SESSION 11
SELENIUM IN LIFESTOCK

NOVEL PORCINE MODELS FOR STUDYING DIABETOGENIC RISK OF HIGH DIETARY SE INTAKE AND UNDERLYING MECHANISM RELATED TO SELENOPROTEIN EXPRESSION

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A number of major human studies have shown intriguing pro-diabetic, hyperglycemic, or hyperlipidemic risks associated with high dietary intakes of Se. Because pigs are an excellent model for human nutrition and medicine, we have developed porcine models to elucidate effects of high dietary Se intake on body glucose and lipid metabolism, and the underlying mechanism related to selenoprotein expression. We initially cloned all 25 porcine selenoprotein genes and determined regulation of their transcripts and protein levels in various tissues of pigs by dietary Se concentrations (0.02, 0.3, and 3 mg/kg). After weanling pigs (7.5 kg body weigh) were fed a corn-soy diet supplemented with 1.0 mg Se/kg (as sodium selenite) for 8 weeks, their fasting plasma glucose or lipid profiles were not different from those fed 0.3 mg Se/kg. In contrast, hyperinsulinemia consistently occurred in pigs fed 3.0 mg Se/kg (as Se-enriched yeast) for 11 to 16 weeks in two independent experiments. Compared with their Se-adequate controls (0.3 mg/kg), these pigs showed altered profiles of plasma glucose and lipid in the early phase of experiment, and elevated ($P < 0.05$) mRNA and protein levels of lipogenesis and protein synthesis pathways in liver and muscle. To create an obese and diabetic porcine model, we fed cross-bred, castrated boars (n = 20, 20 kg body weight) with an Se-adequate (0.3 mg/kg), corn-soy diet (total fat < 0.82%) or the diet added with lard at 3% (20–50 kg), 5% (50–80 kg), or 7% (> 80 kg) for six months. In the end, pigs fed the high fat diet developed moderate obesity and insulin resistance. The high fat intake elevated mRNA abundance of eight selenoproteins and decreased that of nine selenoproteins in various tissues of pigs. This implied a reciprocal regulation between body selenoproteins and lipid metabolism(NIH DK 53018, NSFC Projects 30628019, 30700585, and 30871844, and the Chang Jiang Scholars Program).

COMPARING FUNCTIONAL METABOLIC EFFECTS OF MARGINAL AND SUFFICIENT SELENIUM SUPPLY IN SHEEP

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Link to published paper in J Trace Elem Med Biol, Oct; 27(4):380-90:
http://www.unboundmedicine.com/medline/citation/23611506/Comparing_functional_metabolic_effects_of_marginal_and_sufficient_selenium_supply_in_sheep_

SUPRANUTRITIONAL SELENIUM, GROWTH AND VASCULARITY: IMPACTS OF SUPRANUTRITIONAL SELENIUM DURING PREGNANCY ON NUTRIENT TRANSFERRING TISSUES IN THE DAM AND OFFSPRING

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Inappropriate maternal environment has been documented to impact fetal development and lead to compromised postnatal growth and metabolism in many livestock species. Our laboratory has investigated maternal dietary supranutritional Se supplied throughout pregnancy on growth and vascular development of key nutrient transferring tissues (maternal and offspring intestine, placenta, and mammary gland) during gestation and early neonatal life in the face of inadequate or excess maternal nutrition. Our over-arching hypothesis is that maternal supranutritional Se would mitigate the negative impacts of under- and over-nourishment during gestation in first parity mothers. Our data supports that maternal levels of Se impact growth and vascularity of key nutrient delivering tissues during gestation and early lactation

in dams, as well as in neonates and near adult offspring. Supranutritional Se during pregnancy may play an important role in altering the growth trajectory of poorly nourished offspring. Elucidating the consequences of inappropriate maternal intake and dietary Se supply on the development and plasticity of intestinal, placental, and mammary tissues will allow for enhanced biological understanding and improved therapeutic intervention into compromised pregnancies and offspring.

CLONING, SEQUENCING, AND EXPRESSION OF SELENOPROTEIN TRANSCRIPTS IN THE TURKEY (MELEAGRIS GALLOPAVO)

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The minimum Se requirement for male turkey poults is 0.3 µg Se/g - three times higher than requirements found in rodents - based on liver and gizzard Gpx4 and Gpx1 activities (Exp Biol Med 235:23 (2010)). In addition, turkey liver Gpx4 activity is 10-fold higher and Gpx1 activity is more than 10-fold lower than in rats, and both Gpx1 and Gpx4 mRNA levels are dramatically down-regulated by Se deficiency. Thus we initiated cloning of turkey selenoprotein transcripts to investigate Se regulation of the full selenoproteome. Using homology of mammalian and G. gallus (chicken) transcripts and proteins, primers for qRT-PCR were designed to examine the relative expression of selenoproteins in total RNA isolated from 6 turkey tissues (liver, heart, kidney, gizzard, thigh, breast) of an adult male Nicholas-strain (white) turkey. The turkey selenoproteome in turkeys appears to consist of 24-26 selenoproteins, with greater than 90% sequence identity with the chicken and roughly 70% identity with mammalian selenoproteins. Using relative Ct and expression values, Sepp1 mRNA appears to be the most abundant selenoprotein mRNA in both turkey and rat liver. As expected based on enzyme activity, turkey liver Gpx1 and Gpx4 mRNA levels are 25% and 200% of rat levels; Sepw1 and Sels mRNA levels are over 10-fold higher than in rat liver. Fold-changes in different turkey tissues relative to liver were: for kidney, Gpx1 11X, Txnrd1 4X, Sepn1 3X, Sepw1 3X; for heart, Sepw1 6X, Sepn1 4X, Dio2 4X; for gizzard, Sepn1 6X, Selm 3X, Sepw1 2X; for breast, Sepw1 6X; for thigh, Sepw1 4X, Dio2 3X, Sepn1 2X. 3´ and 5'-RACE has been used to clone and sequence 19 selenoproteins so far, as well as the selenocysteine tRNA which was not found in contigs present in shotgun sequencing of the turkey genome (PloS Biology 8:e1000475 (2010)). These sequences are being used to develop molecular biomarkers to characterize Se regulation in the turkey.

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