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Inactivating PTH/PTHrP signaling disorders (iPPSDs): validation of the new classification in a multicenter large series of 544 patients

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Abstract

Pseudohypoparathyroidism (PHP) and related disorders belong to group of heterogeneous rare diseases that share an impaired signaling downstream of Gsα-protein coupled receptors. Affected patients may present with various combination of symptoms including resistance to PTH and/or to other hormones, ectopic ossifications, brachydactyly type E, early onset obesity, short stature and cognitive difficulties. Several years ago, the delay in diagnosis, the variability in disease presentation, as well as the increasing molecular diversity causing the PHP spectrum have prompted us to propose a novel nomenclature under the term of inactivating PTH/PTHrP signaling disorders (iPPSD). This novel classification relied on criteria chosen by a group of experts based on literature evidence. It is now of utmost importance to validate these criteria and/or improve the basis of this new classification through the thorough analysis of a large international series of 459 probands and 85 relatives molecularly characterized. In this report, we demonstrate that more than 98% of the probands met the criteria initially defined, i.e. resistance to PTH (rPTH) and/or ectopic ossifications (EO) and/or brachydactyly (BR) associated with 2 minor criteria. Noteworthy, most patients (85%) presented a combination of symptoms rather than a single sign suggestive of iPPSD. Although specific clinical patterns did show up such as isolated PTH resistance as the main manifestation of iPPSD3 due to *GNAS* methylation defect, our study confirmed the overlap among the different genetic forms of iPPSD. The clinical and molecular characterization of iPPSD relatives identified familial history as an additional important criterion predictive of the disease.

Overall, the phenotypic analysis of this large cohort confirmed the validity of the major and minor criteria and their combination to diagnose iPPSD. This report shows the importance of having simple and easily recognizable signs to diagnose with confidence these rare disorders and supports a better management of patients.

Introduction

Pseudohypoparathyroidism (PHP) encompasses a spectrum of related, highly heterogeneous and frequently overlapping disorders deriving from molecular defects that impair the hormonal signaling *via* receptors coupled to the adenylyl cyclase by the α-subunit of the stimulatory G protein (Gsα).[1–3]

The term PHP includes several subtypes, including PHP type 1A (PHP1A, MIM#103580), PHP type 1B (PHP1B, MIM#603233) and PHP type 1C (PHP1C, MIM#612462), characterized by biochemical features of hypoparathyroidism due to peripheral resistance to the action of the parathyroid hormone (PTH) caused by genetic or epigenetic defects within or upstream the *GNAS* locus, that encodes for the Gsα.[3] Frequently, patients also suffer from resistance to other hormones acting through Gsα-coupled receptors, such as the thyroid-stimulating hormone (TSH), gonadotropins, growth hormone-releasing hormone (GHRH) and calcitonin.[3,4] Additionally, individuals with PHP1A and PHP1C variably express early-onset obesity together with a series of physical features (pre- and/or post-natal growth retardation, dysmorphic facies, varying degrees of intellectual and/or cognitive impairment and development delay, brachydactyly and ectopic ossifications) termed Albright hereditary osteodystrophy (AHO).[5] The presence of AHO without PTH resistance is defined as pseudopseudohypoparathyroidism (PPHP, MIM#612463), while, in case of ectopic ossifications extending into deep muscles and connective tissues, as progressive osseous heteroplasia (POH; MIM#166350).[6] Acrodysostosis (ACRDYS, MIM#101800), that is associated with genetic defects at the *PRKAR1A* and *PDE4D* genes, does also present signs similar to PHP such as brachydactyly, extensive facial dysmorphism, developmental delay and, frequently, PTH and TSH resistance.[7–9] Molecular alterations at another PDE gene, the *PDE3A* gene, are finally associated with the autosomal dominant hypertension and brachydactyly type E syndrome (HTNB, MIM#112410), characterized by brachydactyly type E, severe salt-independent but age-dependent hypertension, increased fibroblast growth rate, altered baroreflex blood pressure regulation and juvenile death from stroke when untreated.[10]

Several research studies on the clinical and molecular background associated with different PHP subtypes demonstrated that the delay in obtaining a specific diagnosis often derives from the extremely variable presentation, the severity of PHP signs and symptoms among patients, even in those carrying the same genetic alteration, as well as from the significant clinical and molecular overlap both among PHP subtypes and between PHP and the above mentioned related diseases.[11–15] Moreover, a correct early diagnosis in infants and in individuals with atypical features is very rarely achieved because clinical symptoms may be isolated in infancy and considered as poorly specific; biochemical abnormalities typically worsen during childhood.

In 2016, the European Network for the study of PHP (EuroPHPnetwork) conducted an expert initiative to produce a new nomenclature and classification encompassing all disorders with impairments in PTH and/or

PTHrP cAMP-mediated pathway in order to overcome the limits of the historical classification that disregarded related disorders. More importantly, the former classification did not consider molecular defects as distinctive criteria, thus failing to stratify many disorders including PHP and AHO. According to the novel proposal, the term inactivating PTH/PTHrP signaling disorder (iPPSD) was proposed instead of PHP, followed by a numbering for specific subtypes that allows the description of both clinical and molecular features (iPPSD1, loss-of-function variant in *PTHR1*; iPPSD2, loss-of-function alteration in *GNAS*; iPPSD3, methylation defects at one or more *GNAS* DMRs; iPPSD4, *PRKAR1A* pathogenic variant; iPPSD5, *PDE4D* pathogenic variant; iPPSD6, *PDE3A* pathogenic variant; iPPSDx, no molecular defect identified).[6] Such nomenclature will be used, together with the classical one when necessary, through the text.

The main advantages of the new suggested terminology can be summarized as 1) the definition of a common mechanism responsible for all diseases, 2) the inclusion of non-genetically characterized patients into the classification, 3) the avoidance of the ambiguous terms like “pseudo” and 4) the erasure of the clinical and molecular overlap between diseases.

Consequently, it is now of major importance to validate, and improve if necessary, the newly proposed classification. Hence, we propose a second position paper produced by the EuroPHPnetwork on the terminology and the classification of disorders characterized by the inactivation of the PTH/PTHrP signalling pathway. The aim of the present work was to evaluate a large, international case series of highly clinically and molecularly characterized patients by using the criteria recently proposed. In this large cohort of genetically confirmed patients, we investigated whether patients met the clinical major and minor criteria.[16] In addition, we considered still unexplored features to design additional objective criteria to guide an efficient distinction and stratification of iPPSD subtypes.

Patients and methods

This work was designed by clinicians and scientists from 3 tertiary centers (Italy, Spain and France) of the EuroPHPnet. Clinical and molecular data from 459 index patients (Supp.Tab.1) and 85 relatives followed in their clinical centers and laboratories over the last decades were collected.

Inclusion criteria for the study were the availability of complete clinical data at the time of the clinical diagnosis of each patient and a confirmative molecular diagnosis of a (epi)genetic alteration at *GNAS, PRKAR1A, PDE4D* or *PDE3A* loci.

Clinical features were divided into major [PTH resistance (rPTH), ectopic ossifications (EO) and brachydactyly (BR)] and minor criteria (TSH resistance, additional hormone resistances, motor and/or cognitive retardation or impairment, intrauterine growth retardation and/or post-natal growth retardation, obesity or overweight, and flat nasal bridge and/or maxillar hypoplasia and/or round face) according to the new proposal for

diagnosis and classification.[6] The minimum criteria for a clinical diagnosis of iPPSD were initially defined as at least one major criterion, either PTH resistance or ectopic ossifications or brachydactyly; in case of brachydactyly, 2 additional minor criteria were required as well.[6]

The molecular workout to identify iPPSD/PHP-related alterations has been described previously.[6,16]

Only index cases were included in the analysis to prevent bias, while relatives were evaluated separately. All patients, legal guardians for minors and relatives involved in the study subscribed the informed consent for genetic studies and the treatment of personal and clinical data. All procedures were performed in compliance with relevant legislation and institutional guidelines and were approved by the IRCCS Fondazione Cà Granda Ospedale Maggiore Policlinico institutional committee (PHP2019, parere 15_2019bis), the comité consultatif sur le traitement de l'information en matière de recherche dans le domaine de la santé (CCTIRS, #13-028) under the promotion of the INSERM (Institut national de la santé et de la recherche médicale) (#DC-2013-1762), and the Basque Ethics Committee (IRB #PI2013214 and PI2017018).

Results and Discussion

Validation of minimum criteria for iPPSD clinical diagnosis

The first and main aim of the present study was to test the detection rate achieved by re-evaluating our cohort of 459 PHP patients (205 males and 254 females) with a confirmatory molecular diagnosis following the proposals given by the EuroPHPnetwork in 2016. This meant to determine whether patients showed at least one major criterion between resistance to PTH (rPTH) and ectopic ossifications (EO) or brachydactyly (BR) associated with 2 minor criteria.

Out of the 459 patients, all but 8 patients (1.7%) met these minimum criteria, demonstrating a 98.3% detection rate. Thus, the proposed classification showed to work properly and allowed to identify almost all iPPSD patients at a first screening.

Of the 451 patients meeting the minimum criteria, 70 patients (15.5%) presented only 1 major criterion while 381 (84.5%) had either 1 major criterion associated with minor criteria or from 2 up to 3 major criteria with or without minor criteria (Fig. 1). As expected, although the age at diagnosis was not significantly different between these two subgroups, the mean age at diagnosis was slightly lower in the group of individuals with a more complex phenotype (14.9 years *vs* 21.8 years). Altogether, this suggests that the association of several symptoms allows an earlier detection of iPPSD patients. No significant difference associated with gender was found in both groups (Tab.1).

Affected subjects without 1 major criterion, therefore not meeting the new criteria for diagnosis, were 7 females and one male; they were diagnosed clinically between the age of 3 and 15 and genetically between

the age of 6 and 15 years. Two of them presented with brachydactyly only (IT11 and IT231), two other patients (SP85, SP130) presented with brachydactyly and pre- and/or post-natal growth retardation and 4 patients (IT137, FR83, IT16 and FR76) did not match any major criteria for iPPSD; the latter patients presented with TSH resistance (IT16 and FR83) isolated or in association with additional minor criteria or isolated obesity (FR76). Patient IT137 was referred for suspected mild PTH resistance associated with overweight and endocrine hyperfunction (subclinical hyperthyroidism, syndrome of inappropriate natriuresis and mild hypercortisolism) but PTH resistance reverted after vitamin D supplementation (Supp.Tab.1). For most of these patients, we cannot exclude that some features, at an early stage of their development, could be unnoticed at the first evaluation or that, given the young age of the patients, they could develop other signs overtime. Among these 8 patients, we identified 6 iPPSD2 patients carrying a *GNAS* coding mutation, one iPPSD3 patient and one iPPSD5 patient. We can rule out the possibility that the phenotypic variability is due to the genetic background as 2 out of 6 iPPSD2 patients carry molecular defects located in the hot spot regions of *GNAS*, i.e. an exon 1 pathogenic variant (patient IT11) and the only recurrent 4bp-deletion in exon 7 (c.568_571del, patient IT231), while the remaining 4 iPPSD2 subjects showed genetic variants located at aminoacidic positions whose replacement is predicted to have a damaging effect both by bioinformatics, previous reports from the literature [17,18] and Leiden Open Variation Database database (LOVD at https://databases.lovd.nl/shared/genes/GNAS). In addition, among the 6 iPPSD2 patients, 2 were paternal mutations (former pseudopseudohypoparathyroidism), one was a maternal *GNAS* coding mutation while the other 3 were of unknown allele origin.

Age at clinical diagnosis of iPPSD and signs at diagnosis

We divided our cohort in age groups including infancy (from birth up to 2 years, n=53, 11.5%), early childhood (from 3 to 8 years, n=104, 22.7%), middle childhood (from 9 to 11 years, n=64, 13.9%), adolescence (from 12 up to 18 years, n= 94, 20.5%) and adulthood (over 18 years, n=138, 30.1%). The age at clinical diagnosis was not available in 6 patients. We found that, at the time of iPPSD diagnosis, most probands (68.6%) were children or adolescents, with a peak in early childhood (from 3 to 8 years) and in adolescence (from 12 up to 18 years), and the remaining 30.1% were adults (>18 years). In particular, within the whole cohort of probands, the age range at clinical diagnosis was 0-68 years and the mean age was 15.8±13.6 years. Thus, a prompt identification of possible iPPSD cases by pediatricians is very important. We did not observe any gender difference both considering the case series as a whole and the different age groups (Tab. 2).

The next step was to define the clinical presentation at diagnosis, in particular the number and combination of major criteria with or without minor criteria, both considering the whole cohort and the division into age groups (Fig. 2). The most frequent presentation was isolated rPTH, that was found in 57 (12.4%) of patients. The second most frequent isolated sign was BR (associated with two minor criteria) in 12 (2.6%) of probands.

Finally, the less frequent isolated presentation was EO in one (0.2%) patient. On the other hand, 84.8% of the patients presented one of the major criteria combined with either another major or minor criteria.

When the number of criteria used for the diagnosis was analyzed in the different age ranges, we observed that younger people presented more clinical features than elder people (Fig. 2). During infancy, childhood, and adolescence and adulthood, the presence of complex phenotypes associating at least one major criterion and other criteria, minor or majors, was found in 94%, 81-90%, and 76-78% of the patients, respectively (Fig. 2). In the minority of patients presenting with only one major criterion, isolated PTH resistance was the most common.

Clinical presentation and age at diagnosis in patients affected with the different iPPSD subtypes

The identification of a causing molecular defect testing is fundamental to confirm the clinical diagnosis and categorize each patient into a specific iPPSD subtype. No clear genotype-phenotype correlation has been identified so far and clinical and molecular overlap exists among different PHP and PHP-related disorders. We thus investigated the correlation between the genetics and the patients' clinical presentation in our cohort (Tab. 3).

As previously observed in our study on the prevalence of PHP-associated molecular defects [17] we found that the 57 probands presenting with isolated PTH resistance were iPPSD3 due to *GNAS* methylation alterations. In particular, 70.2% had broad methylation defects and no known underlying primary genetic alteration, 26.3% had a deletion at the *STX16* gene and 3.5% presented broad methylation alterations secondary to UPD. As expected, the only patient showing ectopic ossifications with no additional signs carried a paternal *GNAS* point variant. Brachydactyly and 2 minor criteria was found almost in all types of iPPSDs, nearly half of them being iPPSD5, former acrodysostosis. We also confirmed that iPPSD4 and iPPSD5 diagnoses associate with a more complex and dysmorphic phenotype (31/37 patients with several major and minor criteria).

Several cases confirmed that there is a considerable overlap between what we have historically considered as different diseases, the most striking overlap being observed between the two most represented subtypes, i.e. iPPSD2 and 3 (historically PHP1A and 1B) (Fig. 3). As an example, patient IT208 who displayed brachydactyly plus 2 minor criteria, was diagnosed as iPPSD3 due to loss-of-imprinting at all 4 *GNAS* DMRs. Several iPPSD3 patients with resistance to PTH presented additional major criteria and/or signs of AHO (mainly brachydactyly). In addition, patient IT108 diagnosed with iPPSD4 and a *PRKAR1A* pathogenic variant did not develop PTH resistance while 1 iPPSD2 case with *GNAS* alterations on the paternal allele (patient FR87) and 4 iPPSD5 patients (patients FR85, FR74, IT8p and FR62) showed resistance to the action of PTH. These findings further support the usefulness of the new classification and the impossibility for the former one to predict specific phenotypes, therefore preventing a proper follow-up.

Except for an increased prevalence of females in iPPSD5 (4 males *vs* 14 females), and increased age at diagnosis in iPPSD3, we found similar sex ratio and similar age at diagnosis in the different iPPSDs. Only 1 patient with iPPSD3 caused by methylation defects at the *GNAS* locus was identified during infancy; this number increased proportionally with patients' age (48 patients diagnosed in childhood, 48 in adolescence and 94 in adulthood). This might be related to the lack of symptoms associated to the PTH resistance and hypocalcemia (Supp. Tab. 1); we know that, in patients with *GNAS* molecular defects, PTH resistance is absent at birth and develops overtime.[17,19,20] In addition, hypocalcemia may be underdiagnosed for years, when developing slowly. [16,17,19]

In 76 of the 224 iPPSD2 probands, we were able to define the parental inheritance of the genetic defect (63 on the maternal allele and 13 on the paternal one). The iPPSD3 group was mainly represented by patients with sporadic imprinting defects affecting all 4 *GNAS* DMRs. In iPPSD3 patients affected by the autosomal inherited *STX16* deletion, we were able to demonstrate the maternal origin in 8 out of 10 for whom information on parents, mother or father, were available. In addition, 4 women affected with iPPSD3 caused by *STX16* deletion and isolated loss of methylation at the at the *GNAS A/B*:TSS-DMR transmitted the deletion, the methylation defect and the iPPSD3 phenotype to their children. Out of 39 probands affected with non-imprinted genes like (*PRKAR1A* in 19 iPPSD4, *PDE4D* in 18 iPPSD5 and *PDE3A* in 2 iPPSD6), we identified only 2 autosomal transmissions within the same family from mother to son and daughter (iPPSD4).

All the above-mentioned data further support the absence of clear genotype-phenotype correlations. It reinforces the claim that the diagnosis of iPPSDs should be primarily clinical.[16] Nevertheless, the same data strongly support the need to confirm the genetic diagnosis as the the only way to identify a specific subtype, because of the dramatic clinical and molecular overlap among these heterogenous disorders.[16]

Minor criteria: frequency and association with major criteria

Many symptoms of iPPSD are non-specific that exist in many endocrine and syndromic diseases different from this group of disorders. Moreover, the number, the age of appearance and the severity of such features are extremely variable among patients, even when bearing the same molecular alteration. Indeed, patients may develop a sequence of AHO features over time or clinical features may be faint and unnoticed at first examination. Therefore, we decided to determine, among the signs of AHO and other minor criteria, which ones could be considered as pathognomonic and more predictive of the diagnosis. We evaluated, in our cohort, the frequency, age of presentation and possible association of a series of symptoms with specific major criteria.

We counted how many times each single minor criterion was seen in patients, both alone and in combination with additional minor features. The most common symptoms identified were resistance to TSH, dysmorphic facies marked by a flat nasal bridge and/or a maxillar hypoplasia and/or a round face, obesity or overweight,

intrauterine growth retardation and/or post-natal growth retardation, motor and/cognitive retardation or impairment and additional hormone resistances, e.g. to calcitonin, gonadotropins and/or GHRH in 282 (61.4%), 230 (50.1%), 199 (43.4%), 192 (41.8%), 148 (32.2%) and 90 (19.6%) iPPSD probands, respectively (Tab. 4 and Supp. Tab. 1)

When we considered these clinical features as the unique minor criterion present in a given patient (n=91), we found that resistance to TSH, intrauterine growth retardation and/or the post-natal growth retardation, obesity and overweight, and facial dysmorphism were the most frequent features in 41 (45.1%), 19 (20.9%), 13 (14.3%) and 9 (9.9%) patients, respectively (Tab. 4 and Sup. Tab .1). Noteworthy, intrauterine growth retardation and/or post-natal growth retardation were the unique minor criteria found in infants; mental and cognitive impairment was the most frequently reported in early childhood; resistance to TSH was the most frequent sign in the older groups; finally, the number of obese patients increased significantly from early childhood to adulthood (Fig. 4).

Overall and unfortunately, we were not able to detect a specific minor sign nor a combination of signs allowing to establish a precise clinical diagnosis, i.e. the iPPSD subtype, or to predict the underlying genetic alteration. We conclude from our findings that these minor and major signs should be carefully searched during the first examination in order to promote an earlier detection of iPPSD in patients.

Relatives of index iPPSD patients

The great intrafamiliar variability in clinical presentation has been largely reported.[16,21]. We took advantage of this rare, large and unique collection of 459 probands and 85 relatives to investigate this phenotypic diversity and the iPPSD detection in the patient's family circle.

The cohort of 85 relatives includes 36 mothers (M), 3 fathers (F), 12 descendants (D), i.e. 5 sons and 7 daughters, 30 siblings, i.e. 14 brothers and 16 sisters, 3 cousins (C) and one aunt (A) (Table 5).

It is remarkable that one third of the relatives (n=28, 32.9%) were diagnosed through the family history and did not meet the minimum criteria to be classified as iPPSD. Among them, we identified 6 iPPSD3 and 22 iPPSD2 patients, including 6 with a paternal mutation at the *GNAS* gene. In particular, 18 subjects were apparently healthy with no major nor minor criteria, 5 patients had brachydactyly plus one minor criterion (4 growth retardation and one facial dysmorphism) and 5 patients showed minor criteria only (growth retardation, obesity, dysmorphic facies or resistance to TSH). The familial history therefore allowed a diagnosis of iPPSD before the occurrence of symptoms.

We then investigated the already known intrafamiliar phenotypic variability of the disease and we observed that all index patients developed a more severe and complex clinical presentation compared to the parent from whom they inherited the molecular defect, either genetic or epigenetic, displaying a greater number of major and/or minor criteria (the overall presence of major and minor criteria in probands and relatives is

summarized in Fig. 6 Agnes). The same was true for the only aunt of the series. In a specular way, when we considered offsprings of affected patients, we found that, in half cases, the clinical phenotype was aggravated in the next generation. There were few exceptions, most of which being very young patients (1 year or less) in whom probably the phenotype had not become apparent yet (IT191d, FR32d2, FR64d, FR41d); in addition, IT84d is a healthy adult daughter of an iPPSD3 mother with rPTH and FR16d is a patient with 2 major and 1 minor criteria whose mother displayed 3 major and 6 minor criteria.

All mutated siblings were affected and the clinical presentation was comparable to that of the index sibling. Patient IT217s, brother of a proband, was not considered in the analysis since no clinical data were available. Finally, the clinical features of the available couple of cousins were identical to the index case, similarily to what we found in siblings (Tab. 5).

Altogether, and in accordance to observations made in many other complex genetic disorders, our data suggest that, when present, the familial history of iPPSD should be also considered as a major criterion.

Concluding remarks

The investigation of a large, and unique cohort of 544 patients characterized by the inactivation of the PTH/PTHrP signalling pathway allowed us to propose this second position paper on the terminology and the classification of iPPSDs. The term “pseudohypoparathyroidism” has been widely used to describe several highly related, metabolic disorders based on disputable clinical and biochemical grounds. Performing an early and correct diagnosis and a stratification into subtypes is challenging, due to the overlap between PHP and related disorders, and even among PHP subtypes. Additionally, the presentation and the severity are extremely variable among affected individuals, even among those carrying the same molecular alteration. For this reason, in the recent past a new nomenclature and classification has been proposed,[6] and recommendations for the diagnosis and management of these patients have been published as a first international Consensus Statement.[16]

The present study investigated the largest cohort of deeply clinically and molecularly characterized patients affected by iPPSDs and allowed to validate the recently proposed criteria to define and classify these patients, although further prospective studies are needed to prospectically confirm these observations. Overall, the phenotypic analysis of this large cohort confirmed the validity of the major and minor criteria and their combination to diagnose iPPSD, the new classification being able to correctly identify more than 98% of index patients at the time of their first clinical presentation. The further clinical characterization of iPPSD relatives importantly identified familial history as a new major criterion predictive of the disease.

In conclusion, our report shows the importance of having simple and easily recognizable signs to diagnose with confidence these rare disorders and support a better management of patients.

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Conflict of Interest Statement

The authors declare no competing interests.

FIGURE LEYENDS

Supp.Tab.1

Table resuming clinical and molecular data of the whole investigated cohort, including the 459 index cases. Abbreviations: BD, date of birth; iPPSD, inactivating PTH/PTHrp signaling disorder; rPTH, resistance to PTH; EO, ectopic ossifications; BR, brachydactyly; rTSH, resistance to TSH; add HR, additional hormone resistances; M/C imp, motor and/or cognitive impairment or retardation; IUGR/PNGR, intrauterine and/or postnatal growth retardation; OB/OW, obesity or overweight; DF, facial dysmorphism~~; P, proband; M, mother; F, father; D, descendant (son or daughter); S, sibling (brother or sister); C, cousin; A, aunt~~; M, male; F, female; mat, maternal inheritance; pat, paternal inheritance; 0, absence of the criterion; 9, criterion not investigated; 1, presence of the criterion; IVS, intron. Legend of *GNAS* methylation defects: 2, uniparental isodisomy (iUPD); 6, overall methylation defects without known causes; 10, overall partial methylation defects without known causes; 11, partial (p) loss-of-methylation (LoM) at XL, gain-of-methylation (GoM) at *NESP*, LoM at *AB* and LoM at *GNAS-AS*; 12: LoM at *XL*, GoM at *NESP*, LoM at *AB* and pLoM at *GNAS-AS*; 13, pLoM at *XL*, GoM at *NESP*, LoM at *AB* and pLoM at *GNAS-AS*; 15, isolated LoM at *AB* and *STX16* deletion; 16, isolated LoM at *AB* without *STX16* deletion; 17, isolated pLoM at *AB* and *STX16* deletion; 18, isolated pLoM at *AB* without STX16 deletions.