(676) 12.90

SCREENING FOR INHERITED METABOLIC DISEASES AND CONGENITAL HYPOTHYROIDISM IN 4,744 MENTALLY RETARDED SCHOOL CHILDREN IN TAIWAN. K. D. WUU* and K. J. Hsiao**. *Genetics Laboratory, National Yang-Ming Medical College, Taipei. **Clinical Biochemistry Laboratory, Department of Medical Research, Veterans General Hospital, Taipei, Taiwan, Republic of China.

For the purpose of exploring the possibility of implementing a nation-wide screening program for inherited metabolic diseases and congenital hypothyroidism(CHT) in Chinese newborns, a pilot study was initiated in 1982 to detect patients of phenylketonuria(Guthrie's bacterial inhibition assay, BIA), galactosemia(modified Paigen's bacteriophage assay), homocystinuria(BIA), maple syrup urine disease(BIA) and congenital hypothyroidism(double antibody competitive enzyme immunoassay) in moderately mentally retarded (mostly IQ 50-75) school children in Taiwan. 4,744 blood samples collected on filter paper from 246 Primary and Junior High Schools by local public health nurses were sent to the Screening Center at the Veterans General Hospital in Taipei. Suspected positives of 6 PKU and 9 CHT were observed after primary screening. Confirmatory tests for PKU(serum phe and tyr, $FeCl_3$ and gas chromatography) and CHT(RIA to detect serum TSH, T_3, T_4; bone X-ray and 99mTc thyroid scan) were carried out for all the suspected positives. Three PKU(2 classical, 1 hyperphenylalaninemia) and 7 CHT(1 hypoplastic, 2 athyroid, 3 ectopic and 1 dyshormonogenesis) were finally confirmed. The incidence is 1/1581 for PKU and 1/678 for CHT in these children. Protein restriction diet was applied to the PKU patients mainly for having monitoring experiences in food therapy rather than to improve their mental status.

(677) 8.7

PRENATAL DIAGNOSIS IN DIABETIC PREGNANCIES. J. Zunich, D. Willard, N. Rike, and J. Granados. West Virginia Univ., Morgantown.

Infants of diabetic mothers are at increased risk for congenital malformations, most notably congenital heart defects, neural tube defects, and caudal regression sequence. Although prenatal diagnosis is possible for these conditions, screening of diabetic pregnancies is not routine. We have offered such screening since 1983 and our recommended program is as follows: genetic counseling and HbAlc level at the end of the first trimester; detailed fetal ultrasound at 16, 20 and 23 weeks gestation; AFP at 16 weeks; fetal echocardiography at 22 weeks; and exam of infant by us at birth. We report our initial results on the known outcomes of 26 pregnancies in 25 diabetic women. Of the 24 women who elected prenatal diagnosis after counseling, 13 completed the full program, 8 partially completed the program, 2 electively terminated prior to completion (1 for fetal abnormality), and 1 had 2 miscarriages prior to beginning the program. The women ranged in age from 19-41 and diabetic class A-D (A-2, B-11, C-9, D-3). Of 19 pregnancies diagnosed as normal prenatally, 17 were normal at birth, 1 had minor anomalies, and 1 had VATER sequence. Fetal abnormalities were detected in 4 pregnancies. The suspected abnormalities and diagnosis at delivery or autopsy are as follows: renal agenesis and hydrocephalus--confirmed (elective abortion); renal agenesis--caudal regression with normal extremities (intrauterine death); hydrocephalus--holoprosencephaly at birth; and congenital heart defect--confirmed (neonatal death; single kidney also noted). No normal infant was diagnosed as abnormal prenatally. We conclude that prenatal diagnosis should be routinely offered for diabetic pregnancies.

SOMATIC CELL GENETICS

(678) 19.79

CLUSTERING OF GENES ENCODING AMINOACYL-tRNA SYNTHETASES ON HUMAN CHROMOSOME 5. S. Arfin, L. Carlock, S. Gerken, J. Wasmuth, Univ. of Calif., Irvine.

Initial mapping studies of the functionally related group of genes encoding aminoacyl-tRNA synthetases indicated that these genes were scattered randomly throughout the human genome. Thus, the genes encoding leucyl- (LARS), methionyl- (MARS), tryptophanyl- (WARS) and asparaginyl- (NARS) tRNA synthetases have previously been localized to human chromosomes 5, 12, 14 and 18, respectively. However, using interspecific CHO-human cell hybrids, we have recently completed mapping studies of three additional members of this group of genes, those encoding histidyl- (HARS), arginyl- (RARS) and threonyl- (TARS) tRNA synthetases and have found all 3 of these loci to be syntenic with the LARS gene on chromosome 5. Therefore, of the 7 human genes encoding different aminoacyl-tRNA synthetases which have been mapped in humans, 4 are localized to a single chromosome which represents less than 7% of the total human genome. Although regional mapping data is not yet available for the HARS or RARS genes, we have determined that the LARS and TARS genes are very closely linked. Analysis of genes encoding additional aminoacyl-tRNA synthetases as well as further regional mapping studies for those located on chromosome 5 will be required to assess the possible evolutionary or regulatory significance of these findings.