

Sex-specific causal relations between steroid hormones and obesity – a Mendelian Randomization Study

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Supplemental Data – Detailed findings of GWAMA

2.1.1. Progesterone (P4)

For P4, we detected seven loci associated with genome-wide significance, of which three were novel associations. These loci were at cytobands 1q32.2, 7q36.3, and 16p13.3. At 1q32.2 and 16p13.3 there were female-specific effects (no effect in males, interaction after hierarchical FDR correction $q_{IA} = 4.97 \times 10^{-6}$ for 1q32.2, and $q_{IA} = 3.13 \times 10^{-6}$ for 16p13.3). The association at 7q36.3 was sex-related: the lowest p-value was observed in the combined setting, but the effect in females differed significantly from that in men ($\beta_{males} = -0.226$, $p_{males} = 1.14 \times 10^{-4}$; $\beta_{females} = -0.559$, $p_{females} = 1.45 \times 10^{-5}$; $q_{IA} = 0.0187$). Plausible candidate genes are: *CD55* at 1q32.2 (cis-eQTL), whose gene expression is up-regulated by progesterone in mice [1]; *VIPR2* at 7q36.3 (intron modifier), coding for a receptor of the pituitary adenylate cyclase-activating polypeptide which is controlling the hormone release for ovulation [2]; and *RBFOX1* at 16p13.3 (intron modifier), which is androgen-responsive [3].

We also tested the known loci for sex-interaction and replicated the female-specific effects at *KCNH1* (1q32.2), *ARNTL* (11p15.2), and *HSD17B12* (11p11.2). In addition, we observed a novel interaction for *CYP17A1* (10q24.32), which was male-specific. Hence, all seven observed P4 associations had significant sex-interactions: five female-specific, one male-specific, and one sex-related with stronger effect in females.

2.1.2. 17-hydroxy-progesterone (17-OHP)

We found four genome-wide significant loci for 17-OHP, one known (MHC region at chromosome 6), and three novel hits at 1p12, 2p15, and 18q22.3. The first novel locus at 1p12 was male-specific ($\beta_{males} = 0.112$, $p_{males} = 1.03 \times 10^{-10}$; $\beta_{females} = -0.016$, $p_{females} = 0.571$; $q_{IA} = 5.14 \times 10^{-4}$) and was located near *HSD3B1*, coding for the enzyme transforming 17-OH-pregnenolone to 17-OHP. In a previous work, we only detected this locus with suggestive significance [4]. The other two loci were at 2p15 and 18q22.3, with candidate genes *REL* and *CYB5A*, respectively. *Rel* and P4 are part of a DNA loop, which enhances gene expression [5], while *Cyb5* has a redox effector role for *Cyp17A1* [6], another enzyme of the steroid biosynthesis pathway catalyzing the reaction of P4 to 17-OHP. The effect at 2p15 was sex-unspecific, while the other was male-specific ($q_{IA} = 7.81 \times 10^{-2}$ at 2p15; $q_{IA} = 8.21 \times 10^{-7}$ at 18q22.3). The known hit at MHC was sex-unspecific ($q_{IA} = 0.722$).

2.1.3. Androstenedione (A4)

There was only one novel locus for A4 at cytoband 10q26.3, which was male-specific ($q_{IA} = 7.06 \times 10^{-4}$). The most likely candidate gene was *MGMT* (intron modifier). Its genetically regulated gene expression was associated with A4 in all tissues (using MetaXcan and GTex data). P4 has been reported to suppress *MGMT* expression in WHO grade IV human glioblastoma multiforme cell lines [7]. The androgen and progesterone receptor are closely related, and P4 in high dosages can block the androgen receptor [8,9]. This might explain the observed A4 association, but the exact mechanisms behind this are still unclear. In addition, we replicated *CYP11B2* at 8q24.3 [4]. There was no sex-interaction observed for this locus ($q_{IA} = 0.573$).

2.1.4. Aldosterone (Aldo)

For the first time, we were able to detect genome-wide significant hits for aldosterone, one female- and one male-specific locus. The female-specific locus was at 1q23.3 within *HSD17B7*, coding for another enzyme of the steroid pathway ($q_{IA} = 9.62 \times 10^{-6}$). The male-specific hit is within a gene desert, but a trans-eQTL of *CNST*, suggesting a connection to connexins, which play a role in the renin-angiotensin-aldosterone system [13] ($q_{IA} = 0.0281$).

2.1.5. Testosterone to estradiol ratio (T/E2)

We detected two loci associated with the ratio of T to E2. Several independent SNPs (pairwise LD $r^2 < 0.1$) were associated at 15q21.2 with candidate gene *CYP19A1*, which has been described previously for E2 [4], T [11], sex hormone-binding globulin levels [11], and WHR [14]. While this locus showed no sex-specific effect for E2 alone [4], we detected a weak male-specific effect for the T/E2 ratio. However, this interaction did not withstand multiple testing correction ($p_{IA} = 0.0272$; $q_{IA} = 0.054$). The second associated locus was at 6q26 near *PARK2*. It has been reported that T and E2 prevent lymphocytes with a homozygote missense mutation in *PARK2* from oxidative stressors-evoked apoptosis in juvenile Parkinson patients [15]. Here, no sex-interaction was observed ($p_{IA} = 0.707$).

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