Poster #18

Microarray Anaylsis of Human Immortalized Uterine Lieomyoma Cells

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Uterine leiomyomas are benign smooth muscle tumors, which affect at least 25 % of women with a higher prevalence in African American women. Leiomyomas are known to be estrogen dependent tumors, yet a genetic basis for leiomyomas growth still remains to be elucidated.

Previous studies from our laboratory have shown that the levels of Wnt 7a were decreased, and that estrogen receptor alpha (ER □levels were increased in leiomyomas compared to adjacent normal myometrial tissues (Li et al, 2001). In addition, we have shown that DNA Methyltransferases 3A and 3B are decreased while DNA Methyltransferase 1 is increased in leiomyoma tissues (Li et al, 2003). In the current report, we utilize human immortalized uterine myometrial and leiomyoma cell lines, which were developed by Dixon et al, 2002, to further probe the genetic factors involved in growth of uterine leiomyomas. It is clear that leiomyomas growth is estrogen and progesterone related since tumors regress after menopause and treatment of GnRH agonists.

In accordance with this data, we compared myometrial and leiomyoma cells exposed with 10 nM 17 β estradiol to controls. Using microarray analysis as an unbiased approach to identify genes/family of genes that maybe involved in uterine leiomyoma induction.
Array analysis revealed many genes, most of which were not previously associated with uterine leiomyoma formation, that were either up regulated or down regulated more than two fold compared to myometrium. This array offered a large scale screening of mRNA expression, which will help us differentiate between genes and metabolic pathways necessary for regulating leiomyomas.

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