

## **Combined Microarray and linkage studies**

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### **Abstract:**

Microarrays and linkage analysis are in many ways a perfect complement to study complex disease. Both essentially test the entire genome, but they do so in fundamentally different ways. We have developed methods that for combining the results of RIX, test-crosses, and pedigree based linkage results with microarray studies to identify candidate genes for harboring causative variation. Each type of study has its own requirements. There are relatively few RIX strains, thus high precision is required in the gene expression results. In test crosses when the P are not inbred it may be best to microarray the P to identify candidate genes, but when the P are inbred the difference between the phenotype and breeding value of the P may be so large that microarraying the F2 is required. In addition microarraying the F2 will allow for linkage analysis of the gene expression levels using the markers from the primary linkage study. Sampling the phenotypic extremes of the F2 will provide much of the information on difference in gene expression between strains that may be associated with the phenotype being studied. More information for combined microarray QTL studies for the same number of people microarrayed when the individuals are in fewer large pedigrees than many small ones. Combined microarray and linkage studies may provide the ability to identify genes involved in complex diseases and quantitative traits.