Possible Implication of RNF135 in High Type 1 Neurofibromatosis Tumoral Risk

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Abstract

**Background:** Recurrent type 1 and 2 microdeletions of NF1 (neurofibromatosis, type 1) gene leads to a more severe phenotype than heterozygous point mutations. The associated deletion of RNF135 (Ring Finger protein 135), a flanking NF1 gene, is known to be responsible for the childhood overgrowth syndrome but its implication in tumoral severity has never been proven.

**Methods and Results:** A Single Nucleotide Polymorphisms array (715K) was performed in a patient with a very severe form of type 1 neurofibromatosis, as revealed by massive cervico-mediastinal plexiform neurofibromas. It showed a small 126kb atypical deletion encompassing only RNF135 and the first exon of NF1.

**Conclusion:** This observation highlights the possible role of RNF135 in tumoral severity in type 1 neurofibromatosis caused by recurrent type 1 and type 2 microdeletions.

Keywords: Neurofibromatosis; RNF135; Cytogenetics; Atypical deletion; Single nucleotide polymorphism array

Introduction

About 5% of type 1 neurofibromatosis cases are caused by different types of recurrent overlapping 17q11.2 microdeletions that encompass several genes including NF1 (Neurofibromatosis, type 1) [1,2]. These recurrent deletions are mediated by repeated regions NF1-REP1 and NF1-REP2 for type 1 deletions (1.4Mb containing 15 genes) [3], by SUZ12 (Suppressor of zeste 12) and its pseudogene for type 2 deletions (1.2Mb containing 14 genes) [4], and by NF1-REP6 and NF1-REPc for the much rarer type 3 deletion (1.0Mb containing 9 genes) [5,6]. Many atypical deletions have also been reported [5-7].

A severe neurofibromatosis phenotype, including numerous and early-onset plexiform neurofibromas, as well as malignant peripheral nerve sheath tumors (MPNST), is encountered more frequently in type 1 and type 2 deleted patients than in those with NF1 point mutations [3,6,8]. Deleted patients also present an overgrowth syndrome due to the loss of the RNF135 (Ring Finger protein 135) gene [9]. RNF135 is a NF1 flanking gene which is included in type 1 and type 2 microdeletions but its implication in early-onset tumors is not clearly defined so far. By comparing the expression level of the 16 genes included in the 1.4 Mb deletion in dermal plexiform neurofibromas and in MPNST samples with that in benign dermal neurofibromas, Pasman et al. [10] demonstrated that both RNF135 and ADAP2 (ArfGAP with dual pleckstrin homology domains 2) were down-regulated in MPNST biopsies and MPNST cell lines. These results suggested that one or both of these two genes were involved in the increased malignant risk observed in NF1 deleted patients.

Here we report the case of a young but severe NF1 patient carrying a non-previously described 126kb microdeletion encompassing only the RNF135 gene and the NF1 first exon.

Case Report

**Patient clinical data**

This boy was born at 36 weeks of gestation from non-related Caucasian parents. Pregnancy was marked by a diet-treated gestational diabetes, an over 90th percentile macrosomy at 2nd trimester ultrasound examination and a major hydramnios. Birth parameters were 3590kg (> 95th percentile) of weight, 51cm (95th percentile) of size and 37.5cm (> > 97th percentile) of head circumference. Neonatal skin examination revealed a few café-au-lait spots and about 10 hamartomas.

At the age of 3 months, acute respiratory distress led to his hospitalization. Clinical examination revealed laryngomalacia, hyper salivation and axial hypotonia with peripheral hypertonia. Size and weight were below average at this time while head circumference was at +2 SD. During follow-up, a persistence of neurological troubles, a chronic stridor and several oxygen desaturation episodes around 85% were noted. As polysomnography revealed severe obstructive sleep apneas, non-invasive ventilation was introduced during sleep. This latter induced a great improvement of the patient’s tonus. Psychomotor development was normal afterwards, but chronic dyspnea remained and an infiltration of cervical and facial soft tissues was noted. Laryngotraceal endoscopy with biopsies was performed and showed a bulky cervical plexiform neurofibroma behind left arytenoid cartilage, leading to clinical diagnosis of type 1 neurofibromatosis. At the age of 15 months, whole body Magnetic Resonance Imaging (MRI) revealed a massive tumor syndrome with numerous plexiform neurofibromas in the cervical and mediastinal region (Figures 1A and 1B). The patient was included in a therapeutic trial by selective inhibitor of MAPK kinase (MEK) inhibitors at the age of 17 months.
Single nucleotide polymorphisms array analysis

Single Nucleotide Polymorphisms (SNP) array was performed using the Illumina OmniExpress-24 BeadChip array (713,000 markers, Illumina, San Diego, California, USA). BeadChips were imaged using the Illumina Bead Array reader and data analysis was performed by examination of signal intensity [Log R ratio, i.e. ln(sample copy number/reference copy number)] and allelic composition (B Allele Frequency) with the copy number variation (CNV) Partition 3.1.6 algorithm in GenomeStudio v.2011.1 (Illumina). Deletion breakpoints were defined as the first and last SNP comprised in the deleted region. Consequent tumoral phenotype is however as severe as type 1 and type 2 recurrent deletions, corroborating thereby the possible implication of RNF135 in tumors invasiveness.

Figure 1: Whole body 3 Tesla Resonance Magnetic Imaging performed at the age of 15 months.
(A) Cervico-thoracic coronal T2 sequence revealing many neurofibromas compressing upper aero-digestive tracks (thick arrow, iii) and repressing carotido-jugular vessels (thick arrow, iv) and submandibular glands, which seep from upper cervico-dorsal paravertebral spaces (thin arrow i,ii) to supraglottic level (thin arrow, iv) through cervical and mediastinal vascular spaces and posterior cervical spaces. Another neurofibroma from right parotid gland (arrowhead iii, iv) invades right masticator space and right temporo-mandibular joint. (B) Cerebral axial T1 sequence after gadolinium injection showing a 15.4mm x 9mm cerebellopontine angle neurofibroma from cranial nerves IX, X, and XI invading jugular foramen (arrows). A left pinna neurofibroma was also found (not shown).

Figure 2: De novo 126kb 17q11.2 microdeletion encompassing RNF135 and the first exon of NF1. arr [hg19] 17q11.2(29,297,595-29,423,989) x1 (A) Single Nucleotide Polymorphisms array (HumanOmniexpress-24, 713K, Illumina®), whole 17 chromosome, black arrow point out the microdeletion. (B) Zoom on deleted region (between the two dotted lines) and the included genes. (C) 17q11.2 recurrent deletions and encompassed genes (genome.ucsc.edu, hg19). Our patient deletion is much smaller than recurrent ones and has, to our knowledge, never been described. Consequent tumoral phenotype is however as severe as type 1 and type 2 recurrent deletions, corroborating thereby the possible implication of RNF135 in tumors invasiveness.
the first exon of NF1 gene (Figures 2A and 2B). It was confirmed and visualized by fluorescence in situ hybridization (FISH) using bacterial artificial chromosome clone RP11-229K15. This deletion had been reported in the literature and it was shown to have occurred de novo since none of the two parents carried it.

**Discussion**

Autosomal dominant Neurofibromatosis type 1 (MIM#162200) has a complete penetrance but shows highly variable expressivity and severity. Type 1 deletions are responsible for a contiguous gene syndrome leading to learning disabilities, facial dysmorphism and childhood overgrowth [6]. These features are also found, but at lower frequencies, in NF1 mutated patients [6]. However, the only well-established genotype-phenotype correlation is the association between type 1 or type 2 recurrent 17q11 deletions and an increased tumoral severity when compared to that due to NF1 point mutations. Mantripragada et al. [7] described a 6 years old American patient with café-au-lait spots, freckling and neurofibromas due to a very small 6kb atypical deletion, thus suggesting that the loss of the first NF1 exon was sufficient to cause type 1 neurofibromatosis.

We report the occurrence of a very severe tumoral phenotype in a one-year-old boy with neurofibromatosis due to a small 126kb deletion encompassing the NF1 first exon and the RNF135 gene. We hypothesized that the severity of our patient’s neurofibromas, similar to recurrent type 1 and type 2 longer deletions (Figure 2C), was therefore a consequence of the loss of the RNF135 gene. Indeed, heterozygous loss of function mutations of the neighboring RNF135 gene have been described in dysmorphic patients without neurofibromatosis but presenting with a global overgrowth [9]. It could be linked to an increased cell division rate, thus explaining why loss of RNF135 in deleted NF1 patients could worsen tumoral phenotype. At this point, this is just an assumption as it is very difficult to establish genotype-phenotype correlation in a disease with a highly variable expressivity. Describing phenotype of patients with similar deletions could help to conclude about this question.


