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the first report of the involvement of *NUP98* in a lymphocytic leukemia and the first time that a GEF has been directly implicated in the development of human malignancy.

#258 Cloning of the cDNA encoding phenylalanyl tRNA synthetase α-subunit-like protein whose expression is down regulated during differentiation. Zhou, X., Richon, V.M., Rifkind, R.A., and Marks, P.A. *Memorial Sloan-Kettering Cancer Center, New York, NY 10021.*

Hybrid polar compounds, such as suberoylanilide hydroxamic acid (SAHA), induce differentiation of transformed cells. Differential display of RNA was used to identify genes whose expression is changed during SAHA induced differentiation of murine erythroleukemia cells. One such cDNA was identified whose steady-state levels of mRNA (about 2kb in size) decreased about 50% by 8 hours of SAHA treatment as determined by Northern blot analysis. The full-length cDNA (1985bp in length) was cloned by sequencing of an EST clone and rapid amplification of 5' cDNA end (5'-RACE). The predicted amino acid sequence is 589 amino acids that share 45% identity with the yeast cytoplasmic phenylalanyl tRNA synthetase (PheS) regulatory α-subunit. Human EST clones which share over 90% identity of predicated amino acid sequence with this cDNA maps to chromosome 2 distal to PAX3, a region syngenic to mouse chromosome 1. This is the first cDNA reported for the PheS α-subunit from mammalian cells.

EPIDEMIOLOGY 1: Cancer Epidemiology

#259 Comparison of *helicobacter pylori* (HP) infection in the cardia and pyloric parts of the stomach from symptom-free subjects in Northern China. Wang, L-D., Liu, G., Gao, S.S., Zhou, Q., Qi, Y-J., Feng, C.W., and Yang, C.S. *Lab. Cancer Res., Henan Medical Univ., China; Rutgers Univ., Piscataway, NJ 08854.*

To investigate the etiological effect of HP on the precancerous lesions of the cardia and pyloric stomach and its correlation with esophageal lesions, HP infection was determined with Giemsa staining on 88 samples from symptom-free subjects in Henan, China, a high incidence area for both esophageal and gastric cardia cancers, but a low incidence area for cancers in the distal part of the stomach. Two biopsies, one each from cardia and pyloric parts, from the same subject were collected. Blood samples were also collected from these subjects for HP ELISA analysis. ELISA analysis showed that 57 cases (65%) were positive for HP infection. Giemsa staining showed that HP infection was higher in the pyloric stomach (63%, 55/88) than in the gastric cardia (34%, 30/88). A high incidence rate for ELISA and Giemsa staining was observed (86%, 76/88). In the gastric cardia, HP infection rate was low in normal (7%), slightly higher in dysplasia (19%), and much higher in chronic superficial gastritis (67%). Similar results were observed in the pyloric antrum. HP positive infection in gastric cardia appears to be inversely associated with esophageal lesions. All 5 cases with esophageal dysplasia had negative HP infection in their respective gastric cardia. The present results suggest that HP infection is associated with lesions in the gastric cardia, but may be inversely associated with the lesions in the esophageal epithelium. (Supported by National Natural Science Foundation of China grants 39840012 and 39770296, and NIH grant CA65871).

#260 Frequent presence of *Streptococcus* DNA in esophageal cancer, dysplasia of esophagus and gastric cancer. Sasaki, H[1]., Ishizuka, T[1]., Muto, M[1]., Nezu, M[1]., Nakanishi, Y[2]., Kuwahara, Y[1]., Tanabe, C[1]., Ueda, U[1]., Watanabe, H[3]., and Terada, M[1]. *[1]Genetics Division, [2]Pathology Division, National Cancer Center Research Institute, [3]Department of Surgery, National Cancer Center Hospital, 1-1, Tsukiji, 5-chome, Chuo-ku, Tokyo 104-0045, Japan.*

We recently reported cloning of *Streptococcus anginosus* (*S. anginosus*) DNA fragments containing the 16S ribosomal gene from DNA samples of surgical specimens of gastric cancers. Frequent presence of homologous sequence to *S. anginosus* in esophageal and gastric cancers was observed by Southern blot analysis with *S. anginosus* 16S rDNA probe. No *S. anginosus* DNA bands were detected by Southern blot analysis on DNAs from the non-cancerous portions of the esophagus or those of the stomach. It was revealed by PCR and sequence analyses that most of these positive signals in esophageal and gastric cancers were derived from *S. anginosus* and *S. mitis* DNAs. To investigate the frequency of *S. anginosus* infection, PCR analysis with *S. anginosus*-specific primers was performed on 127 DNA samples prepared from seven types of cancers. We found the frequent presence of *S. anginosus* sequences in DNA samples from esophageal cancer, although they were not detected in the normal esophagus mucosa. They were found frequently in gastric cancer tissues as well as in those from dysplasia of the esophagus of esophageal cancer patients. No *S. anginosus* sequences were found in DNAs from cancers in lung, cervix and kidney, while they were found in 1 out of 10 colon cancers. These data suggest that *S. anginosus* infection could be involved in esophageal and gastric carcinogenesis.

#261 Expression of CYP2E1 and AGT mRNA in human esophageal mucosa. Deng, C.J., Zhao, Y.J., Wang, L.D. and Hong, J.Y. *Laboratory for Cancer Research, Rutgers, the State University of New Jersey, Piscataway, New Jersey 08854 and Laboratory for Cancer Research, Henan Medical University, Zhengzhou, China.*

Cytochrome P4502E1 (CYP2E1) catalyzes the metabolic activation of several carcinogenic nitrosamines in which the DNA alkylating species are produced. O^6-Alkylguanine DNA alkyltransferase (AGT) specifically repairs DNA damage induced by alkylating carcinogens. Therefore, both CYP2E1 and AGT play important roles in carcinogenesis induced by alkylating agents. Polymorphic alterations were identified in 5'-flanking region of the human CYP2E1 and AGT genes, which may affect their mRNA expression. In the present study, 38 surgically resected frozen esophageal tissue samples of esophageal cancer patients were collected. These patients resided in a high esophageal cancer incidence area in Northern China, where alkylating nitroso compounds are suspected carcinogens. Total RNA was extracted from tumor-neighboring normal mucosa and was subjected to Northern blot analysis. Expression of CYP2E1 and AGT mRNA, with large inter-individual variations, were detected in almost all of the samples. The correlation of mRNA expression levels of CYP2E1 and AGT with the 5'flanking region polymorphic alterations was investigated. An almost 2-fold increase ($P<0.05$) of CYP2E1 expression was observed in *Rsa*I polymorphic samples. Although a 3-fold increase ($P>0.05$) of AGT mRNA expression was also observed in *Ban*I polymorphic samples, the increase was not statistically significant due to large inter-individual variations (supported by Health Effects Institute contract 96-2 and NIH grant ES03938).

#262 Polymorphisms in NAD(P)H: quinone oxidoreductase 1 (NQO1) in a Japanese population. Susceptibility to head and neck cancers and genotype-phenotype relationships in gastric cancers. Sadler, A., Siegel, D., Tsujinaka, T., Monden, M., Yano, M. and Ross, D. *School of Pharmacy and Cancer Center, Univ. of Colorado Health Sciences Center, Denver, CO 80262 and Dept. of Surgery II, Osaka University Medical School, Osaka 565, Japan.*

Individuals carrying the homozygous C609T polymorphism in NQO1 (*2 allele) have no detectable enzyme activity. The possible relationship between a lack of NQO1 and susceptibility to cancer was investigated in a Japanese control population and in individuals with head and neck cancer. The frequency of the homozygous C609T change in controls (n=156) was 12.2% and increased to 15.4% in head and neck cancer cases (n=130). The C609T homozygous change increased in cases relative to controls but did not reach significance at the 0.05 level, although in patients with pharyngeal cancer (n=39) the frequency of the homozygous C609T change was 23% ($p<0.082$). In 17 gastric cancers and controls, NQO1 could be detected by immunohistochemistry in all normal and neoplastic tissues genotyped as C/C or C/T at 609, but T/T genotypes had no detectable, or only trace levels of, NQO1 protein. The frequency of a second NQO1 polymorphism (C465T, *3 allele) was also examined in controls and in head and neck cancer cases. The frequency of the *3 allele was found to be low (0.03 in controls and 0.01 in cases) with no homozygous mutants detected in 290 samples. Supported by EPA R825281010, CA 51210 and a Grant in Aid for Scientific Research, Ministry of Education, Science, Sports and Culture of Japan.

#263 Genotypes of glutathione S-transferase M1 and N-acetyltransferase 2 in Japanese patients with gastric cancer. Oda, Y., Okada, Y., and Nakanishi, I. *First Department of Pathology, Faculty of Medicine, Kanazawa University, Takara-machi 13-1, Kanazawa, Ishikawa 920-8640 (Y. Oda, I. Nakanishi); Department of Pathology, School of Medicine, Keio University, Tokyo, Japan (Y. Okada).*

Genetic polymorphisms of some metabolizing enzymes have recently been shown to affect individual susceptibility to chemical carcinogenesis. We examined genotypes of *glutathione S-transferase M1 (GSTM1)* by PCR and *N-acetyltransferase 2 (NAT2)* by RFLP following PCR in 147 Japanese patients with gastric cancer and 112 autopsied Japanese patients without gastric or lung cancer. The frequency of the *GSTM1* null genotype was significantly increased in the cancer patients (91 individuals, 61.9%) compared to the controls (55 individuals, 49.1%) ($P < 0.05$; odds ratio = 1.68). The frequency of patients with the homozygously wild genotype of *NAT2* (rapid acetylator) was slightly lower in the cancer group (59 individuals, 40.1%) than in the control group (58 individuals, 51.8%). The proportion of patients with both the *GSTM1* gene and homozygously wild genotype of *NAT2* was significantly smaller in the cancer group (19 individuals, 12.9%) than in the control group (29 individuals, 25.9%) ($P < 0.05$). In addition, in the comparison of 4 subgroups of gastric cancer which were classified by both the genotype of *GSTM1* and the predicted phenotype of NAT2, the subject number of the subgroup '*GSTM1* +/rapid' was significantly smaller than the expected numbers of the other 3 subgroups, '*GSTM1* +/non-rapid, *GSTM1* null/rapid and *GSTM1* null/non-rapid' ($P < 0.05$). These results suggest that a combination of GSTM1 and NAT2 decreases the risk of gastric cancer in Japanese patients.

#264 Virtual trials: An internet-based brain tumor registry. Hayes RL, Levin M, Musella A, Selker RG, Fried A, Schulder M, Williams J, Arbit E, Lederman GS. *Staten Island Univ Hosp (RLH,EA,GSL); Brookdale Med College (ML); NY Med Coll (AF); New Jersey Med Sch (MS); W Penn Cancer Ctr (RGS); Johns Hopkins Med Ctr (JW).*

Developing a medical research registry is technically fairly simple but involves numerous practical, methodological and data management issues. We report our experience in setting up an observation, prospective registry of patients with brain cancer and preliminary findings on the reliability of the collected information. This unique project was conducted by the nonprofit Musella Foundation *http://www.virtualtrials.com*. This site consists of a database of demographics and basic medical information as well as treatment and outcome for each registrant. A confidential self-reporting system that includes written informed consent and ethical safeguards was developed. An on-line registration form is submitted along with a hard copy of pathology and MRI reports. From 3/4/97–3/7/98 (year 1 of operation) 331 patients were enrolled. The reliability of patient self-reporting was assessed by randomly selecting 25 pathology and MRI reports for review. Each were graded by a neurosurgeon and an oncologist (pathology) or a pediatric and a general neurosurgeon (MRIs). The self reported histology and change from baseline MRI were assessed by kappa statistic for nominal variable and weighted kappa for ordinal variables (change from baseline MRI). This analysis revealed a statistically significant high level of agreement between patient and physician interpretation. Data self-reported by patients at our internet site is accurate and reliable. However, several issues remain to be resolved including patient selection bias and confidentiality.

#265 Genetic polymorphism of N-acetyltransferase 2 and the risk of brain tumors. Peters, E.S., Kelsey, K.T., Wiencke, J.K., Chen, P., Wrensch, M. *Harvard Univ, Boston, MA 02115; UCSF, San Francisco, CA 94143.*

A polymorphism in the N-acetetyltransferase 2 (*NAT2*) has been associated with variation in the metabolism of amine procarcinogens. Slow and fast acetylators may differ in their susceptibility to a variety of cancers. Few studies to date have examined the association of *NAT2* with malignant gliomas, with one study observing an elevated risk of gliomas for individuals with the fast acetylator genotype. To further test this hypothesis we conducted a case-control study which examined the association of the *NAT2* polymorphism and the risk of brain tumors. DNA was extracted from 174 cases and 152 age, gender and race matched population based controls who participated in the San Francisco Bay Area Adult Glioma Study. The prevalence of the slow acetylator genotype was observed in 52.6% of controls and 59.8% of cases. No association between the *NAT2* slow acetylator genotype and an increased risk of developing gliomas was found. (OR = 1.3, 95% CI = 0.9, 2.1) After adjustment for age, gender and race the association was essentially unchanged. (OR = 1.3, 95% CI = 0.8, 2.1) These results do not support the hypothesis that the slow acetylator phenotype is associated with development of gliomas. Supported by NIH RO1CA52689 and RO3CA57220.

#266 Relative effectiveness of smoking cessation interventions by three groups of health care professionals. Sheinfeld Gorin, S., Neugut, A.I. Albert, D.A, Sadowsky, D. *Joseph L Mailman School of Public Heath of Columbia University, New York, NY 10032.*

Physician, dentist, and nurse smoking cessation counseling has demonstrated efficacy in reducing tobacco use. Yet, given the intractability of smoking behavior among certain subgroups, and the differing approaches among the three professions, an analysis of their relative effectiveness could better target their tobacco control efforts. Fifty eight tobacco control clinical trials with primarily physician, dentist, or nurse counselors were reviewed (39, physician, 15, nurse, and 4, dentist). Effect sizes (with 95% confidence intervals) for tobacco control interventions delivered by three groups of health professionals by type, number of components, frequency, and length, as well as the primary subjects involved in the study, were obtained. Overall, the effect sizes for the three health care professional groups compared to controls, for patient quitting at 6 months, were significantly different (*Mean*, .046 to .232; *SD*, .087 to .132, $p < .05$). We also observed differences among the three groups in the frequency of their interventions, as well as their efficacy with adults experiencing acute cardiovascular problems relative to those in primary care settings. We suggest modifications in the intervention approaches of each professional group.

#267 Effect of family history of cancer on health-related behaviors in a cancer-screening clinic population. Swede H, Moysich KB, Natarajan N. *Roswell Park Cancer Institute; Buffalo NY 14263.*

In this cross-sectional study we examined the effect of family history of cancer (FH) in relation to demographics and health-related behaviors among individuals attending a cancer-screening clinic. The sample included 1144 women (59%) and 801 men (41%) who completed a self-administered questionnaire on cancer risk factors. We compared 1366 individuals (70%) with a self-reported FH of cancer (FH+) and 579 individuals (30%) without such history (FH−). Overall, FH+ individuals tended to be slightly younger (mean=56 years) and were more likely to be Caucasian (95%) than individuals with FH− (mean = 60 years; 89%, respectively); these patterns maintained regardless of sex. Men with FH+ were similar to those with FH− with respect to education. Women with FH+ were somewhat more likely to be college graduates (32%) and less likely to have not completed high school (10%) than women with FH− (23% and 16%, respectively). FH did not affect smoking behavior in men; although women with FH+ were more likely to have quit smoking (36%) compared to women with FH− (26%). Patterns of weekly alcohol use were very similar for FH− and FH+ individuals regardless of sex. Among women, prevalence of overall FH did not affect the likelihood of performing breast self-exam (BSE). Women with a specific FH of breast cancer were somewhat more likely (48%) to perform BSE regularly than women without such history (40%). FH, or FH of breast cancer in particular, did not affect the likelihood of taking exogenous estrogens, having an annual Pap screen or an annual physician breast exam. Separate analyses for individuals with first or second degree relatives with cancer, and individuals with three or more affected relatives did not substantially alter these results. These data suggest that prevalence of FH does not uniformly affect health behaviors among people attending a cancer-screening clinic.

#268 Development of a new model of cancer care (CC) in the community: A British Columbia Cancer Agency (BCCA) initiative. Williams, C.K.O. *BC Cancer Agency, Vancouver Island Cancer Centre (VICC), Nanaimo Cancer Clinic, Nanamo, B.C., V9S 2B7, Canada.*

Advances in chemotherapy administration and communication technology (CT) are reducing the need for a centralized provision of complex CC in large medical centers. In Canada, CC is provided under a system of provincial and federal fiscal control, usually through provincial institutions such as BCCA, whose CC services are provided at its four major cancer centers through its Systemic Therapy, Radiation Therapy, and Communities Oncology Programs. Community CC in BC occurs through two outreach mechanisms: consultative clinics providing consultative and follow-up care by radiation and medical oncologists who travel at about monthly intervals to outreach centers, and community based regional oncologists providing diagnostic and treatment services in small communities. In order to provide the highest quality of CC in the community setting, BCCA in April, 1997 initiated a new CC model by placing a VICC medical oncologist (VICCMO) at a new treatment unit jointly managed with the Central Vancouver Island Health Region (CVIHR), whose 3×10^5 residents have constrained access to two major cancer centers. Through CT linkage with Vancouver Cancer Center (VCC), VICC and academic affiliation with the University of BC, VICCMO functions as consultant and resource person for primary CC providers and advocacy bodies in a defined sector of CVIHR. Monthly radiation consultative service complements the general and medical oncology services routinely provided at the clinic. A review of the first year of operation of the unit reveals a heavier workload than planned, while a formal survey reveals a high degree of acceptance both by community physicians and patients of this innovative and unique program in tertiary CC provision.

#269 Ethnicity and survival from lung cancer in a managed care organization. Ulcickas Yood M, Blount A, Coates R, Lamerato L, Abrams J, Johnson CC.

Studies indicate African Americans (AA) with lung cancer have poorer survival than non-AA. We measured lung cancer survival among members of a Detroit area health maintenance organization who were served by physicians in a large multispeciality group practice. In this setting, many potential barriers related to insurance are removed, and diagnosis and treatment are relatively standardized. All lung cancer cases diagnosed from 1/86–12/96 among HAP members continuously enrolled for at least one year formed the cohort. Baseline data included race, date of birth, sex, marital status, and stage. Address was geocoded to census block group to obtain an estimate of median household income.

The cohort consisted of 827 patients, 280 AA and 547 non-AA. Mean ages at stage at diagnosis were similar. Median income was substantially different comparing AA ($18,200) and non-AA ($35,600). Overall, AA had poorer survival compared to non-AA (hazard ratio HR=1.20, 95% CI 1.02–1.42). Adjusting for income, the HR decreased to 1.05 (95% CI 0.85–1.31). Adjusting for stage, income, age, sex and marital status, the RR was 1.00 (95% CI of 0.80–1.27).

In a setting that removes a number of health care barriers and potential treatment differences, and after adjustment for stage and other socio-demographic variables, the survival difference between AA and non-AA was eliminated.

#270 Application of a genetically engineered neural network (GENN) to predict progression using radical prostatectomy specimens. Veltri R., Miller M.C., Epstein J.E., Mangold L., and Partin A.W. *UroCor, Inc., Oklahoma City, OK, 73104 and the Johns Hopkins University Hospital, Baltimore, MD 21287.*

One of the leading clinical dilemmas in prostate cancer (CaP) is the inability to accurately predict which patients will recur following surgery. Previously, on retrospective radical prostatectomy (RP) specimens from a single institution (Johns Hopkins Hospital), we determined that the Gleason score and a variable, termed Quantitative Nuclear Grade (QNG), were important variables predicting progression (*Urology* **48(5)**: 685–691, 1996). In the current study, RP patients (average age = 58.9 years, average follow-up time = 7.8 years) were used to assess the ability of age, clinical stage, organ-confinement status, capsular penetration status, surgical margin status, DNA ploidy, post-operative Gleason score, and QNG (41 nuclear descriptors) to predict progression. The progressors (n=130) all had a minimum follow-up time of 5 years. Apply a commercially available GENN software program, the best model for predicting progression utilized a back-propagation neural network with a single hidden layer containing 149 neurons. Training with a randomly selected training set of the following variables were used to predict progression: age, capsular penetration status, surgical margin status, post-operative Gleason score, and QNG. The model had an accuracy of 72.7% and 90.5% in the randomly selected training (n=172) and testing (n=42) sets, respectively. The positive and negative pre-