Strategy for Assaying Gene Expression in Human Brain Malformations

Generate cDNA from poly A mRNA via *in situ* transcription from whole section

Probe cDNA arrays

1) Obtain human tissue - intraoperatively Amplify mRNA from cDNA, incorporate radiolabel -post-mortem Probe cDNA array containing candidate genes 2) Obtain animal tissue Analyze hybridization intensities 3) Fix in paraformaldehyde 4) Immunolabel Microdissect single cells Single cell mRNA amplification

Crino et al., 1996

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Tissue section Large Array

Hybridization intensity Compare with "housekeeping" gene Compare with internal standard Compare to average of entire blot Relative mRNA abundance



Tissue section Small array



Why Single Cell mRNA Analysis? Consideration of Important Variables



Neuronal Heterogeneity Disease Heterogeneity Analysis of Phenotypically Similar Cells Selecting Disease Affected Neurons Speed of Analysis







ICAM-1 mRNA expression in tuber and control cortex. **A**, Top, cDNA arrays showing increased hybridization of ICAM-1 mRNA in whole tuber sections compared with peri-tuberal and control cortex. Note similar N-cadherin hybridization levels in tuber and control cortex sections. Bottom, left, increased expression of ICAM-1 mRNA in tubers compared with control cortex. Right, similar expression levels of N-cadherin mRNA in tubers and control cortex. Graphs depict mean percent hybridization intensity of each mRNA±standard error (* p<0.05). **B**, ICAM-1 mRNA expression is increased in single ICAM-1 immunoreactive GC from tuber compared with single layer III pyramidal neuron (control) that did not exhibit ICAM-1 immunoreactivity. N-cadherin mRNA expression did not differ between these cell types.



Cellular expression of ICAM-1 in 4 representative tuber specimens. A,C note robust immunolabeling of tubers with ICAM-1. Scale bar, 300 microns. B,D higher magnification view of ICAM-1 immunolabeling in GCs (arrows). Smaller ICAM-1 labeled cells include DNs and rare astrocytes.