

MPSS Vs. Microarray:

MPSS Invented by Sydney Brenner

- MPSS is most notable in that it is a technology that has the potential to capture virtually all genes present within the sample, and not just those that have been placed on the microarray.
- No prior knowledge of a gene's sequence is required for MPSS.
- Microarrays have the limitation that homologous genes can cross-hybridise, which makes it impossible to detect individual members of highly homologous gene family members which are not annotated earlier.
- But with MPSS, the signature sequence in the 3' untranslated region, can be different for individual family members. Therefore, it is possible, in many cases, to differentiate highly homologous genes from each other.
- The advantage of microarray is the high throughput analysis of multiple samples.
- The microarray and MPSS technologies as being complementary in nature different tools for different types of experiments. e.g. To generate in-depth and quantitative gene expression data for building complex relational databases, MPSS may be the technology of choice.
- After these databases are mined for interesting biological information, it may be necessary to test whether sets of genes are differentially expressed in a large number of samples (eg tumours of a specific type). Here, the microarray platform be the technology of choice.
- Both MPSS and at least one of the microarray technologies would seem to be ideal for most investigators.
- MPSS has the advantage that it provides in-depth quantitation of virtually all genes that are expressed in a sample.
- Since there is no requirement for prior knowledge of any gene or genome, it is possible to generate quantitative gene expression datasets from any organism.
- MPSS dataset involves one million or more signature sequences, it has the sensitivity to quantitate accurately genes that are expressed at very low levels within a cell.
- No other single technology has these performance characteristics.

Comparison to Serial Analysis of Gene Expression (SAGE)

- Signature sequence of SAGE is 14 nucleotides compared with 17 nucleotides with MPSS:
- Less ambiguity with MPSS when mapping to the mammalian genome
- Easier to connect MPSS tags with known genes
- Typical SAGE data set is 20,000-60,000 tags compared to over a million signatures sequences for MPSS
- MPSS sequencing done on a miniaturized platform that is amenable to high-through
- SAGE conducted with standard cloning and sequencing that are expensive, time consuming and labor intensive
- Larger MPSS data sets provide enhanced depth of analysis