

## Method to Identify Cancer Fusion Genes

**R**esearchers at the University of South Florida have developed a highly efficient method for identifying fusion genes that could be useful in developing tests aimed at cancer diagnosis and treatment, as well as other diseases.

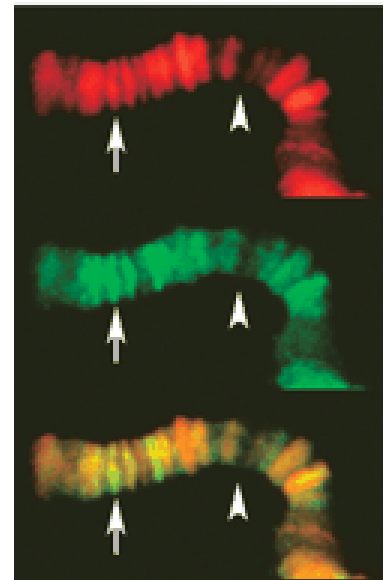
Microscopic methods have traditionally been used to detect chromosome rearrangements. However this is a tedious process especially when identifying the specific segments of DNA involved in the rearrangement process. There are as many as 50,000 potential chromosomal rearrangements, all associated with human pathological conditions and almost all have unknown fusion points. For many genetic diseases caused by these rearrangements, valuable time could be lost in identifying responsible genes using conventional methods.

This statistical analysis tool and associated algorithm is a highly efficient means to determine DNA segments involved chromosomal rearrangements, and allows for an efficient means of screening genes, thereby allowing PCR tests for these rearrangements. PCR primers can be designed to test each of the top three genes as determined by the algorithm, or to test potential mRNA fusions resulting from the three gene fusions. If none of the top three genes is part of the rearrangement, then the top 7 genes are next screened, according to species homology percentage peaks. Our data indicate that with this follow up, there is about an 83% chance of identifying the genes involved in a chromosomal rearrangement. In sum, using this two step procedure for any chromosomal rearrangement, there is a 95% chance of identifying a fusion gene or DNA segment.

### ADVANTAGES:

- **Rapid fusion gene analysis**
- **Can be linked to primer design tools**
- **New web based tool for biomedical researchers**

*Increase primer sales and web traffic*



*Arrows indicating location of fusion genes by microscopic method*

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