Factors Affecting Expression of Transgenes
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It is often observed that transgenes become incorporated into chromosomes, but fail to express. This is referred to as gene silencing.

Two categories:

TGS - transcriptional gene silencing
PTGS - post-transcriptional gene silencing
Eukaryotes inactivate specific genes by methylation of cytosine residues, especially CpG.

In plants, methylation tends to occur at CpG, CpHpG, and CpHpH, where H is any nucleotide other than G.

By preventing transcription, methylation acts as a mechanism for selectively down-regulating genes.

In embryos, methylation is often reversed. Subsequently during development, certain genes are methylated, and are no longer expressed in the adult.

Methylation patterns are often inherited from one generation to the next.
Transcriptional Gene Silencing (TGS)

Genes that insert into hypermethylated regions will usually become methylated, and thus inactive.

Transgenes that insert into active chromatin domains will be expressed.

Transgenes that insert into inactive domains are not transcribed.
Post-Transcriptional Gene Silencing (PTGS)

- Found in all eukaryotes
- Mediated by small interference RNAs (siRNA)
- siRNAs are typically 21 - 24 nt in length
- Can be mediated by sense or antisense transcripts, or by double-stranded RNA
- Typically transmissible intercellularly. In plants, PTGS can be graft-transmissible
- In nature, PTGS is used by plants to inactivate viruses. It is therefore a natural defense mechanism.
- Foreign mRNAs from transgenes can often inactivate other copies of genes in plants with which the siRNAs share sequence similarity.
- PTGS is a very effective way of inactivating naturally-occurring genes in transgenic plants “gene knockout”.


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http://www.eurofinsgenomics.eu/media/561167/gene_silencing_mechanism.jpg
References