hydrolase, eNOS and were found to be associated with REPL. Apart from these results, present study revealed the lack of association between REPL with other variants pressing the need to consider the ethnic background in epidemiological studies. Proteome analysis of platelets revealed a differential expression pattern in three proteins with approximate molecular masses of 65kDa, 35kDa and 20kDa which were exclusively present in REPL females.

CONCLUSION: Present study revealed certain novel and already reported polymorphisms in a multitude of genes to be associated with the risk of REPL. A role of genetic factor in REPL is further strengthened by the proteome analysis of platelets.

Supported by: Financial support for the present work is provided by the Council of Scientific and Industrial Research, India.

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Elimination of Alcohol From Breast Milk: Establishing Guidelines for Resumption of Breast-Feeding After Alcohol Consumption. M. Palmquist, D. Grainger, L. Frazier, A. Topolinski, P. Studts, H. Nipper. University of Kansas, Wichita, KS; Creighton University, Omaha, NE.

OBJECTIVE: The Motherisk organization has promoted use of a pharmacokinetic model to help nursing mothers determine how long they should discard breast milk after taking an occasional alcoholic drink. We performed this pilot study to assess whether alcohol elimination follows this predictive model among nursing mothers of various body sizes.

DESIGNS: Prospective non-random clinical study

MATERIALS AND METHODS: Ten non-pregnant lactating mothers fasted for four hours, then consumed a standard meal with 16 ounces (two glasses) of 13.5% merlot wine. Breath alcohol analysis and breast milk samples were obtained at baseline and at hourly intervals for 12 hours. Ethanol concentration in breast milk was determined using gas chromatography.

RESULTS: The time to a zero alcohol level in breast milk ranged from 4 to 8 hours. Participants' body mass index (BMI) varied from 18.6 to 37.3 (mean, 27.6). Levels of ethanol in breath were highly correlated with levels in milk ($P>0.001$). Overweight women (BMI $>$ 25) cleared alcohol faster than women of normal or low weight (BMI $<$ 25). The mean time to a zero alcohol level in breath was 5.5 + 0.96 (SD) hours vs 7.3 + 0.55 hours, respectively ($P=0.006$), and in milk was 5.2 + 0.75 hours vs 7.3 + 0.96 hours, respectively ($P=0.005$). BMI had an approximately linear relationship with time to a zero alcohol level in breath ($P=0.019$) and in milk ($P=0.008$).

CONCLUSION: Our findings, although limited to only 10 women, are consistent with the pharmacokinetic model promoted by Motherisk. Because alcohol is water-soluble and BMI is an easily measured albeit approximate marker for total body water, BMI is an important variable when determining alcohol clearance. Heavier women will eliminate the same amount of alcohol at a faster rate than women of normal or low BMI. To avoid exposing infants to alcohol, women should wait at least 8 hours after drinking 16 ounces of wine before resuming breast-feeding.

Supported by: Women's Research Institute Ortho Pharmaceuticals

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Regulation of Human Blastocyst Inner Cell Mass and Embryonic Stem Cell Pluripotency and Differentiation. A. M. El-Bareg, S. J. Kimber, D. R. Brison. The University of Manchester, MANCHESTER, United Kingdom.

OBJECTIVE: Embryonic stem (ES) are cells that have the ability to divide for an indefinite period.Under the right conditions and given the right signals, they can give rise to precursors of one or more specialised cells.Although they are derived from the inner cell mass (ICM) of human blastocyst, it is still uncertain precisely which stage of ICM development the ES cells correspond to, what controls their maintenance as pluripotent progenitors and which signals can initiate differentiation. This study addresses the regulation of cell fate decision within the human ICM by analysing expression of genes in the preimplantation human embryos, human embryonal carcinoma (hEC) cells and hES cells.

DESIGN: EC cell line: Comprise a model sytem for the study of molecular mechanisms involved in human ES cells and events regulating cell fate/lineage decision.

MATERIALS AND METHODS: Primary amplified cDNA samples from different stages of human preimplantation embryos;(pronucleus, 2-cell, 4-cell, 8-cell, and blastocyst stages). -Primary amplified cDNA samples of blastocyst stage embyos cultured in absence or presence of growth factors,e.g: Nanog, FoxD3, and the neuonal stem cell gene Galanin, LIF(leukemia inhibitory factor), IGF-1(Insulin like growth factor-1), HB-EGF(heparin binding epidermal growth factor).cDNA samples were subjected to gene specific PCR. -The expression of these genes in the pluripotent EC cell line Ntera-2 and the changes in their expression upon Retinoic Acid (RA)-induced differentiation have also been assessed. -hES 3 cell line cultured on mouse embryonic fibroblast feeder. Passaged by cutting the colonies. -Analysis was performed using immunocytochemistry and RT-PCR for expression of pluripotency and differentiation markers.

RESULTS: Galanin, Nanog, and FoxD3 are expressed from the 8-cell stage of human embryo development. FoxD3 expression shows some up regulation in response to the growth factors studied. In EC cells, Galanin, Nanog and FoxD3 are expressed in undifferentiated cells and their expression is down regulated upon differentiation.

CONCLUSION: The data suggest important role of these genes in pluripotency and differentiation in early human embryo development and ES cells. Galanin might induce an intermediate state between pluripotency and differentiation.

Supported by: I acknowledge Prof.P.Andrew for providing us with EC cells(Ntera-2), also M.Pera for providing hES 3 cell line.

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The Polymorphisms of PPARγ Pro12Ala and PGC-1 Gly482Ser in Chinese Women With Polycystic Ovary Syndrome. X. Wu Sr., Y. Wang, L. Hou. Department of Obstetrics and Gynecology, The First Affiliated Hospital, Heilongjiang University of Chinese Medicine, and Jinling Hospital of Nanjing University, Harbin 150040, China; Human Genetic Identification Laboratory, Medical School of Nanjing University, Nanjing 210093, China; Department of Obstetrics and Gynecology, The First Affiliated Hospital, Heilongjiang University of Chinese Medicine, Harbin 150040, China.

OBJECTIVE: Polycystic ovary syndrome (PCOS) is one of the most common endocrine metabolic diseases and is characterized by ovarian androgen overproduction, polycystic ovary and oligo- or anovulation. Insulin resistance has been implicated in the pathogenesis of ovarian dysfunction in PCOS. Insulin-mediated carbohydrate metabolism and sensitizing effects of thiazolidinedione are regulated at least in part by peroxisome proliferator-activated receptor-γ (PPARγ) and peroxisome proliferator activated receptor γ coactivator-1 (PGC-1).In this study, we defined the role of polymorphisms of PPARγ Pro12Ala and PGC-1 Gly482Ser in Chinese women with Polycystic ovary syndrome.

DESIGN: Controlled clinical study .

MATERIALS AND METHODS: Two hundred and one PCOS patients and 147 controls were recruited in University-affiliated department. Menarche age was recorded. Body mass indices were calculated. Blood samples were obtained for DNA analyses of PPARγ and PGC-1 polymorphisms,and hormone measurements.

RESULTS: In Chinese subjects the frequencies of genotypes were as follows: 0.914 Pro12pro, 0.083 Pro12Ala, 0.003 Ala12Ala for the PPARγ2 gene and 0.329 Gly482Gly, 0.392 Gly482Ser, 0.279 Ser482Ser for the PGC-1 gene. The Ala allele frequency (4.4%) is lower, and Ser allele frequency (34.1%) is higher in Chinese subjects, as compared with that of western countries. Both Pro12Ala polymorphism and Gly482Ser polymorphism distributions are similar between Chinese women with PCOS and control. There are no significant differernces of BMI and reproductive hormones such as Total testosterone (T) levels, FSH, LH, P, E2 and PRL levels between the patients and controls.

CONCLUSION: Our data suggests there is no association between these polymorphisms and the risk of PCOS in Chinese subjects.

Supported by: the Nature Science Foundation of China (30271353/C03030401), the Chinese Ministry of Education, and the Chinese Medical Association

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A Randomized, Controlled, Double Blinded Trial of EmbryoGlue® in Frozen Embryo Transfer Cycles: An Interim Analysis. D. L. Walker,