6]. Classic HED is often diagnosed after infancy in patients showing typical  
106 hypotrichosis, hypohidrosis, and hypodontia. In the male proband the diagnosis of classic HED was  
107 established with the above characteristic features. The identification of a hemizygous *EDA*  
108 pathogenic variant or biallelic *EDAR*, *EDARADD* or *WNT10A* pathogenic variants confirmed the  
109 diagnosis [6, 16].

110 *EDA* mutations had been considered as genetic conditions, without a clear genotype-phenotype  
111 correlation [15, 17]. Burger and Schneider (2014) suggested a reproducible association of common  
112 *EDA* genotypes with XLHED phenotypes. A systematic mapping of *EDA* mutations with an  
113 evaluation of quantifiable clinical data may help to distinguish the pathogenetic gene mutations with  
114 respect to those allowing a residual ectodysplasin A activity [15, 18]. A multigene panel also  
115 including *EDA*, *EDAR*, *EDARADD*, *WNT10A* may be useful for the differential diagnosis.

116 Different pathogenic variants including nucleotide substitutions (missense, nonsense, and splicing),  
117 small deletions and insertions, and gross deletions have been identified in *EDA* [16, 19]. Pathogenic  
118 variants in *EDA* lead to ectodysplasin A molecules that are unable to regulate epithelial-mesenchyme  
119 interactions, resulting in abnormal ectodermal appendages. Several pathogenic variants  
120 in *EDA* produce ectodysplasin A that is unable to be converted to their active forms and mediate the  
121 cell-to-cell signaling regulating the morphogenesis of ectodermal appendages [20, 21]. The missense  
122 variant reported in our study is novel and does not result among those reported in the International  
123 literature (PubMed/Medline), in the Catalog of Human Genes and Genetic Disorders (OMIM), in the  
124 Genome Aggregation, ClinVar and in The Human Gene Mutation Database. According to the  
125 American College of Medical Genetics and Genomics this genetic variant is currently considered  
126 VUS.

127 VUS may or may not be disease-causing or associated with increased risk of an abnormal phenotype;  
128 the identification of a variant of uncertain significance does not confirm or exclude a diagnosis. A  
129 VUS does not meet the criteria to be classified as pathogenic or benign [22].

130 We analyzed the variant in silico by using software Scale-Invariant Feature Transform (SIFT),  
131 DANN, DEOGEN, MutationTaster, for the prediction of possible deleterious variants in human  
132 proteins. Combined Annotation Dependent Depletion (CADD), another algorithm used to help assess  
133 the potential pathogenicity of a variant, display scores for this variant of 26,9. Despite the variant  
134 reported in our study has been described as VUS with an imprecise potential functional impact, the  
135 prediction tools used suggest a potential pathogenetic effect.

136 To our knowledge, this is the first report of a VUS in a XLHED and it may be demonstrate that a  
137 mutation of the EDA gene caused by a hemizygous variant, c.1142G>C on the X chromosome, can  
138 lead to the XLHED clinical spectrum. Therefore, in consideration of the proband phenotype, a  
139 causative role of the variant found in hemizygosis in the gene EDA cannot be excluded.

140 Furthermore, only male hemizygotes are affected by this X-linked disease, being the heterozygous  
141 females clinically normal, as it happens in the vast majority of XLHED cases accounting for gene  
142 mutation.

143

144 In conclusion, despite we know many genetic variations involved in the development of HED, the  
145 latest investigation techniques such as NGS could increase our knowledge about genetic etiology.

146 Present patient seems to demonstrate that his clinical phenotype is due to the c.1142G>C  
147 (p.Gly318A1a) mutation in EDA gene. This novel VUS could broaden the spectrum of genes  
148 mutations involved in the development of HED.

149 The identification of this new mutation may contribute to evaluate the genotype/phenotype  
150 correlations. We deemed it useful to describe and characterize a novel mutation of EDA because we  
151 hope that a great number of further studies on the effect of normal and abnormal function of EDA  
152 protein will lead to a better knowledge of this group of ED. Future studies are mandatory to  
153 elucidate genomic and epigenomic susceptibility factors, which could cause mutations on EDA  
154 gene.

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217 The clinical data used during the current report are available from the corresponding author on  
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219

### 220 **Competing interests**

221 The authors declare that they have no competing interests

222

### 223 **Author's contributions**

224 GA, MF, GM drafted the manuscript and participated in management of the case. TM and GLB  
225 managed the case. CG coordinated the study and participated in its design. All authors read and  
226 approved the final manuscript.

227

### 228 **Ethics approval and consent to participate**

229 Not applicable.

230

### 231 **Consent for publication**

232 Written informed consent was obtained from the patient's parents for publication of this report and  
233 any accompanying images. A copy of the written consent is available for review.

234

235 **Figures**

236 **Fig. 1. X-linked hypohidrotic ectodermal dysplasia.** (a) missing eyebrows, sparse eyelashes; (b)  
237 scaphocephaly, missing hair, eczematous dermatitis

238

239 **Fig. 2. Severe oligodontia.** Two conical anterior teeth and a wide midline diastema.

240

241

## Figures



**Figure 1**

X-linked hypohidrotic ectodermal dysplasia. (a) missing eyebrows, sparse eyelashes; (b) scaphocephaly, missing hair, eczematous dermatitis



**Figure 2**

Severe oligodontia. Two conical anterior teeth and a wide midline diastema.