

North Dakota Tribal College Research Symposium 2015
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Cankdeska Cikana Community College

Factors Influencing Behavioral Health Outcomes

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Purpose This study, describing behavioral health status of students, staff, and faculty in a rural, tribal community and factors influencing behavioral health outcomes, has six research questions: 1) How do level of mental and physical health influence general health and life satisfaction? 2) Does poverty influence general health and life satisfaction? 3) Is having a disability associated with depression, anxiety, and life satisfaction? 4) Is poor mental health correlated with “self-medication” with alcohol? 5) Do men’s health outcomes vary by demographics? 6) Do health needs vary by age? **Methods** Students, faculty, and staff were invited to complete a cross-sectional, electronic survey Fall 2013. The survey, based on the 2012 BRFSS, was completed by 124 people: 59% female, average age 31. Demographics were summarized using frequencies, percents, means, and standard deviations. The research questions employed regression, anova, t-test, and content analysis. **Results:** 1) The higher the number of poor mental health days, the lower the level of general health and life satisfaction. 2) The number of poor physical health days and poverty were not correlated with general health and life satisfaction. 3) People who reported having a disability (limitation) had lower life satisfaction but were not more likely to have depression and anxiety. 4) People who reported a higher number of poor mental health days also reported a higher number of days drinking. 5) Male students had more days where level of activity was impacted by poor physical or mental health days than male faculty. 6) Health needs did not vary by age. **Support:** NARCH, The National Center for Research Resources (P20 RR016471); the National Institute of General Medical Sciences (P20 GM103442) from the National Institutes of Health; grant number 1U79SM058389-01 from the Substance Abuse and Mental Health Services Administration (SAMHSA), U.S. Department of Health and Human Services (HHS). The views, policies, and opinions expressed are those of the authors and do not necessarily reflect those of SAMHSA or HHS.

Terrestrial oil absorption of *Agaricus brunnescens*.

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This survey observes how *Agaricus brunnescens*, or the button mushroom, can absorb the intake of used motor oil. Previous studies have shown oyster mushrooms absorb oil in the water when grown on straw filled booms. This method has been used in tanker oil spills in the Pacific Ocean and the Gulf of Mexico. However, little research has been completed on terrestrial oils spills. This survey will examine oil absorption process in local soils with varying amounts of oil to simulate small oil spills, such as from vehicular maintenance. *Agaricus brunnescens* are being used in lieu of oyster mushrooms due to lack of

woody vegetative matter in local soils. Survey will be completed with the help of the Cankdeska Cikana Community College STEM department.

Indigenous Corn Reintroduction Project:

Analysis of Lipid Content and Dietary Health Implications

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Corn or maize is known to the Lakota/Dakota people as *Wagmiza*; which translates to “*that which sustains life*”. It is one of the most important food crops in the United States and is a staple of backyard home gardens. Corn is a high-energy food source with adequate nutritional value. Historical accounts show it was a staple food in the diet of many Native American tribes. This study was part of a larger project carried out to assess the value of Native American corn varieties, especially their nutritional health benefits. The objective of this study was to analyze the lipid profiles of corn associated with eight native varieties compared to two hybrid varieties. Three research study sites on Standing Rock and Cheyenne River Sioux Reservations were identified for planting based on soil, hydrology and topographic properties. Planting occurred in early May, 2013 using a No Till system with black plastic mulch used to heat up the soil. This method was instituted to promote a firm seedbed for uniform plant emergence and germination success. Analyses were conducted for germination success, seed moisture content, colorimetric profile, total lipid content, and fatty acid profile composition of the harvested varieties. ANOVA tests showed a statistically significant difference in the total lipid profiles between native corn varieties and the hybrid varieties ($PV = 0.001$, $\alpha=0.05$). Native varieties contained more unsaturated lipids than the hybrid varieties. This has dietary health implications for encouraging their consumption if the aim of a diet is to minimize unhealthy lipid foods.

Characterizing water quality parameters in a typical livestock pasture on the Standing Rock Reservation: health and productivity implications

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Water is essential to all terrestrial living organisms. It is important to the health of humans and all livestock species. Its quality and quantity also play a significant role in animal productivity. Unlike humans who require safe and high quality water, animals can subsist on less-than-perfect drinking water quality without any major negative impacts. However, there are tradeoffs with health and productivity implications. The purpose of this study was to evaluate inorganic nutrient water quality parameters of area surface and ground water. Evidence points to a large gap in water quality data on ranch water sources on Standing Rock. Representative water samples were collected from five watering points on a livestock range research site in Mahto SD. The watering points included 2 stock dams, 2 wells, and a stream. Six samples were collected for chemical analysis at each watering point to generate a representative sample using standard protocol methods. The samples were preserved with acids and stored in ice. These were transported to the Sitting Bull Analytical Laboratory at Sitting Bull College where the samples were processed and analyzed using EPA approved methods. Results show mineral

and salt concentrations were greater than recommended standards set for livestock water quality. These high concentrations of salts in the surface and ground water have health implications to cattle and people. More analyses need to be performed on more analytes that could be problematic for cattle, as well as ways to implement remediation practices to minimize any negative impacts.

Expression of Genes TRIB3 and EPHB2 in Kidney PT Cells in Response to Elevated Levels of Glucose

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Purpose: In this study, high glucose effect in kidney proximal tubule cells was gauged in terms of gene expression of two genes often associated with epithelial-to-mesenchymal transition (EMT), a process linked to cancer generation and metastasis, and also possibly linked to fibrotic changes brought about by renal nephropathy. The genes TRIB3 and EPHB2, described in the literature as connected to EMT processes, were monitored for overexpression in high-glucose treated cells; establishment of the presence of various genetic entities will help elucidate genetic roles in diabetes pathological processes. **Method:** Human kidney proximal tubule cells were cultured under varying concentrations of glucose; RNA extracted from cells was used for RT cDNA synthesis and the resulting cDNA was evaluated for relative quantitation by qPCR in comparison to the normocytic cell glucose concentration (5.5 mM). **Results:** It was found that only EPHB2 was overexpressed relatively, at approximately twice the control concentration in the 7.5 and 11 mM samples. **Conclusion:** Literature indications show that EPHB2 is strongly correlated with cell migration in cancer tissue, although the nature of the migration is unclear. The presence of EPHB2 in high-glucose cells may show a cancer/metastasis linkage or may be related to cell movement in fibrotic tissue formation or angiogenesis; delineation of pathological processes is crucial to diabetic information, which particularly impacts Native populations. **For further information:** Ashley M. Parisien, student intern, TMCC, 701-477-6341, 701-477-3995 (fax), ash.parisien@tm.edu

A Variant of the C-Reactive Protein gene (rs2027471) is not Associated with Risk of Pre-Eclampsia in an American Indian Population

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The cause of pre-eclampsia (PE) is unknown; but it is known that normal pregnancy represents a challenge to the maternal immune system. Genetic changes coding for a component of the innate immune system, C-reactive protein (CRP), is associated with preeclampsia. Our goal was to investigate the effects of additional CRP variants. There were 118 cases of PE and 144 matched controls from an American Indian population that participated in the study. An allele specific, real-time PCR method (Applied Biosystems “Taqman” assay) was used to genotype the CRP gene. Conditional logistic regression was used to analyze the potential association of CRP rs2027471 with pre-eclampsia. The minor allele frequency was 45.6% (95% CI 41.3-49.9%); and there was no significant deviation from Hardy-Weinberg equilibrium. We found no significant association between CRP rs2027471 and PE,

using either univariate or multivariate analysis of dominant, recessive or additive genetic models. There was a significant association between preeclampsia and nulliparity and body mass index (BMI) with an Odds Ratio (OR) of 5.58 (95% CI 2.81-11.12) p<.001 and OR 1.06 (95% CI 1.02-1.10) p<0.002 respectively. The CRP SNP rs2027471, is in the 5' flanking region, and doesn't appear to be associated with PE in this American Indian cohort. In both primarily Caucasian and Filipino populations the SNP affects CRP levels, but not among African Americans. Supported by NIH NIGMS grant P20GM103442.

Novel sequences of the C-Reactive Protein Gene among an American Indian Population

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The etiology of pre-eclampsia (PE) is unknown; but normal pregnancy represents a distinctive challenge to the maternal immune system; and C-reactive protein (CRP) is a prominent component of the innate immune system. We previously reported an association between three *CRP* variants and PE in this cohort. Our aim was to sequence the CRP gene, to potentially identify variants that are more directly associated with PE. The region sequenced totaled 18,300 bp, including the 5', 3' untranslated regions, the two coding exons (675bp), the single intron, and both 3' and 5' flanking regions. Sequencing was performed using an Illumina TruSeq Custom Amplicon project on a MiSeq Personal sequencer; reads (91% with quality score >/=Q30) and variant calls were aligned to the human reference genome (hg19). We sequenced 95 PE cases and detected a total of 67 single nucleotide variants (SNVs). Of this total, 61 variants were recorded in genome build GRCh38; and the remaining 6 SNVs have not been reported. None of the newly identified variants were within the coding or untranslated regions of the gene. All 6 of the novel SNVs were located within a 4,800 bp region upstream of the 5' UTR. These results show that a significant degree of novel genetic variation remains to be discovered among minority populations and further analysis of these additional variants will improve our ability to identify which variants are directly influencing the pathophysiology of pre-eclampsia rather than being associated through linkage disequilibrium. Supported by NIH grant P20 RR016741 from the NCRR

Cultural Incongruence: MMPI-2 Pd Scale and Native Americans

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This project examines differences in Native American and White Caucasian item response on the Psychopathic Deviate (Pd) Scale in the Minnesota Multiphasic Personality Inventory-2 (MMPI-2) personality test. The analysis is a follow-up of data from the “Impact of Cultural Identity on MMPI-2 Profiles in Northern Plains American Indians,” (Kagan, 2014). A sample of 115 Native Americans and 152 White Caucasians participated in the study. The results from Kagan’s (2014) dissertation concluded that the Native American participants scored slightly higher on the Pd Scale as compared to White Caucasian participants. The 18 of the 50 Pd scale items were evaluated and categorized into theme areas by independent raters. Content analysis of the 18 identified items focused upon two primary themes: historical trauma and self-image. The Pd Scale measures personality characteristics such as; trouble with authority figures and social introversion. Historical trauma is still felt today by many Native Americans because of the historical loss of population, land, family and culture and could contribute to participant’s

responses. As a minority in a white dominated culture feelings of hardship and conflict can also occur. White Caucasian participants scored slightly higher than Native Americans on the social image aspect of the Pd scale. These findings may indicate, White Caucasians subjects are more aware and protective of their social image as compared to the Native American subjects. Being able to keep things “bottled up” to maintain reputation could cause one to feel unpleased with oneself.

Metallothionein Isoform 3 Expression in Human Skin, Related Cancers and Human Skin Derived Cell Cultures

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Human skin is a well known target site of inorganic arsenic with effects ranging from hyperkeratosis to dermal malignancies. The current study characterizes the expression of a protein known to bind inorganic, As³⁺, metallothionein 3 (MT-3). Expression of this protein was assessed immunohistochemically with a specific MT-3 antibody on human formalin-fixed, paraffin-embedded biopsy specimens in normal skin, squamous cell carcinoma (SCC), basal cell carcinoma (BCC) and melanoma. Assessment in normal skin using nine normal specimens showed moderate to intense MT-3 staining in epidermal keratinocytes with staining extending into the basal cells and moderate to intense staining in melanocytes of nevi. MT-3 immunoexpression was shown to be moderate to intense in 12 of 13 of SCC, low to moderate in 8 of 10 BCC, and moderate to intense in 12 melanoma samples. MT-3 expression in cell culture models (normal human epidermal keratinocytes, normal human melanocytes, and HaCaT cells) showed only trace expression of MT-3, while exposures to the histone deacetylase inhibitor, MS-275, partially restored expression levels. These results indicate that the epidermis of human skin and resulting malignancies express high level of MT-3 and potentially impact on the known association of arsenic exposure and the development of skin disorders and related cancers.

Potential Involvement of Cadmium in the Induction of the Polyol Pathway of Hyperglycemic Glucose Metabolism in Human Proximal Tubule Cells

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Diabetic nephropathy (DN) is a major cause of end-stage renal disease (ESRD), where prolonged exposure to hyperglycemia induces damage to proximal tubule cells of the kidney. Since progression to ESRD correlates to pathological changes in the tubular segments of the kidney, the effects of hyperglycemia in the proximal tubule portion of the nephron may be particularly relevant to the progression of DN. Development of this disease also is likely to occur in the context of exposure to other renal toxins, and the heavy metal cadmium may be the most relevant due to the accumulation of this metal in proximal tubule cells. Preliminary microarray analysis has shown human proximal tubule (HPT) cells exposed acutely and chronically to cadmium have an increased expression of an aldose reductase isoform, AKR1B10. This isoform along with AKR1B1 and sorbitol dehydrogenase (SORD) are involved in glucose metabolism under hyperglycemic conditions via the polyol pathway. The goal of this study was to verify and extend these observations in culture of HPT cells. For this purpose, HPT cells were exposed to one of the three

following treatments; 5.5 (control), 7.5, 11, or 16 mM glucose concentrations for 8 days, 9, 27, 45 μ M cadmium for 24 hours (acute), or 4.5, 9, 27 μ M cadmium for 13 days (chronic). Real-time PCR was used to measure the expression level of these enzymes. Exposures to either hyperglycemia or cadmium stimulated a significant induction of AKR1B10 in HPT cells; however, no effect was seen in AKR1B1 or SORD expression. These results are suggestive of potential synergistic effects of cadmium and hyperglycemia in the toxic responses of the proximal tubule during the development of DN.

The Unique N- and C-Terminal Domains of Metallothionein-3 Alter the Expression of hnRNP A2 in MCF-7 Breast Cancer Cells.

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Previous work from our laboratory has shown that over-expression of MT-3 in breast cancers is associated with poor patient outcome. Furthermore, MT-3 has shown to inhibit the growth of breast cancer and prostate cancer cell lines. Studies have shown that the MT-3 protein contains 7 additional amino acids that are not present in any other member of the MT gene family, a 6 amino acid C-terminal sequence and a Thr in the N-terminal region. The unique N-terminal sequence is responsible for the growth inhibitory activity of MT-3 in the neuronal system. The goal of this study was to characterize the function of the N and C-terminal domains of MT-3 in the breast cancer cell line, MCF-7. For this purpose six different constructs of MTs were prepared which were as follows: wild type (WT) MT-3, MT-3 N-terminal mutation (MT-3 Δ NT), MT-3 C-terminal deletion (MT-3 Δ CT), WT MT-1E, and MT-1E mutated to contain the N-terminal of MT-3 or the C-terminal or both the N- and the C-terminal of MT-3. Each of these constructs was stably transfected into MCF-7 cells which were then sent out for microarray analysis. Microarray analysis indicated that both glycerophosphodiester phosphodiesterase domain containing 3 (GDPD3) and human nuclear ribonucleoprotein (hnRNP) A2 were repressed. Past research indicates that GDPD3 is up regulated in breast cancer due to the differential expression of phospholipase A2 isoforms, while hnRNPA2 has been known to be over expressed in lung cancer and various other cancers such as breast, pancreas and liver. Validation data obtained in this study indicated that GDPD3 expression was not significantly altered. The expression of hnRNP A2 was significantly repressed in the MT3 Δ CT cell line, and expression was significantly induced in the CT-1E cell line. Expression of hnRNP A2 may be increased or decreased depending on the activity of the N- or C-terminal of MT-3. The activity of the N- or C-terminal domains of MT-3 and the alteration in expression of hnRNP A2 may affect the oncogenic activity of the cancer cell.

An Investigation into the Differential Expressions of SCN1A and PFKFB3 Based on Absence or Presence of the N- or C-Terminal Domains of MT-3

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N-cadherin upregulation and EMT progression in As³⁺ and Cd²⁺-transformed urothelial cells.

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Purpose: The heavy metals As³⁺ and Cd²⁺ are known causes of bladder cancer. Our lab has shown that As³⁺ and Cd²⁺ cause malignant transformation of immortalized urothelial cells, which can form tumors in nude mice. Microarray analysis of repeated transformation in parallel revealed that N-cadherin was the most upregulated gene in As³⁺ transformants, and a top induced gene in Cd²⁺ transformed cells. N-cadherin is an indicator of the epithelial-to-mesenchymal transition (EMT). The goal of the present study was to determine how As³⁺ and Cd²⁺ regulate N-cadherin expression, if this expression is maintained in heterotransplant models, and if N-cadherin is promoting EMT. **Methods:** Real-time PCR and Western blot for N-cadherin and E-cadherin was performed on As³⁺ and Cd²⁺-transformed cell lines and their tumor heterotransplants. Immunohistochemistry was also performed. N-cadherin levels were determined after treatment of the epigenetic modifiers MS-275 and 5'-AZC and long-term Cd²⁺ exposure. **Results:** N-cadherin was greatly increased in the As³⁺ and Cd²⁺-transformed cell isolates, with focal expression present in intraperitoneal heterotransplants. The transcription factor Twist was also elevated. Treatment with the histone acetyltransferase inhibitor MS-275 altered expression of N-cadherin. Exposure of nontransformed UROtsa to Cd²⁺ induced N-cadherin. **Conclusion:** N-cadherin is significantly elevated in As³⁺ and Cd²⁺-transformed cell isolates and intraperitoneal heterotransplants, as well as the transcription factor Twist, indicating progression through the initial stages of EMT. Long-term exposure to Cd²⁺ induced N-cadherin, suggesting that heavy metal exposure regulates N-cadherin expression. As³⁺ and Cd²⁺ may utilize epigenetic modification to induce N-cadherin and progression through EMT in bladder cancer. **For Further Information:** Elizabeth Sandquist, B.S. Department of

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Anterior Gradient 2 Expression in MCF-10A Cells Exposed to Arsenite and Cadmium.

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Background: The environmental carcinogens arsenic and cadmium have been implicated in various cancers. Our laboratory has shown that arsenite and cadmium can cause malignant transformation of a breast epithelial cell line, MCF-10A. Previous studies have shown that the proto-oncogene, Anterior Gradient 2 (AGR2) expression promotes breast tumorigenesis in mice. This gene is known to play a role in promoting cellular transformation, tumor growth, and metastasis in various cancers. In this study, we determined the expression level of AGR2 in arsenite and cadmium transformed MCF-10A cells.

Methods: Real-time PCR and Western analysis was performed on samples isolated from the arsenite and cadmium transformed MCF-10A cells. Exposure of the parent MCF-10A cells to 4, 8, and 16 μ M arsenite for 48 hours resulted in a significant increase in the expression of AGR2 whereas exposure to Cd⁺² did not increase the expression of AGR2. MCF-10A cells were also transfected with the AGR2 gene to further examine the effects of AGR2 expression. MCF-10A cells were treated with the histone deacetylase inhibitor MS-275 and the demethylating agent, 5-Aza-2'-deoxycytidine (5-AZC) which increased AGR2 expression. **Results:** The data obtained indicated that expression of AGR2 was significantly increased in MCF-10A cells transformed with arsenite. Over-expression of AGR2 in MCF-10A cells increased cell migration in the wound scratch assay. **Conclusions:** These results suggest that arsenite has the potential to induce AGR2 in MCF-10A cells, which may increase the metastatic potential of the cancer cells. Epigenetic modifications may be involved in regulating the expression of AGR2 in MCF-10A cells. **For further information:** Jamie L. Van Gieson – Graduate Research Assistant, 501 N. Columbia Rd. Stop 9037, Grand Forks, ND, jamie.vangieson@med.und.edu

Metallothionein-3 Increases the Expression of the Na+/K+ exchanger ATP1B1 in MCF-7 Breast Cancer Cells

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Previous work from our laboratory has shown that over-expression of MT-3 in breast cancers is associated with poor patient outcome. Furthermore, MT-3 has shown to inhibit the growth of breast cancer and prostate cancer cell lines. Studies have shown that the MT-3 protein contains 7 additional amino acids that are not present in any other member of the MT gene family, a 6 amino acid C-terminal sequence and a Thr in the N-terminal region. The unique N-terminal sequence is responsible for the growth inhibitory activity of MT-3 in the neuronal system. The goal of this study was to characterize the function of the N and C-terminal domains of MT-3 in the breast cancer cell line, MCF-7. For this purpose six different constructs of MTs were prepared which were as follows: wild type (WT) MT-3, MT-3 N-terminal mutation (MT-3 Δ NT), MT-3 C-terminal deletion (MT-3 Δ CT), WT MT-1E, and MT-1E mutated to contain the N-terminal of MT-3 or the C-terminal or both the N- and the C-terminal of

MT-3. Each of these constructs was stably transfected into MCF-7 cells which were then sent out for microarray analysis. Caveolin-1 (CAV-1) was up regulated based on microarray analysis; however only the CT-1E mutant cell line had significantly increased expression based on real time PCR. ATP1B1 is one of five biomarkers that are over expressed in aggressive breast cancers of African American women. All of the MT-3 mutants had increased expression of ATP1B1 regardless of only the N- or C-terminal being present. Increased expression of MT-3 and the subsequent increase in expression of ATP1B1 may correlate to an aggressive breast cancer phenotype.

Metallothionein-3 Represses the Expression of Regenerating Islet-Derived 1 Beta in MCF-7 Breast Cancer Cells.

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Previous work from our laboratory has shown that over-expression of MT-3 in breast cancers is associated with poor patient outcome. Furthermore, MT-3 has shown to inhibit the growth of breast cancer and prostate cancer cell lines. Studies have shown that the MT-3 protein contains 7 additional amino acids that are not present in any other member of the MT gene family, a 6 amino acid C-terminal sequence and a Thr in the N-terminal region. The unique N-terminal sequence is responsible for the growth inhibitory activity of MT-3 in the neuronal system. The goal of this study was to characterize the function of the N and C-terminal domains of MT-3 in the breast cancer cell line, MCF-7. For this purpose six different constructs of MTs were prepared which were as follows: wild type (WT) MT-3, MT-3 N-terminal mutation (MT-3 Δ NT), MT-3 C-terminal deletion (MT-3 Δ CT), WT MT-1E, and MT-1E mutated to contain the N-terminal of MT-3 or the C-terminal or both the N- and the C-terminal of MT-3. Each of these constructs was stably transfected into MCF-7 cells which were then sent out for microarray analysis. Microarray analysis revealed that Diacylglycerol lipase, beta (DAGLB) was up regulated 2.1 fold and regenerating islet-derived 1 beta (REG1B) was up regulated 2.05 fold. Validation with the RT-qPCR showed a significant down-regulation of REG1B and showed no significant alteration in expression for DAGLB. The repression of REG1B may have further downstream implications since its expression can up regulate the expression of interleukin-6 (IL-6).

Differential Expression of AHSA-2 & BST-2 Based on Presence or Absence of the N- and C-terminal of MT-3

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Over-expression of MT-3 in breast cancers is associated with poor patient outcome, and MT-3 has been shown to inhibit the growth of breast cancer and prostate cancer cell lines. The MT-3 protein contains 7 additional amino acids that are not present in any other member of the MT gene family, a 6 amino acid C-terminal sequence and a Thr in the N-terminal region. The unique N-terminal sequence is responsible for the growth inhibitory activity of MT-3 in the neuronal system. The goal of this study was to characterize the function of the N- and C-terminal domains of MT-3 in the breast cancer cell line, MCF-7. For this purpose six different constructs of MTs were prepared which were as follows: wild type

(WT) MT-3, MT-3 N-terminal deletion (MT-3 Δ NT), MT-3 C-terminal deletion (MT-3 Δ CT), WT MT-1E, and MT-1E mutated to contain the N-terminal of MT-3 or the C-terminal or both the N- and the C-terminal of MT-3. Each of these constructs was transfected into MCF-7 cells. BST2 expression in cancer cells as an early targeting strategy to assist in surmounting resistance to pro apoptotic therapies. AHSA2 co-chaperoning with Hsp90 is a molecular chaperone essential for the activation and assembly of many key eukaryotic signaling and regulatory proteins. In vivo experiments have demonstrated that Aha1 and Hch1 contributed to efficient activation of the heterologous Hsp90 client protein v-Src. Moreover, Aha1 and Hch1 are crucial for cell viability under non-optimal growth conditions when Hsp90 levels are limiting. BST-2 is a potential activator of invasion and migration in tamoxifen-resistant breast cancer cells. Array validation demonstrated repression of AHSA2 in all cell lines except MT-3 Δ NT, and an up regulation of BST2 in all cell lines except MT-3 Δ CT.

3 Cycle Comparison of Native American Elder Abuse Indicators

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The National Resource Center on Native American Aging is making valuable strides to increase awareness of Native American elder health and social issues. One resource is the NRCNAA's "Identifying Our Needs: A Survey of Elders", which is an assessment of health and social needs for Indigenous elders in tribal communities all over the country. Collection of data is a three year long process, during this time the results for each community are then compiled and documented to assist in tribal planning and grant writing. I have compared selected information from 3 consecutive data periods (Cycle III, Cycle IV, and Cycle V) to identify factors of possible indicators of Native American elder abuse. The comparison of Cycles shows an increase in the use of many services available to Native American elders such as; caregiver programs, financial assistance, home modifications, and legal assistance. This increase may be contributed to awareness of social services offered to Native Americans elders since 2007. Comparisons also showed the need for continued awareness for elder abuse prevention programs, as it was least reported service being used.

Comparison of the Expression of stem cell markers in monolayer and spheroid CELL CULTURES OF HUMAN RENAL EPITHELIAL CELLS WITH THAT EXPRESSED IN THE IMMORTALIZED human proximal tubule cell line, HK-2

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Renal proximal tubules are a common site of toxic insult, cell death and regeneration as well as a major site for the development of renal tubular diseases. Toxic insult can result from chemicals such as heavy metals, pharmaceutical products or from diabetes induced nephropathy. In this study, we characterized stem cell populations within mortal human proximal tubule cell (HPTs) cultures and compared them to the immortalized proximal tubule cell line, HK-2, and also in HPTs exposed to various levels of cadmium (Cd^{2+}) or glucose. In-vitro cell culture systems have demonstrated that spheroids are often considered to be enriched in stem cells, in the current study spheroids were prepared by culturing HK-2 and HPT cells in non-attachable culture flasks. Four stem cell markers CD24, CD44, CD133 and ALDH1A1 were chosen

and their expression was assessed with real-time PCR. Our results show that the mortal cultures of HPTs and spheroids derived from them expressed high levels of all four markers suggesting that they contain a cell-population that exhibit many stem-like markers whereas expression levels of these markers decreased in HK-2. HPTs treated with Cd²⁺ resulted in a decrease in the expression of these stem cell markers, whereas long term exposure to glucose did not show significant effect on their expression. Expression levels of an epithelial to mesenchymal transition (EMT) marker, smooth muscle actin (ACTA2) was also determined in the Cd²⁺ and glucose exposed HPTs. Exposure to Cd²⁺ resulted in an attenuated expression level of ACTA2 whereas glucose exposure increased its expression level.