Beer, Brains, and Bioinformatics:
Exploring the Response of SGK to Ethanol and its Interactions with Other Genes

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Alcoholism is a significant health issue for the United States and other Western countries. Chronic alcohol use may lead to behavioral changes including tolerance, dependence, sensitization, and craving. Alcohol has been shown to result in changes in brain gene expression which have been suggested to contribute to these characteristic behaviors. Since behaviors are rarely regulated by a single gene, by employing microarray technology we are able to examine the effects of ethanol on thousands of genes simultaneously. By comparing microarray results from ethanol treated mice and saline treated control mice, it is possible to identify genes that are significantly upregulated by ethanol. Past microarray analysis conducted in our laboratory has identified a gene called serum- and glucocorticoid-regulated kinase (SGK) which is strongly upregulated by ethanol. SGK also plays a vital role in the regulation of many ion channels including the epithelial sodium channel ENaC, the voltage-gated potassium channel KCNE1, and the glutamate transporter EAAT1, making SGK an important candidate for study. Immunohistochemical methods were employed to confirm that SGK is induced by ethanol and is most strongly expressed in the prefrontal cortex (PFC) of the mouse brain. In addition, a functional network for SGK was created using literature mining tools to discover genes regulated with SGK. This functional network will help to discern genes and gene networks involved in the behavioral responses caused by chronic ethanol use.