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**DEVELOPMENT OF INSULIN RESISTANCE IN OBESE
ADOLESCENTS INTRODUCES GENOME REPROGRAMMING
AND CHANGES THE EXPRESSION OF NUMEROUS
ENDOPLASMIC RETICULUM STRESS RESPONSIVE GENES**

Minchenko D. O.

*Candidate of Medical Sciences, Associate Professor,
Associate Professor at the Department of Pediatrics
Bogomolets National Medical University
Kyiv, Ukraine*

Viletska Yu. M.

*Ph.D.,
Assistant Professor at the Department of Molecular Biology
Palladin Institute of Biochemistry of the National Academy
of Sciences of Ukraine
Kyiv, Ukraine*

Minchenko O. H.

*DrSc,
Professor at the Department of Molecular Biology
Palladin Institute of Biochemistry of the National Academy
of Sciences of Ukraine
Kyiv, Ukraine*

The development of obesity and its metabolic complications is associated with dysregulation of various intrinsic mechanisms, which control basic metabolic processes through changes in the expression of numerous regulatory genes. Endoplasmic reticulum stress is an important component of obesity related metabolic dysregulation as well as the development of insulin resistance and other complications of obesity.

The expression level of different genes as well as microRNA was measured in the blood of obese adolescents without signs of resistance to insulin and with insulin resistance in comparison with the group of relative healthy control individuals without signs of obesity. It was shown that in the blood of obese adolescents with normal insulin sensitivity the expression level of *IGFBP4*, *IGFBP5* and *HTRA1* genes was down-regulated, but *IGFBP2* and *IGFBP7* genes up-regulated as compared to control (normal)

group. At the same time, no significant changes in *IGF1* and *IGF2* gene expressions in this group of obese adolescents were found. Insulin resistance in obese adolescents led to up-regulation of *IGF2*, *IGFBP2*, and *IGFBP7* gene expressions as well as to down-regulation of the expression of *IGF1*, *IGFBP5* and *HTRA1* genes in the blood in comparison with the obese patients, which have normal insulin sensitivity. Furthermore, the level of *IGFBP4* gene expression was similar in both groups of obese adolescents.

Previously was shown that the expression of genes encoding IGF factors and IGF binding proteins as well as IRS1 are endoplasmic reticulum stress responsible and play important roles in the control of variable metabolic processes [1 – 4, p.3]. It was also shown that obesity is associated with up-regulation of the expression level of gene encoding polyfunctional protein insulinase (insulin degrading enzyme, IDE) and down-regulation of pitrilysin metallopeptidase 1 (PITRM1) independently from insulin resistance. Furthermore, suppression of ERN1 signaling pathway of endoplasmic reticulum stress down-regulates the expression of both these genes [5, p. 3]. It was also shown that obesity is associated with up-regulation of the expression level of genes encoding *HLA-DRA* and *HLA-DRB1*, which responsible for immune response, in the blood as compared to control group of relative healthy adolescents. At the same time, significant down-regulation was observed in the expression level of *HLA-G* gene in the blood of this group of obese adolescents. Furthermore, development of insulin resistance in obese individuals leads to significant down-regulation of *HLA-DRA*, *HLA-DRB1*, *HLA-G*, and *HLA-F* gene expressions as well as to up-regulation of *NFX1* gene as well as microRNA miR-190b in the blood as compared to obese patients without signs of insulin resistance.

Results of this study provide evidence that obesity affects the expression of the subset of genes related to glucose metabolism, cell proliferation and immune response in the blood and that development of insulin resistance in obese adolescents is associated with gene specific changes in the expression of *IGF1*, *IGF2*, *IGFBP2*, *IGFBP5*, *IGFBP7*, and *HTRA1* genes as well as with strong down-regulation of the expressions of *HLA-DRA*, *HLA-DRB1*, *HLA-F*, and *HLA-G* genes, which may be contribute to the development of obesity complications. It is possible that transcription factor *NFX1* and miR-190b participate in down-regulation of *HLA-DRA* gene expression in the blood of obese adolescents with insulin resistance.

References:

1. Minchenko D.O., Kharkova A.P., Hubenia O.V., Minchenko O.H. Insulin receptor, IRS1, IRS2, INSIG1, INSIG2, RRAD, and BAIAP2 gene expressions in glioma U87 cells with ERN1 loss of function: effect

of hypoxia and glutamine or glucose deprivation. *Endocr. Reg.* 2013. 47 (1): 15-26.

2. Minchenko D.O., Kharkova A.P., Karbovskiy L.L., Minchenko O.H. Expression of insulin-like growth factor binding protein genes and its hypoxic regulation in U87 glioma cells depends on ERN1 mediated signaling pathway of endoplasmic reticulum stress. *Endocr. Reg.* 2015. № 49 (2): 73-83.

3. Minchenko D.O., Kharkova A.P., Halkin O.V., Karbovskiy L.L., Minchenko O.H. Effect of hypoxia on the expression of genes encoded insulin-like growth factors and some related proteins in U87 glioma cells without IRE1 function. *Endocr. Reg.* 2016. 50 (2): 43-54.

4. Minchenko D.O., Tsymbal D.O., Luzina O.Y., Riabovol O.O., Danilovskiy SV, Minchenko O.H. Silencing of NAMPT leads to up-regulation of insulin receptor substrate 1 gene expression in U87 glioma cells. *Endocr. Reg.* 2020. 54 (1): 31-42.

5. Minchenko D.O., Khita O.O., Tsymbal D.O., Danilovskiy S.V., Rudnytska O.V., Halkin O.V., Kryvdiuk I.V., Smeshkova M.V., Yakymchuk M.M., Bezrodnyi BH, Minchenko O.H. Expression of IDE and PITRM1 genes in IRE1 knockdown U87 glioma cells: effect of hypoxia and glucose deprivation. *Endocr. Reg.* 2020. 54 (3): 183-195.

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СУЧАСНИЙ ПЕРЕБІГ ЕНТЕРОВІРУСНОЇ ІНФЕКЦІЇ У ДІТЕЙ

Онофрійчук О. С.

кандидат медичних наук,

доцент кафедри дитячих інфекційних хвороб

Вінницький національний медичний університет імені М. І. Пирогова

Гончарук А. М.

асистент кафедри дитячих інфекційних хвороб

*Вінницький національний медичний університет імені М. І. Пирогова
м. Вінниця, Україна*

В останні роки намітилася чітка тенденція активації ентеровірусної інфекції в світі, про що свідчать постійно зареєстровані в різних країнах світу епідеміологічні підйоми захворюваності й спалахи [1]. З одного боку, це пов'язано із зменшенням рівня захворюваності