(3), suggesting that environmental factors may play a role in this PCOS-specific IR. Yet, the molecular mechanisms regulating IR remain unclear (4). Previous work suggested that Transforming Growth Factor Beta (TGFβ) superfamily ligands may be involved in the metabolic morbidity associated with PCOS (5). In this study, we investigated the effects of TGFβ1 (1, 5ng/ml), and the Anti-Müllerian hormone (AMH; 5, 10, 30ng/ml), a novel TGFβ superfamily ligand elevated in women with PCOS, as causal factors of IR in cultured myotubes from women with PCOS (n=10) and healthy controls (n=10). AMH negatively affected glucose uptake and insulin signalling increasing p-IRS1 (ser312) in a dose-dependent manner in myotubes from both women with and without PCOS. AMH did not appear to activate the canonical TGFβ/BMP signalling pathway. Conversely, TGFβ1 had an opposite effect in both PCOS and control myotubes cultures, decreasing phosphorylation of IRS1 (ser312) and enhancing glucose uptake via Smad2/3 signalling. In conclusion, these results suggest that AMH may play a role in skeletal muscle IR observed in PCOS, however, further research is required to elucidate its mechanisms of action and broader impact in this syndrome. **References:** (1) Stepto *et al. Hum Reprod* 2013 Mar;28(3):777-784. (2) Cassar *et al. Hum Reprod* 2016 Nov;31(11):2619-2631. (3) Corbould *et al., Am J Physiol-Endoc* 2005 May;88(5):E1047-54. (4) Stepto *et al. J Clin Endocrinol Metab*, 2019 Nov 1;104(11):5372-5381. (5) Raja-Khan *et al. Reprod Sci* 2014 Jan;21(1):20-31.

Cardiovascular Endocrinology
FROM BEDSIDE TO BENCH AND BACK AGAIN: LIPID METABOLISM & VASCULAR DISEASE

Retinol Binding Protein 4 Predicts Functional Vascular Disease in Early Postmenopausal Women

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Introduction: The impact of gender on the development of cardiovascular disease has long been recognized. The potential effect of sex-specific cardiovascular risk factors on molecular mediators of oxidative stress has received limited attention and the results remain conflicting.
Hypothesis: To assess the link between retinol binding protein 4 (RBP4) and menopause-specific cardiovascular risk factors, on indices of early subclinical atherosclerosis, in a sample of apparently healthy young, postmenopausal women.

Methods: This cross-sectional study included a total of 123 healthy postmenopausal women, recruited from a University Menopause Clinic. Participating women were, not on hormone therapy, antihypertensive or hypolipidemic treatment and had a menopausal age of up to 10 years. Fasting venous blood samples were obtained for hormonal and biochemical assessment, including levels of RBP4. Sonographical studies were performed on the same day and included carotid-femoral pulse wave velocity (PWV) and calculation of the carotid artery stiffness index (SI).
Major results: Univariate analysis showed that RBP4 values correlated positively with age, total cholesterol, triglycerides, LDL-cholesterol, testosterone-to-estrogen ratio; negatively with circulating estrogen and almost significantly with homocysteine levels. Levels of homocysteine were inversely associated with RBP4 (homocysteine: RBP4 <10.5ng/ml vs ≥10.5ng/ml: 11.2±2.81µmol/L vs 12.52±3.44µmol/L, p-value=0.049 ANCOVA, adjusted for age, BMI, HOMA-IR). Multivariate analysis showed that PWV values were predicted by RBP4 (b-coefficient=0.435, p-value=0.006), age, pulse pressure, homocysteine. S.I. beta was predicted independently by RBP4 levels (b-coefficient=0.324, p-value=0.039). Both models were adjusted for menopausal age, LDL-cholesterol, FEI, smoking, HOMA-IR.
Conclusion: RBP4 levels are linked with measures of local carotid and aortic arterial stiffness, in this sample of healthy postmenopausal women. This association seems to be mediated by higher levels of homocysteine, which may interfere with retinoic acid synthesis. Larger studies are required to further elucidate the significance of our findings.
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Diabetes Mellitus and Glucose Metabolism
LIPIDS, OBESITY AND METABOLIC DISEASE

The Gut Microbiome Regulates Host Glucose Homeostasis via Peripheral Serotonin

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The gut microbiome is an established regulator of aspects of host metabolism, such as glucose handling. Despite the known impacts of the gut microbiota on host glucose homeostasis, the underlying mechanisms are unknown. The gut microbiome is also a potent mediator of gut-derived serotonin synthesis, and this peripheral source of serotonin