### Somaclonal Variation

Somaclonal variation is the variation seen in plants that have been produced by plant tissue culture. Chromosomal rearrangements are an important source of this variation. Somaclonal variation is not restricted to, but is particularly common in, plants regenerated from callus. The variations can be genotypic or phenotypic, which in the latter case can be either genetic or epigenetic in origin. Typical genetic alterations are: changes in chromosome numbers (polyploidy and aneuploidy), chromosome structure (translocations, deletions, insertions, and duplications), and DNA sequence (base mutations). Typical epigenetic-related events are gene amplification and gene methylation. If no visual, morphogenic changes are apparent, other plant screening procedures must be applied. There are both benefits and disadvantages to somaclonal variation. The phenomenon of high variability in individuals from [plant cell cultures](https://www.sciencedirect.com/topics/pharmacology-toxicology-and-pharmaceutical-science/plant-cell-culture) or adventitious shoots is called somaclonal variation . Therefore, it can be defined as the variation that occurs because of genetic mutation caused by in vitro conditions or by chimeral separation. Somaclonal variation is usually undesirable. In some cases, somaclonal variation can lead to new cultivars (e.g., disease resistance, new leave pattern) that may have desirable ornamental characteristics or increased pest resistance.

The occurrence of somaclonal variation can be reduced by:

Avoiding long-term cultures.

Using axillary shoot induction systems where possible.

Propagating chimeras by other clonal systems.

It is well known that increasing numbers of subcultures increase the likelihood of somaclonal variation, so the number of subcultures in micropropagation protocols should be kept to a minimum.

Regularly reinitiating clones from new explants, which might reduce variability over time.

Avoiding 2,4-D in the culture medium, as this hormone is known to introduce variation.

### How to Exploit Transgenic Plants Bearing Somaclonal Variation

Somaclonal variation can disturb both basic and applied studies on [transgenic plants](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/transgenic-plant). The use of transgenic plants in order to assign a role to cloned genes of unknown function may be impaired by concomitant variant traits due to somaclonal variation. For example, in the agronomic and industrial exploitation of transgenic plants, transgenic elite [cultivars](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/cultivar) might show undesirable changes compared with the original plant. For instance, when insect-resistant, transgenic sugarcane plants were produced, they were found to be morphologically identical, but the agronomic analysis of selected plants showed changes in some [agronomic traits](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/agronomic-traits). Rare DNA changes were also observed by [AFLP](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/amplified-fragment-length-polymorphism) analysis.

Nevertheless, a large array of commercially exploitable transgenic plants has been produced. In fact, several different approaches can be applied to overcome the problem of somaclonal variation in transgenic plants. One may be that of using recurrent backcrossings to restore the original genotype while retaining the foreign gene. A second approach may be to utilize the best-performing transgenic plants, regardless of genomic changes. The former approach is particularly suitable for annual crops, such as rice, while the latter is suitable for plants that are commercially reproduced by cuttings, such as sugarcane or [poplar](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/populus). But these approaches are not appropriate for all cases. For instance, in the hypothetical case of transgenic olive trees, it would not be practical to wait years before verifying that somaclonal variation had not affected flavor, yield, ripening, or other industrial traits in selected trees.