Strong Gender-Specific Additive Effects of the NYD-SP18 and FTO Variants on BMI Values

J. A. HUBACEK¹, D. DLOUHA², V. LANSKA², V. ADAMKOVA³

¹Center for Experimental Medicine, Institute for Clinical and Experimental Medicine, Prague, Czech Republic, ²Statistical Unit, Institute for Clinical and Experimental Medicine, Prague, Czech Republic, ³Department of Preventive Cardiology, Center for Experimental Medicine, Institute for Clinical and Experimental Medicine, Prague, Czech Republic

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Summary
The role of the FTO gene in obesity development is well established in populations around the world. The NYD-SP18 variant has been suggested to have a similar effect on BMI, but the role of this gene in determining BMI has not yet been verified. The objective of our study was to confirm the association between NYD-SP18 rs6971091 SNP and BMI in the Slavic population and to analyze i) the gender-specific effects of NYD-SP18 on BMI and ii) the simultaneous effect of FTO rs17817449 and NYD-SP18 on BMI. We analyzed a sample of a large adult population based on the post-MONICA study (1,191 males and 1,368 females). Individuals were analyzed three times over 9 years. NYD-SP18 rs6971091 SNP is related to BMI in males (2000/1 GG 28.3±3.7 kg/m² vs. +A 27.5±3.7 kg/m² P<0.0005; in other examinations P<0.05 and <0.005), but not in females (all P values over 0.48 in all three examinations). Further analysis revealed the significant additive effect (but not the interaction) of FTO and NYD-SP18 SNPs on BMI in males (all P<0.01). These results suggest that association between NYD-SP18 rs6971091 SNP and BMI may be restricted to males. Furthermore, variants within NYD-SP18 and FTO genes revealed a significant additive effect on BMI values in males.

Key words
FTO • NYD-SP18 • BMI • Polymorphism

Introduction
Obesity is one of the serious non-communicable diseases, which further increases the risk of cardiovascular diseases, cancer and diabetes development. In the most affected populations, about 60% of individuals are overweight or obese and prevalence of obesity is significantly increasing even in children (Pastucha et al. 2013, Vrablik et al. 2014). Generally, overweight and obesity result from a positive energy balance, caused by the combination of low physical activity and high-energy intake. However, “non-traditional” factors like sleeping deficits, side effects of commonly prescribed drugs (mainly insulin, hypertensives, hormonal contraceptives) or social factors can significantly contribute and should not be omitted (Hubacek 2009, Adamkova et al. 2009, McAllister et al. 2009).

Body weight/body mass index (BMI) is also significantly influenced by genetic factors. Twin studies have estimated that genetic factors can be responsible for even about 60% of body mass index (BMI) variability. However, despite intensive efforts in recent decades, BMI heritability is still poorly understood and remains hidden within the context of concrete genes and variants.

Using the genome-wide analysis approach, two genes (among others), with largely unknown mechanisms by which they may influence the risk of obesity development, have been detected – FTO and NYD-SP18.

The association between BMI and FTO (“fat mass and obesity-associated gene”) was discovered by
many groups simultaneously (Dina et al. 2007, Frayling et al. 2007, Scuteri et al. 2007). FTO has a potential to
demethylate DNA (Gerken et al. 2007) and function as a
possible transcriptional cofactors (Wu et al. 2010). To
date, the general consensus is that FTO variants within
the first intron are the strongest determinants of BMI
among different ethnic groups around the world
(reviewed by Cheung and Yeo 2010, Dlouha and
Hubacek 2014). The association between rs17817449
SNP and BMI has also been confirmed in the Czech
However, studies that have focused on the functional
association between FTO and BMI reveal no clear results.
Thus, it is not completely clear whether FTO affects BMI
through its effect on physical activity, basal metabolism
or energy intake (Berentzen et al. 2008, Cecilia et al. 2008,
Haupt et al. 2009, Hubacek et al. 2011, Liu et al. 2010,
Harbron et al. 2014).

In contrast, NYD-SP18 (a protein with a largely
unknown function except for its role in testes
development via its influence on circulating testosterone
levels) has been identified using fine mapping of the
region on chromosome 7, widely known for its high LOD
score for obesity. In an original study (the NHLBI Family
Heart Study; replicated in the Framingham study), the
effect of the NYD-SP18 rs6971091 variant on BMI was
even larger than the effect of the widely-analyzed 1st
intron FTO variants (Wilk et al. 2008). However, the
effect of NYD-SP18 on BMI was never confirmed or
disproved in later studies.

The aim of our study was to confirm the original
finding of the association between NYD-SP18 and BMI
and to analyze the possible FTO – NYD-SP18 interaction
determining BMI.

Materials and Methods

Analyzed subjects

We analyzed NYD-SP18 SNP rs6971091 in
a group of representatively and randomly selected adult
individuals with the known FTO genotype, rs17817449
(1,191 males and 1,368 females, aged 25-64 years at
the age of first examination; mean age of 49.0±10.7 years)
(Hubacek et al. 2009, 2015). The individuals had
participated in the post-MONICA study (Cičkova et al.
2010). The WHO MONICA Project protocol (Tunstall-
Pedoe et al. 2003) was aligned to examine risk factors of
cardiocascular disease development, including BMI and
WHR. The subjects were examined in 9 Czech districts
(Kromeriz, Chrudim, Cheb, Jindrichuv Hradec, Pardubice, Litomerice, Plzen, Prague East, and Benesov)
in 1997/1998 and were completely re-examined in
2000/2001 (cohort from 2000/2001) and mostly (95.1 %)
also in 2007/8. Written, informed consent was given by
all individuals. The study was approved by the institute’s
Ethics Committee at the Institute for Clinical and
Experimental Medicine, Prague and is in agreement with
the Helsinki Declaration of 1975.

Genotyping

Genomic DNA was extracted from peripheral
blood white cells using a standard salting-out method
(Miller et al. 1988).

NYD-SP18 SNP rs6971091 was genotyped using
the PCR-RFLP technique. All PCR chemicals were
obtained from Fermentas International Inc., Burlington,
Ontario, Canada and PCR reactions were performed on
a PCR device – DYAD Disciple (MJ Research). Briefly,
DNA was amplified in a total volume of 25 μl with the
oligonucleotides, 5’ aag gcc tta acc acc tgg ttc tgc and
5’ cct tgg tca tta gct gaa tga gaa gct. The final PCR
product (105 bp) was cut with 5 units of the restriction
enzyme, HindIII (Fermentas International Inc.,
Burlington, Ontario, Canada) and restriction fragments
were separated on 10 % polyacrylamide gel using the
MADGE platform (Day et al. 1996). Restriction
fragments, 26 bp and 79 bp, represented the minor
A-allele, while the presence of the uncut product
represented the major G-allele.

FTO SNP rs17817449 has already been analyzed
in more detail, as described previously (Hubacek et al.

Statistical analysis

Deviations in Hardy-Weinberg equilibrium
were tested using the following link:
http://www.tufts.edu/~mcourt01/Documents/Court%20la
b%20-%20HW%20calculator.xls.

ANOVA was used for statistical analyses. Males
and females were analyzed separately. For individual
gene analyses, we pooled minor AA homozygotes
(7.2 %) and GA heterozygotes together because of the
relative low frequency of the minor A-allele of rs6971091
homozygotes. A P value of 0.05 was defined as
significant.

We analyzed the simultaneous effect of the
NYD-SP18 and FTO variants in three subgroups defined
by the presence of different numbers of risky alleles
Results

Basic characteristics of examined individuals at the 2000/2001 examination are presented in Table 1.

Table 1. Baseline characteristics for individuals analyzed in 2000/2001.

<table>
<thead>
<tr>
<th></th>
<th>Post-MONICA Males</th>
<th>Post-MONICA Females</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>1,191</td>
<td>1,368</td>
</tr>
<tr>
<td>Age (years)</td>
<td>49.2 ± 10.8</td>
<td>48.8 ± 10.6</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>28.2 ± 4.0</td>
<td>27.6 ± 5.5</td>
</tr>
<tr>
<td>WHR</td>
<td>0.929 ± 0.064</td>
<td>0.810 ± 0.072</td>
</tr>
<tr>
<td>Cholesterol (mmol/l)</td>
<td>5.75 ± 1.06</td>
<td>5.80 ± 1.15</td>
</tr>
<tr>
<td>Triglycerides (mmol/l)</td>
<td>1.98 ± 1.28</td>
<td>1.46 ± 0.85</td>
</tr>
<tr>
<td>HDL-cholesterol (mmol/l)</td>
<td>1.26 ± 0.33</td>
<td>1.50 ± 0.36</td>
</tr>
<tr>
<td>Diabetes (%)</td>
<td>6.0</td>
<td>4.4</td>
</tr>
<tr>
<td>Hypertension (%)</td>
<td>41.1</td>
<td>33.4</td>
</tr>
<tr>
<td>Smoking prevalence (%)</td>
<td>32.7</td>
<td>25.4</td>
</tr>
</tbody>
</table>

Call rates (calculated for individuals examined in 1998/9 and 2000/1, respectively) were 96.4 % for FTO and 97.8 % for NYD-SP18 SNPs.

Distributions of individual genotypes were in Hardy-Weinberg equilibrium. Frequencies of the individual alleles and genotypes were similar to the frequencies observed in other Caucasian populations (for example Dina et al. 2007, Frayling et al. 2007, Scuteri et al. 2007, Dušátková et al. 2013, Wilk et al. 2008).

As described before in the Czech post-MONICA population study, we detected a significant association (P<0.02) between FTO genotypes and BMI in males in cases where a co-dominant model of analysis was used (Table 2). In females, the effect progressed in the same direction but the observed differences did not reach statistical significance (Hubacek et al. 2009), which suggests that age or menopausal status in females is a significant determining confounder of BMI through the FTO gene. Results for females were similar in all three examinations.

Furthermore, similar gender-specific results were also obtained in the case of the NYD-SP18 polymorphism. We confirmed the findings from the original study (Wilk et al. 2008) in males only and detected higher BMI values in NYD-SP18 GG homozygotes than in A-allele carriers (GG 28.3±3.7 kg/m² vs. +A 27.5±3.7 kg/m²; P<0.0005). Similar significant differences were observed in both other examinations (P<0.05 and <0.005, respectively) (Table 2). In females, no effect of rs6971091 within the NYD-SP18 gene on BMI values in any of the three examinations was observed (all P values over 0.48; results are not shown in detail).

Table 2. Genotype frequencies of analyzed individuals and the association between FTO rs17817449 and NYD-SP18 rs6971091 polymorphisms and BMI values (kg/m²) in the Czech post-MONICA study of 2000/2001.

<table>
<thead>
<tr>
<th></th>
<th>rs17817449</th>
<th>N</th>
<th>%</th>
<th>BMI p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>177</td>
<td>15.9</td>
<td>28.7 ± 3.7</td>
<td></td>
</tr>
<tr>
<td>GT</td>
<td>572</td>
<td>51.4</td>
<td>28.3 ± 4.1</td>
<td>0.014</td>
</tr>
<tr>
<td>TT</td>
<td>364</td>
<td>32.7</td>
<td>27.8 ± 3.9</td>
<td></td>
</tr>
<tr>
<td>Females</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>249</td>
<td>18.4</td>
<td>27.9 ± 5.7</td>
<td></td>
</tr>
<tr>
<td>GT</td>
<td>652</td>
<td>48.1</td>
<td>27.5 ± 5.4</td>
<td>n.s.</td>
</tr>
<tr>
<td>TT</td>
<td>453</td>
<td>33.5</td>
<td>27.4 ± 5.0</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>rs6971091</th>
<th>N</th>
<th>%</th>
<th>BMI p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>630</td>
<td>53.6</td>
<td>28.3 ± 3.7</td>
<td>0.0005</td>
</tr>
<tr>
<td>+A</td>
<td>545</td>
<td>46.4</td>
<td>27.5 ± 3.6</td>
<td></td>
</tr>
<tr>
<td>Females</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>696</td>
<td>52.4</td>
<td>27.4 ± 5.3</td>
<td>n.s.</td>
</tr>
<tr>
<td>+A</td>
<td>632</td>
<td>47.6</td>
<td>27.5 ± 5.4</td>
<td></td>
</tr>
</tbody>
</table>

In males, we further analyzed whether the combination between the FTO rs17817449 and NYD-SP18 rs6971091 polymorphisms had an influence on BMI or whether it had an additive effect, or whether these SNPs exhibited any interaction. Distinct combinations, based on the number of risky alleles of
FTO and NYD-SP18 SNPs, revealed a significant effect on BMI in the additive model (all three P values were over 0.004; all three analyses remained significant after Bonferroni correction for multiple testing). However, no interaction (all three P values were over 0.56) between the analyzed SNPs was found (Table 3). Briefly, carriers of at least three risky alleles had the highest BMI values and carriers of at least three protective alleles had the lowest, with carriers of exactly two risky and two protective alleles exhibiting medium values (P<0.0001 in 2000/2001; for more details see Table 3). Adjustment for age did not change the differences significantly.

Table 3. Additive effects of the FTO rs17817449 and NYD-SP18 rs6971091 polymorphisms on BMI (kg/m²) in males from the 2000/2001 Czech post-MONICA study, according to subgroups with different numbers of risky alleles.

<table>
<thead>
<tr>
<th>FTO/NYD-SP18 genotypes</th>
<th>N</th>
<th>BMI</th>
<th>P&lt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>GG/GG and GG/GA and GT/GG</td>
<td>393</td>
<td>28.8 ± 4.1</td>
<td></td>
</tr>
<tr>
<td>GG/AA and TT/GG and GT/GA</td>
<td>442</td>
<td>27.9 ± 3.9</td>
<td>0.0001</td>
</tr>
<tr>
<td>GT/AA and TT/GA and TT/AA</td>
<td>199</td>
<td>27.3 ± 3.9</td>
<td></td>
</tr>
</tbody>
</table>

Discussion

Body weight is a polygenic trait, which means that many variants within dozens of genes can significantly affect final individual values (Day and Loos 2011). It is estimated that single negative alleles increase body weight to a maximum of about one kilogram (FTO, NYD-SP18 genes). However, most of the risky alleles add about 200-300 g “only”. Some studies have focused on gene score in the context of BMI association (Peterson et al. 2011, Domingue et al. 2014). However, knowledge is sparse in the following areas: simultaneous presence of more risky alleles; additive effects and interaction; the critical number of risky alleles that leads to obesity in all cases; and at what stage alleles appear.

In our study, we analyzed the simultaneous effect of the two major BMI determinants, namely the genes for FTO and NYD-SP18. Briefly, we confirmed that the simultaneous presence of the distinct alleles of these genes is associated with enhanced BMI values. Importantly, we detected that there is a significant gender-specific effect of these genes on BMI. We also found a significant association between the variants of these genes and BMI in males only.

Dozens of papers have confirmed the role of the FTO gene in genetic determination of obesity (Hubacek et al. 2008, Dušátková et al. 2013, Tönjes et al. 2010, Hakanen et al. 2009), renal failure (Hubacek et al. 2012), type 2 diabetes (Scott et al. 2007), Alzheimer’s disease (Reitz et al. 2012), suicide (Chojnicka et al. 2014) and even with infection diseases, such as tuberculosis (Feng et al. 2014).

In relative contrast to the well-established role of FTO, our study is the first to confirm the role of the NYD-SP18 rs6971091 polymorphism in BMI determination, as suggested by Wilk et al. (2008). Furthermore, we have recently presented data suggesting that this gene could be a significant predictor of body composition changes in adult females after intensive ten-week life-style interventions, based on intensive physical activity and age-adjusted optimal energy intake (Suchanek et al. 2015). This finding is of interest mainly because BMI is not strongly affected by this variant at the female population level.

Interestingly, in both genes, details in relation to the mechanism of action are unclear. It has been suggested that FTO first intron variants may have effects on epigenetic changes (Almén et al. 2012), transcriptional activity (Wu et al. 2010), RNA modification (Berulava et al. 2013) and leukocyte telomere length (Dlouha et al. 2012), which, surprisingly, point to some very heterogeneous regulatory effects. The function of the NYD-SP18 gene is largely unknown, although it has been suggested that it may influence testosterone production.

The major limitation of our study is that we did not have a confirmatory group of individuals at our disposal. However, our subjects were examined three times within the nine-year period, of which all analyses led to identical conclusions, thus lowering the risk of false-positive results.
We conclude that the NYD-SP18 rs6971091 polymorphism could be a significant genetic determinant of BMI values in males, but not in females. Furthermore, we observed an additive effect on BMI between the FTO rs17817449 and NYD-SP18 rs6971091 genetic variants in males, which underlines the importance of the simultaneous context-dependent analyses of variants in multiple genes.

Conflict of Interest
There is no conflict of interest.

Acknowledgements
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