

Oxidative Stress in Trisomy 13 and 18 Evaluation

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Autosomal aneuploidies are the most frequently occurring congenital abnormalities and are related to many metabolic disorders, hormonal dysfunctions, neurotransmitter abnormalities, and intellectual disabilities. Trisomies are generated by an error of chromosomal segregation during cell division. Accumulating evidence has shown that deregulated gene expression resulting from the triplication of chromosomes 13 and 18 is associated with many disturbed cellular processes. Moreover, a disturbed oxidative stress status may be implicated in the occurrence of fetal malformations.

oxidative stress

trisomy 18 syndrome

trisomy 13 syndrome

1. Introduction

Trisomy 13 (T13), resulting in Patau syndrome, is a chromosomal condition with a prevalence rate of 1/5000 to 1/20,000 ^{[1][2][3]}. Trisomy 18 (T18), causing Edwards syndrome, is another frequent autosomal aneuploidy after Trisomy 21 (T21), affecting 1/6000 to 1/8000 live-birth fetuses ^{[2][4]}. The most frequent mechanism responsible for the apparition of complete homogenous T13 occurrence is the complete triplication of chromosome 13, generally resulted from maternal nondisjunction in meiosis. Additionally, less frequently, T13 occurs as a result of an unbalanced Robertsonian translocation and mosaicism formation ^[5]. T18 occurs most frequently as a result of complete 18 trisomy due to a maternal meiotic nondisjunction, which is the most common form (94%) ^[6]. Mosaic trisomy 18 is the second cause corresponding to fewer than 5% of occurrences, and fewer than 2% of cases are caused by an additional copy of long arm chromosome 18q ^[7]. These chromosomal aberrations generate many congenital abnormalities such as heart defects, gastrointestinal defects, tracheoesophageal abnormalities, endocrine disorders, vision and hearing disorders, and limb and nervous system anomalies ^{[8][9][10]}. Following the complexity of existing comorbidities, numerical chromosomal aberration, such as T13 and T18 are one of the main causes of miscarriage or stillbirth ^[11]. However, along with improvements in clinical management, an increasing survival rate of patients with these syndromes has been reported ^{[4][12][13][14][15][16][17]}.

Recently, a broad range of genetic diseases have been investigated for the implications with oxidative stress and mitochondrial dysfunction in their pathogenesis ^[18]. Moreover, a growing number of studies have recently demonstrated that oxidative stress formation results from trisomy occurrence ^{[19][20][21][22][23]} and was observed to be responsible for the T21 phenotype ^{[24][25][26]}. T13 and T18 are the most frequently autosomal chromosome aberrations, excluding T21, where the pathogenesis of this chromosomal aberration is largely known, and

numerous studies have been conducted [5][7][27][28][29]. The pathogenic changes related to T13 and T18 may also be associated with oxidative stress with important causative genes being primarily involved in the redox balance regulation. Comprehensive studies concerning the evaluation of the trisomies' pathomechanism could explain the development of some malformations and the importance of oxidative stress, which can lead to a better understanding of the effects of the occurrence of these trisomies [4][30][31].

2. Oxidative Stress: An Overview

All biological processes constitute a redox equilibrium, i.e., balanced oxidation and reduction reactions, to ensure convenient homeostasis [32]. Oxidative stress occurs due to a reduction in antioxidant defense caused by defects in the defense mechanisms and/or increased reactive oxygen species (ROS) synthesis [33]. ROS generation is directly associated with oxidized damage in biological components such as proteins, lipids, and DNA [34]. These deteriorations are mostly caused by O_2^- (superoxide radical), OH^- (hydroxyl radical), and H_2O_2 (hydrogen peroxide) [35][36]. Recent studies have shown that mitochondrial dysfunction caused by oxidative stress plays an important role in neuronal damage and neurodegenerative diseases, which can be directly connected to the trisomic phenotype [34][37]. Mitochondrial respiratory chain complexes (MRCCs) play a key role in antioxidant defense by acting through the electron transport chain to oxidize hydrogen from the oxidation of organic acids with atomic oxygen to neutralize and expel hydrogen into water [34]. These complexes subsist as V cooperating units, which catalyze the phosphorylation of adenosine diphosphate (ADP) to adenosine triphosphate (ATP). Complex I is composed of nicotinamide adenine dinucleotide (NADH) coenzyme Q; complex II is composed of succinate dehydrogenase coenzyme Q; complex III is composed of coenzyme Q-cytochrome c reductase; complex IV is composed of cytochrome c oxidase; and complex V is composed of ATP synthase [38]. The MRCC is mostly exposed to oxidative stress through an increase in the possibility of oxidative damage caused to mitochondrial DNA (mtDNA), antioxidant proteins, and enzymes such as superoxide dismutase, catalase, glutathione peroxidase, and glutathione reductase in this complex, which may result in a subsequent additional increase in the intensity of the oxidative stress [39].

3. Previously Established T13 and T18 Pathogenesis—An Indicator for Oxidative Stress Testing

It has been shown that the composition of amniotic fluid, which is produced daily by the fetal urinary and respiratory systems using products of fetal skin keratinization, is similar to that of fetal plasma at the end of the second trimester [40][41]. Consequently, the concentrations of fetal proteins in second-trimester amniotic fluid are directly correlated with the concentrations in fetal serum, the analysis of which would facilitate the discovery of trisomy 13 and 18 pathogeneses [42][43][44][45]. Due to this fact, amniotic fluid appears to be the most useful material for analyzing abnormalities occurring in T13 and T18 fetal development [46].

One of the first studies, performed by Vrachnis, focused on resistin and leptin evaluations and showed that their deregulation may be implicated in T13 and T18 pathogeneses [31]. Resistin is a 12.5 kDa polypeptide secreted by

adipocytes involved in insulin resistance development. Moreover, resistin is a potential marker of chronic inflammation associated with increased oxidative stress [47]. More interestingly, resistin can affect the function of nitric oxide synthase (eNOS) systems, resulting in a significant decrease in eNOS expression and nitric oxide (NO) production, thereby having antioxidative properties [31][48]. Leptin, a hormone released from the adipocytes, in addition to influencing the feeling of hunger, is also involved in antioxidant defense by decreasing ROS production [49].

Another study, performed by Hsu et al., aimed to evaluate T18 pathogenesis and was conducted on second-trimester amniotic fluid samples collected from six confirmed T18 pregnancies. The other six euploid pregnancies were enrolled as the control group [30]. The comparative proteomics analysis was performed using fluorescence-based two-dimensional difference gel electrophoresis (2D-DIGE) with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS). The concentration of amniotic fluid apolipoprotein A1 (ApoA1) was increased in the T18-delivered samples compared to the euploid fluid samples [30]. Furthermore, the study demonstrated the deregulation of four proteins in T18 pregnancies: alpha-1-antitrypsin (A1AT, also known as serpin 1), vitamin D-binding protein (VDBP), insulin-like growth factor-binding protein 1 (IGFBP-1), and transthyretin (TTR) [30] (**Table 1**). ApoA1 is frequently used as a biomarker to predict cardiovascular diseases [43]. Its involvement in T18 could be associated with impaired lipid metabolism due to cardiovascular and neurological comorbidities during T18 early fetal development [44][50][51]. Moreover, the dysregulated ApoA1 expression could also correspond to the oxidative damage observed in trisomy 21-based studies [22][52]. Concluding, ApoA1 plays a meaningful role in the pathogenesis of ES. A1AT is involved in the protection of neurons and glial cells from oxygen and glucose deprivation [53]. VDBP is an important component of many biochemical processes, including the transport of vitamin D and its metabolites, ensuring proper homeostasis. VDBP also controls essential proteins for proper bone metabolism, binding fatty acids, sequestering actin, and modulating oxidative and immune defenses [54][55]. IGFBP-1 serves as a carrier protein for insulin-like growth factors 1 and 2 (IGF1 and IGF2)—important determinants of fetal growth during pregnancy [56]. TTR gene mapped on 18q12.1 encodes a serum- and cerebrospinal fluid-binding protein for thyroxine and retinol implicated in fetal development [57]. Using a biological network analysis of T18 pathogenesis, Hsu et al. showed that the protein expression profile is associated with a lipid- and hormone-disturbed metabolic processes, improper immune response mechanisms, and cardiovascular comorbidities potentially connected to increased oxidative stress [30] (**Table 1**).

Table 1. Disturbances in protein concentrations related to T13 and T18 pathogeneses [30][31].

Material	Protein	Full Name	Form of Dysregulation	Reference
Amniotic fluid T18 pregnancy	A1AT	alpha-1-antitrypsin	down	[30]
Amniotic fluid T18 pregnancy	ApoA	apolipoprotein A	up	[30]

Material	Protein	Full Name	Form of Dysregulation	Reference
Amniotic fluid T18 pregnancy	IGFBP-1	insulin-like growth factor-binding protein 1	down	[30]
Amniotic fluid T13 and T18 pregnancy	leptin	-	down	[31]
Amniotic fluid T13 and T18 pregnancy	resistin	-	down	[31]
Amniotic fluid T18 pregnancy	TTR	transthyretin	down	[30]
Amniotic fluid T18 pregnancy	VDBP	vitamin D binding protein	down	[30]

4. Genetic Basis of the T13 and T18 Pathogeneses

There are several genes mapped on chromosomes 13 and 18 recognized as the players in the maintenance of redox balance [58]. Chromosome 13 mapping demonstrated the presence of genes associated with copper transport (ATPase copper transporting beta; *ATP7B*), tumor suppression (breast cancer 2; *BRCA2*), the inhibition of cell cycle processes, chromatin remodeling (retinoblastoma transcriptional corepressor 1; *RB1*), chromosome stability maintenance and regulations of chromosome segregation in mitosis (chromosome alignment-maintaining phosphoprotein 1; *CHAMP1*), and oxidative mitochondrial processes (mitochondrial intermediate peptidase; *MIPEP*), all of which are relevant in T13 pathogenesis [59][60][61][62]. The proper expression of the *ATP7B* gene is implicated in copper homeostasis, the deregulation of which may result in the development of many pathologies, especially those related to metabolic, cardiovascular and neurodegenerative diseases, and cancer [63]. Interestingly, the proper expression of *ATP7B* is crucial for mitochondrial protection against increased oxidative stress conditions, being an essential micronutrient for proper SOD-1 and mitochondrial complex IV activities [64]. In this case, this gene triplication may lead to an increased possibility of mtDNA mutation, resulting in subsequent oxidative stress disturbances according to the lack of mitochondrial antioxidant defense [65]. The *BRCA2* gene is also responsible for oxidative stress homeostasis; its overexpression correlates with increases in oxidative stress-restricted mtDNA replication, resulting in a disturbed mitochondrial oxidative balance [66]. Moreover, alterations in *MIPEP* expression, involved in oxidative phosphorylation (OXPHOS)-related protein maturation, may additionally indicate a connection between mitochondrial dysfunction and T13 development [62][67]. Moreover, the study performed by Renaudin et al. showed that *BRCA2* deficiency impairs ribonuclease H1 (RNaseH1) function, which is required to ensure mtDNA maintenance [66]. Interestingly, other genes, such as *RB1* and *CHAMP1*, are also related to oxidative-stress-related processes. It has been suggested that disturbances in *RB1* gene expression are

involved in DNA damage sensor activity, forkhead box O (Foxo) transcription factors, and p38 mitogen-activated protein kinase processes, for which a disturbed expression affects cell-cycle progression, antioxidant capacity, mitochondrial mass, and cellular metabolism [68][69][70][71][72]. *CHAMP1* encodes a protein with a function in kinetochore–microtubule attachment and in the regulation of chromosome segregation. These properties are performed by their interaction and regulation of cell structure organization preceding mitosis, both of which are known to be important for proper fetal development [73][74]. Moreover, proper *MIPEP* expression is essential to maintain the normal level of mitochondrial sirtuin 3, which is considered a key regulator of oxidative stress by the deacetylation of the substrates involved in both ROS production and detoxification [75][76][77]. These mechanisms link oxidative stress to mitochondrial dysfunction and may be induced by the triplication of genes implicated in mitochondrial protective processes [78]. Referring to the fact that mitochondrial dysfunction is assumed to be one of the main T21-related symptoms [28][79], similar dysfunctions seem to be implicated in T13 development [59][66].

Furthermore, several important genes involved in intracellular cholesterol trafficking (Niemann–Pick C1 protein; *NPC1* gene), proper DNA transcription and signal transduction (mothers against decapentaplegic homolog; *SMAD*), and mitochondrial membrane function (ferrochelatase enzyme, coded by ferrochelatase; *FECH* gene) are mapped on chromosome 18 [80][81][82]. The *NPC1* gene encodes a crucial protein and affects the excitability of endosome and lysosome membranes, with characteristic mediation properties in intracellular cholesterol trafficking through cholesterol binding [80][83][84]. Interestingly, *NPC1* deficiency is related to neurodegenerative disease development due to oxidative damage. In this case, the *NPC1* gene's correct expression is essential for oxidative stress balance [85]. Moreover, *SMAD* proteins are signal transducers and transcriptional modulators involved in multiple signaling pathways, such as cell growth, apoptosis, morphogenesis, and immune responses [81][86][87]. Research conducted by Xui et al. showed that *SMAD* overexpression results in increased oxidative stress and a reduction in cell viability with subsequent induction of apoptosis [88]. The *FECH* gene, which encodes the ferrochelatase enzyme, essential for the proper catalyzation of the insertion of the ferrous form of iron into the protoporphyrin heme synthesis pathway, is also related to oxidative stress homeostasis [82][89][90][91] (Table 2).

Table 2. Gene expression related to T13 and T18 pathogeneses.

Gene Location	Gene	Full Name	Function
Chromosome 13	<i>ATP7B</i>	ATPase Copper Transporting Beta	copper transport
Chromosome 13	<i>BRCA2</i>	Breast Cancer 2	tumor suppression
Chromosome 13	<i>CHAMP1</i>	Chromosome Alignment-Maintaining Phosphoprotein 1	chromosome alignment maintenance with zinc finger protein regulations of chromosome

Gene Location	Gene	Full Name	Function
			segregation in mitosis
Chromosome 13	<i>MIPEP</i>	Mitochondrial Intermediate Peptidase	oxidative mitochondrial processes
Chromosome 13	<i>RB1</i>	Retinoblastoma Transcriptional Corepressor 1	inhibition of cell cycle processes, chromatin remodeling
Chromosome 18	<i>FECH</i>	Ferrochelataase	mitochondrial membrane function
Chromosome 18	<i>NPC1</i>	Niemann–Pick C1 Protein	intracellular cholesterol trafficking
Chromosome 18	<i>SMAD</i>	Mothers Against Decapentaplegic Homolog	transcription and signal transduction

tion and oxidative status. Therefore, a detailed evaluation of disturbed transcriptomic pathways related to T13 and T18 and the subsequent metabolic pathway disturbances may result in novel findings regarding trisomy-related abnormalities. Undoubtedly, studies may highlight deregulated pathways, and their detailed identification might become the basis for further research in T13 and T18 [\[45\]](#)[\[92\]](#).

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