Determining the Tissue Distribution and Specificity of JM27/ G antigen, family C, 1, a Prostate Cancer-associated Gene

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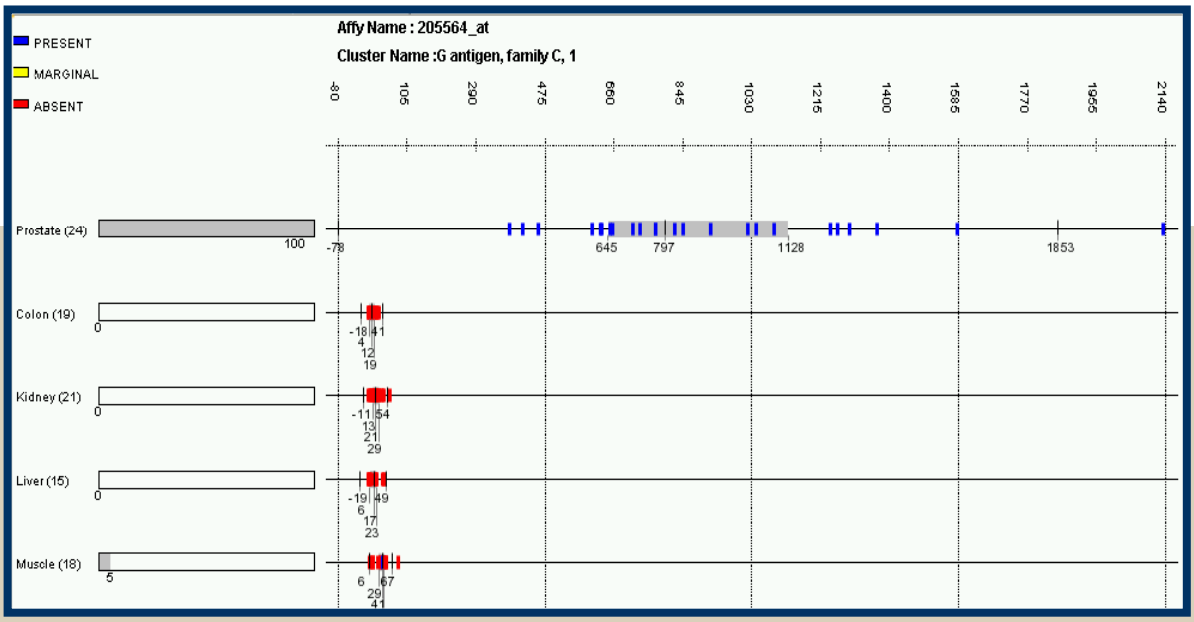
Overview

Recent microarray studies of prostate diseases such as prostate cancer and benign prostatic hyperplasia (BPH) have revealed several differentially expressed genes that had not been previously associated with these diseases[1-2]. However, additional studies are required in order to determine if any of these genes represent potential therapeutic targets or markers of disease. Determination of the distribution of these genes within a large panel of relevant normal human tissues will assess the specificity of each potential marker and target to help prioritize the list of genes for further target development and validation studies.

As proof of principle we've selected the gene JM27, a newly identified gene that is dramatically up-regulated both in prostate cancer[1] and in symptomatic but not asymptomatic BPH[2]. Very little is known about this gene or its function(s) other than its homology to a family of MAGE/GAGE-like proteins that contain RGD motifs frequently found in cell adhesion proteins. The following study is designed to survey a panel of 20 normal human tissues for the expression of JM27 to determine its native tissue distribution. The results provide further understanding of the role JM27 may normally play in the human body, as well as indicate the viability of exploring any diagnostic or therapeutic applications of this gene.

Methodology

Microarray data generated from Affymetrix GeneChip® U_133 experiments from a broad selection of normal human tissues were grouped by organ or tissue type and placed into sample sets. JM27 gene expression values from the microarray experiments found in each sample set were statistically analyzed and graphically displayed using the e-Northern™ Analysis Tool in the BioExpress™ Human Atlas Suite.



The JM27 expression values for each sample are plotted as colored, vertical bars indicating whether the JM27 gene is called present (blue), marginal (yellow), or absent (red). The two extreme outer marks (numbers) along each graph represent a 95% confidence interval for this gene's expression value; the two next inner marks represent the 25th and 75th percentile markers (bound by a gray box); and the innermost mark represents the sample set's median expression values. On the left-hand side of the figure, the number of samples in each tissue set is noted within the parenthesis with the adjacent bar graphs indicating the percentage of tissues in which the gene is present.

Results and Discussion

The above e-Northern™ depicts the range of expression values for JM27 across five sample sets. The results reveal that among the organs surveyed, JM27 mRNA is selectively expressed in prostate. Similar results are obtained using 15 additional tissue sample sets except the uterine tissue (results not shown). This analysis shows a remarkably restricted pattern of expression of JM27 across normal tissues. Its prostate-restricted expression coupled with a near complete absence from all other non-reproductive tissues suggests a function associated with male reproduction. Combining previously known information about JM27 (association with prostate cancer and symptomatic BPH) with the knowledge provided by the above *in silico* study of its prostate specificity could help prioritize JM27 for consideration for further functional and target validation studies.

Conclusion

The BioExpress™ Human Atlas Suite allows researchers to rapidly compare the relative expression and tissue distribution of genes of interest across all major organ systems. The suite provides access to data sets from a large panel of relevant normal tissues not easily obtained through standard laboratory procedures and can save substantial resources associated with the tissue procurement and gene expression data generation. The BioExpress™ Human Atlas Suite has the potential to positively impact drug discovery efforts in several ways:

- Rapid characterization of expression of potential drug targets and bio-markers in normal (non-diseased) tissues
- Prioritization of targets for further validation studies
- Discovery of biological processes and biochemical pathways associated with genes of interest
- Accelerate the understanding of the molecular basis of normal biology and disease

REFERENCES

[1] Bull, J.H. et al (2001). *Br.J.Cancer* **84**, 1512-1519.

[2] Prakash, K. et al (2002). Proc.Natl.Acad.Sci. (USA) **99**, 7598-7603

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