postmenopausal women. A total of 78 subjects completed the study, with 12 subjects dropping out due to non-compliance and medical reasons. Supplementation with fish oil attenuated the thrombin receptor PAR4-induced platelet aggregation, whereas primrose oil supplementation attenuated aggregation mediated by PAR4 or collagen. Supplementation with âµ-3 or âµ-6 fatty acids decreased platelet dense granule secretion and attenuated basal levels of integrin âºIIbÎ²3 activation. Post-washout following supplementation with primrose oil, the thrombin receptor PAR1-induced platelet aggregation was similarly attenuated. For either treatment, the observed effects post supplementation on dense granule secretion and basal integrin activation were sustained after the washout. DISCUSSION/SIGNIFICANCE: Postmenopausal women are at increased risk for a cardiovascular event due to platelet hyperactivity. This study indicates that supplementation with âµ-3 and âµ-6 fatty acids may offer significant protection for postmenopausal women against cardiovascular diseases and occlusive thrombotic events by reducing platelet reactivity.

208

Identification of Trichomonas vaginalis 5-nitroimidazole resistance targets to inform future drug development

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OBJECTIVES/GOALS: 5-nitroimidazoles are the only FDA-approved medications for T. vaginalis treatment. Resistance has been observed in 5-10% of cases, but may be rising. We aimed to delineate mechanisms of resistance in isolates of T. vaginalis using transcriptome profiling of resistant and sensitive T. vaginalis isolates. METHODS/STUDY POPULATION: T. vaginalis isolates (4 metronidazole (MTZ)-resistant were grown in triplicate in Diamond's Trypticase-Yeast-Maltose medium. MTZ susceptibility testing confirmed MTZ MLCs of T. vaginalis isolates. Total RNA extraction was done using Trizol reagent (Invitrogen; Carlsbad; CA); according to the manufacturer's instructions. RNA sequencing (RNAseq) and bioinformatics analyses were performed to identify significantly differentially expressed genes (DEGs) in MTZ-resistant vs. sensitive isolates. Subsequent qPCR was performed to confirm and extend RNAseq data and gene targets related to 5-nitroimidazole resistance. RESULTS/ANTICIPATED RESULTS: RNAseq identified key DEGs in MTZ-resistant vs. sensitive isolates. DEGs from MTZ-resistant isolates included those involved in metabolic pathways relevant to 5-nitroimidazole resistance such as energy production (glycolytic enzymes) and oxygen-scavenging (thioredoxin). Other DEGs included those encoding transcription factors (MYB DNA-binding protein), ribosomal proteins (30S, 40S, 50S, 60S), protein kinases (CAMK, ser/thr, CMGC), Ankyrin repeat proteins, surface proteins (Surface antigen BspA-like) and various uncharacterized hypothetical proteins. RT-qPCR experiments confirmed reduced expression of genes encoding ferredoxin (drug activation) and flavin reductase 1 (oxygen scavenging) in MTZ-resistant T. vaginalis isolates as compared to MTZ-sensitive isolates. DISCUSSION/SIGNIFICANCE: In this study, we identified several DEGs in resistant T. vaginalis isolates. Further studies with large number of isolates representing a broad range of MTZ-susceptibility patterns are needed to identify genes that may represent new targets for future drug development.

209

A CTS Team Approach to Modeling Migration and Suppression of CCR2+/CX3CR1+ Myeloid Cells in Glioblastoma

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OBJECTIVES/GOALS: Evaluate the migration and immune suppressive functions of CCR2+/CX3CR1+ myeloid-derived suppressor cells (MDSCs). Integrate experimental data and biologically relevant mathematical models of infiltrating MDSCs in the context of glioblastoma (GBM). METHODS/STUDY POPULATION: CCR2+/CX3CR1+ cells were enriched from bone marrow obtained from CCR2(+/RFP)/CX3CR1(+/GFP) glioma-bearing mice to evaluate their immune-suppressive phenotype and ability to migrate to CCL2 and CCL7. Fluorescent imaging and quantification were performed on a range of tumor sizes to acquire vasculature, tumor, T cell, and MDSC densities. A system of ordinary differential equations was constructed to represent the temporal dynamics of glioma cells, T cells, and MDSCs within the tumor microenvironment. The Approximate Bayesian Computation method was used to determine probability distributions of important parameters, such as the suppression rate of T cells by MDSCs. RESULTS/ANTICIPATED RESULTS: CCR2+/CX3CR1+ M-MDSCs isolated from the bone marrow of tumor-bearing mice suppress CD8+ T cell proliferation and IFNÎ³ production. CCR2+/CX3CR1+ cells migrate to recombinant and KR158B glioma sourced CCL2 and CCL7. Parameter values determined by the Approximate Bayesian Computation method agreed with parameter values from experimental data. This result further validated the structure and results of the mathematical model when performing computer simulations; thus, we can predict CCR2+/CX3CR1+ M-MDSC infiltration over time. DISCUSSION/SIGNIFICANCE: The immune-suppressive microenvironment in GBM contributes to poor outcomes despite standard of care. This study integrates biological and mathematical models to better understand infiltrating immune-suppressive cells, namely CCR2+/CX3CR1+ M-MDSCs. Future directions include modeling immunotherapies.

210

Antibody function, antigenic target and glycans determine the transfer of herpes simplex virus (HSV) antibodies (Abs) from mothers to newborns and transfer is altered by SARS-CoV-2*

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OBJECTIVES/GOALS: Murine and clinical data suggest that antibody-dependent cellular cytotoxicity (ADCC) is associated with greater protection against disseminated neonatal HSV disease. To quantify the relative transfer of Abs with different functions and targets, we conducted a prospective study of mother-infant term and

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