



Mandate for an ENGL Working Group on good practice/quality of DNA sequencing data (WG-seq)

Background

GMO analysis, targeting GM plants, animals and microorganisms, is becoming more complex with a further diversification of questions that may relate to the detection, identification and quantification of EU-authorized GMOs and well-characterised unauthorised GMOs. Furthermore, the identification and authentication of unauthorised GMOs, for which only limited or fragmentary information is available so far, are also becoming important. In addition, new breeding techniques are increasingly applied and the determination of the whole genome sequence (WGS) of these plants or animals may be required for detailed molecular characterisation.

In this context the identification of DNA sequences by Sanger sequencing and next generation sequencing (NGS) techniques are gaining more importance. This may relate to the sequencing of:

- PCR amplicons;
- captured DNA fragments;
- enriched DNA populations;
- whole genomes.

Some of these sequencing approaches are already routinely applied, while others are only used in exceptional cases based on more experimental protocols. However, on a case-by-case basis, all methods may contribute to the effective and cost-efficient detection and identification of all GMOs in a given sample. At the same time quality aspects of DNA sequence data in the field of GMO detection and characterisation have so far received only limited attention¹. The guidance and requirements provided in relevant EURL GMFF documents should be also considered².

This WG aims to provide minimum quality performance criteria for the methods used for decoding DNA sequences of given samples and how to report such sequencing information. The WG will draft guidance to ascertain the quality of sequencing data and of the results of sequencing strategies that are used for GMO detection and identification and molecular characterisation, as well as of the related data analysis, interpretation and reporting.

¹ Minimum Performance Parameters for molecular analytical methods. Arne Holst-Jensen, Gro Johannessen, Camilla Sekse, Bjørn Spilberg, David Dobnik, Tanja Dreo, Teresa Crespo, Frédéric Gaspar, Ana Simplício Petra Richl, Mathias Welsche, Esther Kok, Martijn Staats. Report Decathlon project (www.decathlon-project.eu).

² Guideline for the submission of DNA sequences derived from genetically modified organisms and associated annotations within the framework of Directive 2001/18/EC and Regulation (EC) No 1829/2003

Tasks

The WG will assess the minimum performance parameters (MPPs) and their associated acceptance values (AAVs) for sequencing based analyses¹ and the guidelines of the EURL GMFF², including the related reporting, with the aim to ascertain the quality of DNA sequence data and of specific applications and strategies. Other sources (e.g. ISO, EFSA etc.) should be considered. The WG will require the participation of an adequate number of DNA sequence analysis experts from ENGL laboratories and JRC covering the different applications.

Timeline

At the first meeting a work plan will be established. A total of 4 meetings (virtual or physical) should be sufficient to finalise the work.