

Versailles, January 25th 2008

To whom may be interested in the Task-Force

Object : Establishing temporary task-force and core collection for taxa reference systems in GMO detection

Dear Madam, Sir,

The current European legislation need for labelling products derived from or containing GMOs above a threshold of adventitious or technically unavoidable presence, requires the quantification of the relative GMO content. Such a quantification is made by using either the ratio of GMO to non-GMO masses or, more generally (ENGL recommendation; Rec. 2004/787/EC), by calculating the number of GMO specific sequences per Haploid Genome Equivalent (HGE). Here, quantification of the HGE has been technically translated into quantification of GMO specific molecules to a representative reference gene. This reference gene is defined by taxon specific sequences (species, subspecies, etc.).

According to the EU legislation, the notifiers have to provide to the Community Reference laboratory for GM Food and Feed (managed by the European Commission Joint Research Centre – JRC) detection methods related to both GMO and taxon specific sequences. Article 30 § 5 of Regulation 1829/2003/EC allows notifiers to use methods developed by third parties, what should have conducted the notifiers to harmonize their taxa reference systems, numerous taxa identification systems have been developed worldwide and have been provided to the JRC. Such non-harmonized detection systems are inducing a redundancy in the available detection systems, a lack of reliability of the quantification methods and furthermore results in cumbersome, expensive and long validation of quantification methods.

This situation is recognized by all stakeholders in the GMO detection area, in particular by the scientists working in the EU FP6 funded research program Co-Extra and ENGL members. The need for harmonization is thus requested and led the Co-Extra WP5 towards the organization through ILVO (BE), of a meeting on this issue, which was held in Brussels on January 23rd. This meeting brought together Co-Extra partners, including JRC, EuropaBio and several of its companies members, ISTA, as well as several external laboratories invited for their expertise in establishing or managing core collections, taxonomy, phylogeny or breeding.

The results presented by both Co-Extra partners and JRC, as well as the following discussions between all partners, confirmed the issue and solutions were looked for by attendees on that complicated matter at the intersection of legislation, agronomy, taxonomy, phylogeny, and technical approaches for detection and quantification.

The Co-Extra coordinator and WP5 leader then proposed to reallocate a part of the Co-Extra funding to WP5 for establishing a temporary task-force (February 2008-February 2009) with the aim of developing an open “core collection” of crops open to all stakeholders after approval by the task-force, whatever the considered taxonomic level of the taxon, with appropriate varieties (inbred and commercial varieties) and related taxa, used for introgression programs as well as related species not to be detected (e.g. fodder beet, chard, etc. versus sugar-beet).

Accordingly, a proposal is currently sent through this letter to the Brussels’ attendees and all interested parties for participating in such a task-force for establishing a core collection on taxa reference systems in the domain of GMO detection. A very short description of the task-force organization and tasks is provided in the annex.

I now have to underline that this proposal is the first practical opportunity provided to harmonize reference systems for different taxa, and for decreasing the costs and uncertainty in this GMO detection domain for improving the consumers’ confidence.

In view of the current Co-Extra agenda (General Assembly to be held on 4-7 February 2008 during which the budgets will be voted), the principle agreement of the attendees and interested parties is fixed on February 4th 2008.

The WP5 leader together with the Co-Extra partners in charge of this task, will make sure to provide estimates of budget and to practically organize the task-force.

Looking forward to hearing from you before February 4th 2008.

Yves Bertheau
Co-Extra coordinator

Institut National de la Recherche Agronomique

Centre de Versailles-Grignon - RD 10 – (Route de St Cyr) – F 78026 Versailles Cedex

Tél : 01 30 83 32 00 – Télécopie : 01 30 83 31 95

Etablissement public à caractère scientifique et technologique placé sous la tutelle conjointe des ministres chargés de la recherche et de l’agriculture

Technical Annex of the Task-Force:

Draft on its organization and tasks

to be formalized through a signed agreement

- The task-force is established by the association of Co-Extra partners, the JRC, EuropaBio and its partners as legal entities, ISTA and third parties such as public laboratories in charge of core collections.
- This “**task-force**” will establish during its life span (February 2008-February 2009), by means of bibliographic studies, internal and confidential expertise, material furniture, material treatment such as seeds grinding or growth in greenhouses, etc., a **core collection** of varieties and related taxa (to be or not to be detected as being or not used into introgression programs) for several cultivated taxa.
- The first step of the core collection establishment will be focused on some *Triticeae* (maize, rice), *Fabaceae* (soybean), *Solanaceae* (potato, tomato, egg-plant), *Amaranthaceae* (sugar-beet, fodder beet), *Brassicaceae* (rapeseed) and *Malvaceae* (cotton).
- A confidentiality agreement between the Co-Extra coordinator and WP5 leader and EuropaBio and ISTA members will be signed ensuring thus the intellectual and industrial property rights of each participant.
- The Co-Extra EU FP6 funded program will reallocate a part of **its budget** to WP5 for establishing such a core collection. The other partners will look for their own corresponding budget.
 - The task-force will establish a **synthesis** of the available data on reference genes, including all sequences (using all available ones such as the Chinese database) phylogenic and taxonomic data, which will be made available to all members, all partners involved.
 - The task-force will summarize the already used and new **strategies** for establishing new taxa reference sequences based systems (e.g. starting from a known sequence such as gene for establishing profiles, taxa regulating elements such as promoters, or transposons towards defining new sequences by e.g. SCAR or genomic subtraction between taxa genomes).
 - Establish the core collection in the facilities of the JRC or any agreed facility for storing material such as ground seeds flour, growing seeds provided by partners, and **distribution** of leaves or flour to partners. The type and size of the samples will be jointly determined.
- The Co-Extra coordinator and/or the WP5 leader will receive confidential and public information from partners about the reasons (phylogeny, taxonomy, taxon used in introgression programs, taxa to be distinguished) of using such varieties or related taxa, and for avoiding duplicates of samples.
- The received samples will be anonymized by either the Co-Extra coordinator, the WP5 leader or a staff member of the JRC for further distribution to stakeholders and Co-Extra partners after its approval by the task-force.
- After agreeing on the content of the taxa families to be tested, the partners will
 - define jointly the issues and bottlenecks (e.g. through a confidential INRA circulation list) for each taxon to be identified;
 - define the validation and comparisons to be carried out with existing reference systems;
 - alternatively define the new techniques to be used for validating a current reference system or developing a new one such as SCAR or genomic subtraction.
- During its life period the task-force will look for any possibility of perennializing the core collection after the end of Co-Extra, e.g. the core collection being taken in charge by the JRC.