

Guidelines for Molecular Characterisation of Genetically Modified Higher Plants for a Standard Part B Consent

ACCORDING TO ANNEX III B OF DIRECTIVE 2001/18/EC

Version: February, 2020

- Any relevant scientific articles and reports referred to should accompany the dossier
- The quality of the experimental data should be sufficient to verify clearly any statements made by the applicant.

1. Description of the genetic material used for the transformation

1.1. For each of the vectors used for transformation, provide a detailed map including the genetic elements listed in 1.2 indicating their location, order and orientation in the vector, and the position of relevant restriction sites.

1.2. For each of the vectors used for transformation, provide a **list** (and a table summarizing name, position and brief description) of all genetic elements, including coding and non-coding sequences (e.g. origins of replication, T-DNA borders of *Agrobacterium*, bacterial transposable elements, promoters). For each of these elements:

1.2.1. Provide a **description** of the genetic element, or a **citation** where the genetic element was isolated and characterized (include an accession number in a publicly available database).

1.2.2. Indicate the **portion** and **size** of the genetic element that was inserted in the vector, and its **location** in the vector.

1.2.3. Provide information about its **source**. Give the scientific and the common or trade name of the donor organism. Describe the history of use of the donor organism (or that of relevant elements thereof) and its relevance to risk assessment: indicate whether the donor organism is responsible for any disease or injury to plants or other organisms (e.g. produces toxicants, allergens, pathogenicity factors or irritants).

1.2.4. Indicate whether the genetic element itself is coding for or involved in the production of proteins responsible for **disease** or **injury** to plants or other organisms (e.g. a toxicant, allergen, pathogenicity factor or irritant).

1.2.5. Provide information about the molecular, biochemical and physiological **properties** of its products, as known in the donor organism and aimed at in the transgenic plant.

1.3. For direct transformation methods, provide data on how the part(s) of the vector(s) used for the transformation was purified and indicate how **purity** was assessed.

2. Description of the transformation method

2.1. **Describe** the transformation protocol and provide relevant **references** for the transformation method. In case of direct transformation pure DNA has to be used, implying the absence of carrier DNA.

2.2. For *Agrobacterium*-mediated transformation, provide the **strain** designation of the *Agrobacterium* used during the transformation process, and indicate if and describe how the Ti/Ri plasmid based vector was **disarmed**.

2.3. For transformation methods that involve the use of **helper plasmids**, describe these plasmids in detail.

3. Information on sequences actually inserted/deleted

3.1 Provide experimental data revealing the **copy number**.

4. Transcript and protein characterization

4.1. Analyse the **expected expression** of the inserted genes. Describe the methods that were used for the expression analysis and assess their sensitivity. For open reading frames intended to be expressed in the transgenic plant, provide data on the levels and the spatial and temporal specificity of the expected expression. In case the purpose of the transformation is to alter the expression of endogenous genes (e.g. by antisense constructs, ribozymes, or via the mechanism of RNA silencing), provide data on the expression of the target.

4.2. Describe the **properties** of the expressed **proteins** or the target proteins referred to in 4.1.

4.3. If there has been a DNA modification that affects the amino acid sequence of the plant expressed protein, the **modified amino acid sequence** must be provided. Indicate whether the modifications are known or expected to result in changes in the properties of the protein.

4.4. In case not all data on expression are available, more stringent containment measures may be required.