adducts called oxidation specific epitopes (OSEs), which are proinflammatory moieties present on oxidized low density lipoproteins and on apoptotic cells and, unless removed, cause extensive cell damage. Natural antibodies (NAb) produced by B-1 lymphocytes, bind OxPL and prevent their inflammatory activity. E06 is a NAb that recognizes the phosphocholine moiety of OxPL. We previously showed that transgenic expression of a single chain (scFv) form of the antigen-binding domain of E06 IgM (E06-scFv) increases cancellous and cortical bone mass in both male and female mice by increasing bone formation. Age-related bone loss is characterized by a decline in osteoblast number and bone formation, associated with increased oxidative stress and lipid peroxidation. These findings, together with the evidence that serum anti-OxPL IgM titers decrease with age, suggest that increased OxPL formation and decreased anti-OxPL antibodies may contribute to age-related bone loss. Like humans, mice exhibit an age-dependent worsening in glucose tolerance, mainly due to alteration in body composition and increased fat tissue. Chronic low grade inflammation and oxidative stress are associated with development of diabetes mellitus and B-1 lymphocytes have been shown to be protective against obesity associated inflammation, glucose intolerance, and insulin resistance. We tested the hypothesis that overexpression of E06-scFv could attenuate age-related bone loss and glucose intolerance. Serial BMD measurements by DXA of both female and male C57BL/6 E06-scFv transgenic mice (and their WT littermates) up to 22 and 24 months, respectively, showed that E06-scFv attenuated age-related bone loss at the spine and femur in both sexes. As revealed by microCT analysis, this effect was due to the attenuation of the age-associated decline in cancellous bone in both sexes. Additionally, both male and female E06-scFv transgenic mice accumulated less fat mass than WT littermates during aging. Intraperitoneal glucose tolerance test, at 15 months of age, revealed that glucose tolerance was greater in both male and female E06-ScFv mice than in respective WT littermates and did not differ from the glucose tolerance of young mice, indicating that E06-scFv improves glucose metabolism. These data suggest that OxPL impair both age-related bone loss and age-related glucose intolerance. Therefore, targeting OxPL with a neutralizing antibody such as E06, represents a prototypic therapeutic intervention that may simultaneously ameliorate important age-associated diseases.

Genetics and Development (including Gene Regulation)

GENETICS AND DEVELOPMENT AND NON-STEROID HORMONE SIGNALING II

The Chromatin Landscape of Glucocorticoid Regulated Genes in Mouse Embryonic Neural Stem / Progenitor Cells

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The Chromatin Landscape of Glucocorticoid Regulated Genes in Mouse Embryonic Neural
Stem/Progenitor Cells
Antenatal administration of Dexamethasone (Dex), a synthetic glucocorticoid (GC), is a common clinical intervention for women at risk for preterm birth or in preterm labor that effectively
reduces fetal risk of mortality and bronchopulmonary-related comorbidities. Despite the
therapeutic potential of Dex, excess GC act adversely in the developing central nervous system
to reprogram distinct neural circuits in the brain by acting through the glucocorticoid receptor
(GR). For example, prenatal exposure to excess GCs can impact neural stem and progenitor cell
(NSPC) proliferation leading to long-term alterations in prefrontal cortical neuronal complexity,
which could contribute to behavioral and cognitive impairments later in life. The GR is a
member of the nuclear receptor superfamily that, when bound by a ligand, translocates from
the cytoplasm to the nucleus and associates indirectly or directly with DNA elements (e.g.
glucocorticoid responsive elements or GREs) resulting in the activation and/or repression of
target genes. While GR-regulated transcriptomes have been identified in many NSPC models,
the mechanisms responsible for programming these cells for GC-responsiveness remain largely
unknown. We therefore used transposase accessible chromatin followed by genome-wide
sequencing (Omni ATAC-seq) to characterize the chromatin landscape of primary embryonic
mouse NSPCs in response to an acute *in vitro* treatment with Dex. We identified a small, yet
distinct fraction (0.002%, $p<0.05$) of open chromatin sites that were Dex-inducible. 95% of
these Dex-induced changes in chromatin accessibility occur within intronic or intergenic
regions, suggesting the presence of long-range enhancer-promoter contacts that mediate NSPC
transcriptional responses to Dex. Motif enrichment analysis revealed putative GRE sites located
in Dex-inducible open chromatin within -5kb/+2kb of a Dex-induced gene, providing possible
DNA targets of GR for further validation. A number of other transcription factors implicated in
neurodevelopmental processes were found to underlie both Dex-inducible and constitutively
open chromatin regions. Characterization of the precise epigenetic and transcriptional response
to excess GC *in-utero,* and its influence on acute and chronic neurological outcomes, will
encourage the development of alternative GC treatment regimens that could protect the
developing brain from insult while providing optimal health outcomes in neonates.

Tumor Biology

TUMOR BIOLOGY: GENERAL, TUMORIGENESIS, PROGRESSION, AND METASTASIS

An Uncommon Case of Squamous Cell Carcinoma of the Vulva with Metastasis to the Thyroid Gland

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