codex alimentarius commission

FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS

WORLD HEALTH ORGANIZATION

JOINT OFFICE: Viale delle Terme di Caracalla 00153 ROME Tel: 39 06 57051 www.codexalimentarius.net Email: codex@fao.org Facsimile: 39 06 5705 4593

Agenda Item 7 **CX/MAS 09/30/8-Add.1**

JOINT FAO/WHO FOOD STANDARDS PROGRAMME

CODEX COMMITTEE ON METHODS OF ANALYSIS AND SAMPLING
Thirtieth Session
Balatonalmádi, Hungary, 9 - 13 March 2009

PROPOSED DRAFT GUIDELINES ON CRITERIA FOR METHODS FOR THE DETECTION AND IDENTIFICATION OF FOODS DERIVED FROM BIOTECHNOLOGY

GOVERNMENT COMMENTS AT STEP 3

(Australia, Brazil, Colombia, Japan, Kenya, United States, EUROPABIO, ICGMA, ILSI)

AUSTRALIA

General Comments:

- While the document is technically sound, it would benefit from some judicious editing to remove redundancies, duplication and inconsistencies both within the main text of the paper and particularly between the main text and the Annexes.
- The document could be condensed into a much more concise document without losing meaning by removing the Annexes and including much of the text in the main body of the document.
- Throughout the text “gene” should be replaced by “DNA”
- Where applicable, definitions in the document should be aligned with those detailed in the Draft Guidelines on Analytical Terminology being considered by CCMAS or other international documents.
- Given the document also deals with quantification, quantification should be included in the title of the document

Specific Comments

Page 2, INTRODUCTION (Method Criteria), *Para 3*

To clarify wording, suggest replacing the first sentence of this para with: “The two most common approaches to the analysis of foods derived from biotechnology (Anklam *et al.*, 2002) are those based on DNA-based methods to detect a specific DNA (target) sequence (Lipp *et al.* 2005; Holst-Jensen *et al.*, 2004, Miraglia *et al.*, 2004) and those based on the detection of proteins themselves or their activities (Grothaus *et al*., 2007).

Page 3, Measurement Uncertainty, *Para 2*

Guidance on how to include uncertainty arising from zygosity would be a valuable addition to this document. Reference materials would also be required with a stated zygosity.

Furthermore, since this paragraph relates to uncertainty of quantitative measurements it is not appropriate to use 'screening methods' as an example since they should not be used for quantitative analysis. The uncertainty arising from stacked events would be of relevance when more than one event is detected and quantified in a sample. Currently, it is not possible to determine if such a situation is due to a mixture of events in the sample or whether the events are stacked in a single genetically modified organism. In this situation, measurement uncertainty would need to take into account both of these possibilities.

Page 4, Modular Approach to Method Validation

Current wording is confusing as the word 'method' is used to refer to the complete experimental process and also used to refer to parts of the method such as DNA extraction. Suggest revising the text and refer to the sub-parts of a method as 'processes' to distinguish between the complete method and separate components of the method

Page 5, Principle Conditions

Suggest replacing "an endogenous gene" with "an endogenous DNA sequence"

Page 6, Collaborative Trial Test Materials *Para 2*

Revise text ton read: "In a PCR-based method, DNA (isolated from plant material, or if validated, as a plasmid calibrator) is used as the calibrator."

ANNEX I

Sensitivity Testing

Page 11, Delete "in terms of haploid genome equivalents" so sentence reads "LOD should be determined for each PCR system separately" ……".

PRACTICAL APPLICATION OF THE METHOD

Operational characteristics and practicability of the method

Second sentence is confusing. Suggest change to read: "Information on costs, practical difficulties, and of any other factor that could be of importance for the operators should be provided. "

Annex III

This section appears to reflect the European Network of GMO Laboratories 'Definition of Minimum Performance Requirements for Analytical Methods of GMO testing' **(**http://gmo-crl.jrc.ec.europa.eu/doc/Min_Perf_Requir_Analyt_methods_131008.pdf**).** However, as the interlaboratory validations described in this document normally apply to extracted DNA, the participating laboratories do not undertake the extraction step. Therefore, the performance criteria for RSD etc relate to the PCR process only. This should be clearly stated in the CX/MAS 09/30/8 as it may be difficult to achieve these criteria from the complete method (including DNA extraction). This may then result in further inconsistency between Annex III (PCR methods) and Annex V (protein methods) since Annex V criteria may be referring to the complete method including protein extraction.

ANNEX V

REFERENCE MATERIALS

Replace first sentence with "The reference material consists of the same matrix as the commodity or food to be tested whenever possible. Reference materials for calibration may be of a different matrix, if they are shown to be validated for the purpose (e.g. for calibration).

Delete "of introduced proteins in recombinant-DNA agricultural commodities" from second last sentence of the first para.

BRAZIL

Brazil supports the document, however it is important to harmonize the definitions with the "Guidelines on Analytical Terminology" and others relevant documents of the Committee on this issue.

COLOMBIA (versión en español)

Colombia expresa su agradecimiento a todos los países que han trabajado en la generación y estructuración del documento de trabajo titulado Anteproyecto de directrices sobre criterios relativos a los metodos de deteccion e identificacion de alimentos obtenidos por medios biotecnologicos CX/MAS 09/30/8 (Trámite 3 de 8), y para el cual fueron solicitados comentarios por parte del Comité del Codex sobre Métodos de Análisis y Toma de Muestras.

Colombia desea expresar sus comentarios al Anteproyecto de Directrices en el sentido de manifestar que teniendo en cuenta el desarrollo actual de las técnicas de detección biomoleculares, y una vez revisado el contenido del anteproyecto de directrices no se encuentra una justificación científica que conduzca a la necesidad de generar un proyecto de documento especifico para la detección de Alimentos Obtenidos por

Medios Biotecnológicos, diferente al que se seguiría para el uso de técnicas moleculares para cualquier otro tipo de alimento, por ejemplo para la detección de patógenos, toxinas, alérgenos y otros contaminantes.

No consideramos pertinente que se generen unas directrices centrándose principalmente en el método de obtención del alimento y no en el producto en si mismo, generando una diferenciación frente a los alimentos obtenidos por medios biotecnológicos, pese a que las técnicas moleculares empleadas para su detección son las mismas, y el contenido de la propuesta de directrices expone los aspectos técnicos y de validación de PCR tiempo real y de ELISA, independientemente de que sean empleadas o no para la detección de alimentos derivados de la biotecnología.

El anteproyecto de directrices debe enfocarse en las provisiones relacionadas con los métodos moleculares empleados para la detección basada en métodos de ADN o proteína para cualquier tipo de alimentos, sin que fuese exclusivo para los alimentos obtenidos por medios biotecnológicos, logrando así un enfoque más amplio, que no es excluyente o especifico por el tipo de técnica por el cual fue obtenido el alimento.

El anteproyecto de directrices hace referencia a la identificación como uno de sus elementos, no obstante Colombia considera que estas directrices deben excluir cualquier referencia a trazabilidad o etiquetado, teniendo en cuenta que el Codex Alimentarius se encuentra trabajando en proyectos específicos al respecto, y las directrices sobre detección en alimentos, no solo en alimentos derivados de la biotecnología, deben centrarse en los aspectos técnicos de los métodos a emplear, las metodologías para su validación y aceptación como métodos de referencia.

El trabajo adelantado por el CCMAS, en este tema, debería asegurar que sea consistente o complementario con el trabajo adelantado por ISO y otras organizaciones internacionales.

Colombia manifiesta su interés porque en la discusión que se adelante sobre el tema de detección, sean tenidos en cuenta los avances de la tecnología, de manera específica las consideraciones referentes a eventos conjuntos, mejoras nutricionales, alimentos derivados de animales modificados genéticamente y cisgénicos, entre otros aspectos considerados dentro de las líneas de desarrollo.

Teniendo en cuenta lo anterior Colombia propone se modifique el titulo de la norma en el siguiente sentido: "**Anteproyecto de directrices sobre criterios relativos a los metodos de deteccion por tecnicas moleculares en alimentos para consumo humano**", ya que el alcance y contenido del documento propuesto es aplicable al uso de técnicas de biología molecular basadas en ADN o proteína en cualquier alimento, como se menciono anteriormente para la detección de patógenos, alergenos, toxinas, contaminantes, OGM, entre otros.

COLOMBIA (English versión)

Colombia expresses its appreciation to all countries who worked in the preparation and structuring of the working document Proposed Draft Guidelines on Criteria for Methods for the Detection and Identification of Foods Derived from Biotechnology CX/MAS 09/30/8 (Step 3 of 8) on which comments were requested by the Committee on Methods of Analysis and Sampling.

Colombia wishes to express its comments on the Proposed Draft Guidelines to point out that, taking into account present development of biomolecular detection techniques, and after reviewing the contents of the proposed draft document, there is no scientific justification for the need to produce a specific project document for the detection of foods derived from biotechnology, which would be different from what would be applied for the use of molecular techniques for any other type of food, for example detection of pathogens, toxins, allergens or other contaminants.

We do not consider it relevant to develop guidelines focused mainly on the production method of the food and not on the product itself, differentiating foods obtained through biotechnology, while the molecular techniques used for their detection are the same, and the proposed guidelines contain aspects of real time PCR and ELISA, irrespective of whether they are used or not for the detection of foods obtained from biotechnology.

The proposed draft guidelines should focus on the provisions related with molecular methods used for detection based on DNA or protein for all types of foods, without being exclusive to foods obtained through biotechnology, achieving therefore a wider scope, which is not exclusive or specific for the type of technique through which the food was obtained.

The proposed draft guidelines refer to identification as one of its elements, however Colombia considers that these guidelines should exclude any reference to traceability of labelling, taking into account that Codex Alimentarius is working on specific drafts in this respect, and the guidelines on detection, not only for foods

derived from biotechnology, must focus on technical aspects of the methods to use, methodologies for their validation and acceptance as reference methods.

The work put forward by CCMAS on this subject should ensure that it is consistent of complementary with the work developed by ISO and other international organisations.

Colombia expresses its interest to ensure that, in the discussion what will take place on the issue of detection, technological advances are taken into account, in particular aspects related to joint events, nutritional improvement, foods derived from genetically and cisgenic modified animals, among other aspects considered in the framework of its scope.

Taking into account the above, Colombia propose to modify the title of the standard as follows: "**Proposed Draft Guidelines on Criteria for Detection Methods using Molecular Techniques in Foods for Human Consumption**", as the scope and content of the proposed document are applicable to the use of molecular biology techniques based on DNA or protein in any food, as mentioned above, for the detection of pathogens, allergens, toxins, contaminants, GO, among others.

JAPAN

I. General comments

Japan appreciates the UK and Germany for their longstanding efforts to lead the electronic Working Group and prepare the basis of this proposed draft guidelines before us.

We consider that we should focus on the setting of the criteria to evaluate the methods in the main body of guideline with numerical value. We hope that the practical guideline will be made to evaluate whether performance of the developed methods is acceptable. If it is necessary, the specific information for each method should be described in the ANNEX.

We propose to include the section of "Scope" in order to clearly describe the aspects to be covered by the guidelines. We also propose to change the order of sections to make them easier to understand as follows:

1. INTRODUCTION (including the purpose of the guideline)

2. SCOPE

3. DEFINITIONS

4. GENERAL METHOD VALIDATION

4.1 Criteria Approach

4.2 General Method Criteria

- trueness
- applicability (matrix, concentration range and preference given to "general" methods)
- limit of detection
- limit of quantification
- precision; repeatability intra-laboratory (within laboratory), reproducibility inter-laboratory (within laboratory and between laboratory)
- selectivity
- sensitivity
- linearity

4.3 Validation Process

- pre-validation of the method
- full validation of the method

5. SPECIFIC CONSIDERATION FOR THE VALIDATION OF METHODS FOR THE DETECTION AND IDENTIFICATION OF FOODS DERIVED FROM BIOTECHNOLOGY

5.1 METHOD DEVELOPMENT TO FORMAL VALIDATION

5.1.1 Method Acceptance Criteria (Required condition for full validation)

5.1.2 Applicability of the Method

5.1.3 Principle condition

5.1.4 Modular Approach to Method Validation

5.2 COLLABORATIVE TRIAL REQUIREMENTS

5.2.1 General Information

5.2.2 Minimum Performance Requirements

5.2.3 Collaborative Trial Test Materials

5.2.4 Specific Information on the Validation of Methods (In CX/MAS 09/30/8, the title of "VALIDATION OF METHODS")

5.3 UNIT OF MEASUREMENT

5.4 MEASUREMENT UNCERTAINTY

(6. SAMPLING)

7 QUALITY CONTROL REQUIREMENTS

7.1 Laboratory Quality

7.2 Guidance on the Laboratory Set-up and Operation

7.3 Reference Material

7.4 Concentration Distributions

8 REFERENCES

In each group, the guidance and/or requirements should clearly state that they are relevant to the qualitative and/or, quantitative methods, and protein-based and/or DNA-based methods.

II. **Specific Comments**

APPENDIX I

Method Criteria

p.2, 3rd para; The document prepared by ISO on DNA based methods, ISO 21570:2005, is already included in the list of references. This document should be presented in the Introduction section. Similarly, ISO has produced a document for protein based methods, ISO 21572:2004. This document should also be included in the Introduction section as a reference. Therefore, we would like to propose to amend paragraph 3 of Introduction as follows:

> However, the two most common approaches (Anklam et al., 2002) are those based on DNA-based methods to detect a specific DNA (target) sequence (Lipp et al. 2005; Holst-Jensen et al., 2004, Miraglia et al., 2004, **ISO21570:2005**) and those based on the detection of proteins themselves or their activities (Grothaus et al., 2007, **ISO21572:2004**). For DNA-based analysis, the PCR approach is presently most widely applied, although other DNA-based methods that achieve measurement with or without a PCR step may be employed if properly validated. Both DNA and protein-based approaches are considered here.

p.2, 4th para; Four bullets for the DNA-based methods and a bullet for the protein based methods should be deleted, because we think that they are information for the characteristics of DNA and Protein-based methods and not criteria for evaluation of the methods in the validation process as well as other criterion such as a trueness.

~~These Guidelines address these requirements in the Foods Derived from Biotechnology sector, and anticipates that is likely that these will have to be further expanded (e.g. for PCR) by other items such as:~~

> ~~for the DNA-based methods~~
>
> - ~~Amplicon length~~
> - ~~Whether the method is instrument specific~~
> - ~~Whether there are differences between qualitative and quantitative PCR-based detection methods~~
> - ~~Wherher single- or multi-plex PCR amplification are undertaken~~

~~and~~

~~for the protein based methods~~

- ~~Equivalency of reagents over time~~

p.3, 3rd para. Measurement Uncertainty

This paragraph should be moved to a suitable part such as sampling, method development, and/or explanation in Annexes or deleted, because we should not take into account of variation of analytes arising from the biological factors in which gene stacking and the expression levels of proteins etc. are included, to estimate the measurement uncertainty.

We also request to clarify the term “Sub-sampling”. We guess that any sampling approach is not effective procedure to reduce the biological variations effect on the measurand unless the measurement units are clearly stated. On the other hand, we think a suitable sampling approach such as a sequential sampling from the specified sample such as a laboratory sample etc. will be effective procedure to obtain the more accurate test-result for the sample. Therefore, when this paragraph is moved to a suitable part, the last sentence “However, both DNA- and protein- based methods may be used via a sub-sampling approach, or on single seeds, where the potential impact of any such biological variation is minimized” should be modified as follows,

> “However, when DNA- and protein-based methods are used on single seeds, or via a suitable sampling approach, the variation of analytes in the specified sample will be reduced even if biological factors affect the variation of analytes.”

The description for the “**MEASUREMENT UNCERTAINTY**” is repeated in page 7, para.2 again. These two parts should be combined, and it is necessary to reconsider what is the measurement uncertainty we can estimate from the analytical data. We propose to describe the general recognition for measurement uncertainty we can estimate form the analytical data for quantitation of the foods in page 3 as follows,

> **MEASUREMENT UNCERTAINTY**
>
> Codex has developed guidelines on Measurement Uncertainty (CAC/GL54-2004). These guidelines require laboratories to estimate the uncertainty of their quantitative measurements. This is particularly important and has consequences for measurements in the sector dealing with foods derived from biotechnology where analytical controls may not be as effective as found in other areas of analysis in the food sector. It is frequently not appreciated that the magnitude of the measurement uncertainty is considerably greater in this analytical sector than would normally be expected.
>
> Sample preparation and analytical methods are two significant sources for error that must be considered when evaluating an analytical measurement. Analysts using methods which have been validated according to these guidelines will have sufficient information to allow them to estimate the uncertainty of their result. Quantitation based on the protein expressed can also significantly contribute to the uncertainty of the analysis. Guidance on both the estimation and use of any measurement uncertainty estimation has been/are being developed and adopted by the Codex (Codex Guidelines on Measurement Uncertainty and the draft Guidance Document on “The Use of Analytical Results”).

p.4, 7th para. Modular Approach to Method Validation

Since there seems to be no experimental report demonstrating the applicability of modular approach to either protein-based or DNA-based methods, it is necessary to clearly state that the modular approach is theoretical one and there is no widely accepted protocol to apply this approach.

p.4-6. Principle Conditions

Please correct the number of each topic because the number (1) is null.

We recommend listing the more information on protein-based methods in Principle Conditions. For example, the controls for qualitative method using lateral flow device should be listed.

p.7, UNITS OF MEASUREMENT

The term “multiple sub-sampling” is not defined in the terminology of Codex use or any other international technical guidelines such as ISO guideline. We request to clarify this term.

According to the comments **on p.3 3rd para. Measurement Uncertainty,** we suggest it would be better to revise the phrase “as a multiple sub-sampling approach on grain” to “as on single seeds, or via a suitable sampling approach”, if the description for sampling will remain in this section.

p.8, SAMPLING

The necessity of including the section “SAMPLING” in this document should be carefully considered. If these aspects have already been covered by the existing Codex document (*e.g.*, Codex General Guideline of Sampling), this section can be deleted.

p.9, References

We propose to insert the following reference according to our comment;

> ISO 21572 Foodstuffs - Methods for the detection of genetically modified organisms and derived products -Protein based methods (ISO 21572:2004)

Editorial errors

“Protein based methods” should be corrected to “protein-based methods” and “DNA based methods” should be corrected to “DNA-based methods” for consistency. We recommend that the editorial check should be made through the document.

ANNEX I

p. 10, INFORMATION ABOUT THE METHOD OPTIMISATION

Generally, the information on the protein-based methods is insufficient. For example, the information on the antibody is as important as information on the primer pairs in DNA-based methods, however, it is not referred in the topics. We propose to separate the topics following protein-based methods and/or DNA-based methods, and the information on the antibody and calibrators for ELISA methods should be added as the topics for protein-based methods.

p.11, 9th para. METHOD VALIDATION /PERFORMANCE

Three characteristics listed in this part including amplicon length, restriction of the methods (e.g. instrument or chemistry specific), and multiplicity of PCR are not included in the criteria listed in the Codex Check-list. Moreover, we doubt why it is necessary to compare validation criteria between PCR-based method and immunological methods.

We think the information on these characteristics should be provided to the Codex as a part of description of the methods if it is required.

ANNEX II

"**Accuracy**" should be changed to "**Trueness**" to harmonize with the analytical terminology for Codex use in the procedural manual discussed now in CCMAS. In the CL2008/28-MS, accuracy when applied to a set of test results or measurement results, involves a combination of random components and a common systematic error or bias component.

"**Recovery**" should be deleted because the concept of recovery is not applicable to the relative quantification methods used in analysis for foods derived from biotechnology.

ANNEX III

P15, 1st para. INTRODUCTION

The term “protein” should be deleted, because this annex focused on the validation of the quantitative PCR methods in which DNAs is analyte.

> DNA-based analysis is commonly performed using Polymerase Chain Reaction (PCR). This technique amplifies a specific (short) segment of DNA to the extent that its quantity can be measured instrumentally (e.g., using fluorometric means). As DNA is a molecule that is easily degraded during food processing operations (e.g., due to heat, enzymes and mechanical shearing), we urge that this be considered in the performance criteria assessment of this technique. This is

relevant as in most foods raw ingredients are not present, but are in a processed form, which has an effect on ~~proteins and/or~~ DNA present in food. Furthermore, these ~~protein(s) and/or~~ DNA may be degraded, or its total amount may be decreased due to processing. As a result, any current detection method (DNA ~~or protein~~ based) is affected.

P15, 5th para. VALIDATION

The term "accuracy" should be changed to "trueness" for consistency.

A number of the parameters involved in validation of the performance of a quantitative PCR assay will be discussed in detail. These are scope, LOD and LOQ, ~~accuracy~~ trueness, precision, sensitivity and ruggedness (robustness). Other important factors are acceptance criteria and interpretation of results, and the issue of the units in which results are expressed.

P15, 7th para. (just before "Accuracy"): editorial

Please delete the last punctuation mark, as it is an editorial error.

KENYA

Background

Kenya recognizes the importance of the development of the Criteria for the methods for Detection and Identification of Foods Derived from Biotechnology and supports the same effort.

Comments

We intensively went through the document and acknowledge its importance to our country. We plan to actively participate on its development so we can adopt it for our national use when endorsed by the CAC. We therefore support consideration of this document by the 30th session of CCMAS. We have no technical comment on the issue raised at this step 3 of the procedure.

UNITED STATES

General Comments

The United States commends the Electronic Working Group led by the United Kingdom and Germany for the development of a scientifically sound document that identifies criteria which should be considered when validating methods to detect specific DNA sequences and proteins in foods. This document provides information and criteria that will enable laboratories engaged in molecular testing to design and conduct collaborative studies to demonstrate the acceptability of methods for a wide variety of DNA-based and Protein-based applications.

Recognizing that the 31st Session of the Codex Alimentarius Commission (CAC) approved the Guidelines as new work, the United States notes the discussion on this document that occurred at this Session of the CAC and the outcome of that discussion, specifically:

> "The Commission approved new work on the Guidelines on the Criteria and recommended that the Committee consider the concerns and recommendations regarding the scope expressed at the current session." (ALINOM 08/31REP, Paragraph 97)."

Reflecting the concerns expressed at the CAC regarding the scope of the work, the United States believes that further work is needed on the draft Guidelines as indicated in our specific comments below and that the document should be retained at Step 3 for further revision

Specific Comments

Given the recommendation of the Commission, the United States offers the following specific comments on this document.

1. Change the title of Appendix 1 The United States feels the current title, "Guidelines for the Validation and Quality Control Requirements for the Analysis of Foods Derived from Biotechnology", is too limited. Protein-based methods have been used for many years to analyze food matrices for a number of analytes; and DNA-based methods can be used to identify molecular markers used in conjunction with conventional breeding, as well as markers associated with r-DNA techniques. We also note that the focus of the document is on validation of methods and not on quality control requirements. As a result, the United States proposes changing the title to: "Guidelines for the Validation of Methods Used for the

Analysis for DNA Sequences and Specific Protein in Foods." This title change is consistent with the intent to broaden the scope of the document as directed by the 31st CAC.

2. Add a Statement of Purpose and Scope to Appendix I. To be consistent with the change in title, we believe that there should be a statement of purpose and scope that states that the criteria specified in the document for the evaluation of methods of analyses are appropriate for all DNA- and Protein-based methods.

3. Revise the text and pertinent Annexes to reflect the broader scope of the document.

4. Organize the document to eliminate duplication, especially with regards to definitions. Annex II provides definitions of terms used throughout the document; however, many of the definitions are then repeated in Annexes III, IV and V, either verbatim or with some method specific variation. Definitions are important, and the definitions used in this document should be consistent with those in the Draft Guidelines on Analytical Terms which is currently of being revised by the Codex Committee on Methods of Analysis and Sampling (CCMAS).

5. Reorganize and streamline the main part of the document to improve the structure and flow of the document. For example, reorganize the text into the following main sections: introduction; purpose and scope, definitions, general considerations, validation of methods, and references. The "general considerations" section would include the following sections: applicability of a method; basic components of a method; determining a specific method to validate; criteria for acceptance; collaborative trial requirements; units of measurement; measurement uncertainty; guidance on laboratory set-up and operation; reference materials; and, sampling.

6. Eliminate references to Codex purposes and method endorsement throughout the document. The performance data for a method is clearly identified in Annex III, Validation of a Quantitative PCR Method; Annex IV; Validation of a Qualitative PCR Method; and Annex V, Validation of a Protein-Based Method, therefore, we believe Annex 1, "INFORMATION TO BE PROVIDED TO CODEX WHEN A METHOD IS TO BE CONSIDERED FOR ENDORSEMENT BY CCMAS" is unnecessary and should be eliminated. . This is consistent with the Commission's recommendation to consider broadening the scope of the document, and consistent with the Terms of Reference for CCMAS. Additionally, the CCMAS methods endorsement process arises from the work of Codex committees/task forces developing standards for which methods of analysis are required, and there are no Codex committees/task forces developing standards for which methods covered by the proposed guidance are directly applicable.

Given the above comments, and the statement of the Commission, the United States recommends the Committee return this document to the Electronic Working Group for revision, and, as noted above, retain the document at Step 3.

EUROPABIO

On behalf of EuropaBio**,** we appreciate the opportunity to provide comment on the document CX/MAS 09/30/8 under development within CCMAS, "Consideration of the methods for the detection and identification of foods derived from biotechnology: General Approach and Criteria for Methods."

While we appreciate the work on the document, as developed, we strongly believe there is no scientifically based justification for the specific guidance related to DNA/protein testing for foods derived from biotechnology owing to method of production of the food. Therefore, we recommend that emphasis in the document be placed on expanding the scope to include protein-based and/or DNA-based analysis, rather than directing the guidance specifically to protein/DNA present as a result of r-DNA technology.

EuropaBio would therefore prefer to see the document framed as relating to health and safety provisions for detection of DNA/protein in all food (not specifically or exclusively those derived from recombinant DNA technology). This would allow CCMAS to focus on the use of DNA and protein detection platforms that can also be applied in other areas of the food supply chain, such as pathogens, toxins and other contaminants.

We note that in the 17th Edition of the Codex Alimentarius Procedural Manual (beginning page 73), Guidelines exist for the "Inclusion of Specific Provisions in Codex Standards and Related Texts", with specific reference to "Working Instructions for the Implementation of the Criteria Approach in Codex, and Conversion of Specific Methods of Analysis to Method Criteria by the CCMAS". However these guidelines and existing criteria do not adequately address guidance for protein or DNA testing. If the scope were

expanded, allergens, toxins and other elements, as well as DNA/protein from r-DNA derived foods would be objectively and distinctly covered by Codex text.

• Specifically, we propose that the Guidance to be developed to:

- Relate to health and safety provisions for detection ofDNA/protein in all food (not specifically or exclusively those derived from r-DNA technology);
- Exclude rationale for the work that do not relate specifically to the
- health and safety of consumers;
- Exclude any reference or link to traceability and/or labeling;
- Focus on the use DNA and protein detection platforms that can be broadly applied to other areas of the food supply chain, such as pathogens, toxins and other contaminants; and
- Ensure that any amended guidance or guidance document work not duplicate and also be consistent with the work of ISO and other international organizations.

Again, we appreciate the work that has been developed to date and the opportunity to comment on its progress. Further, we commit to working within the Codex system to assist in development of a relevant, scientifically-based system for detection of protein and/or DNA in all food and feed matrices.

ICGMA

On behalf of the International Council of Grocery Manufacturers Associations (ICGMA)[1], we appreciate the opportunity to provide comment on the document under development within CCMAS, "Consideration of the methods for the detection and identification of foods derived from biotechnology: General Approach and Criteria for Methods." ICGMA appreciates the work on the Guidance as developed, and suggests broadening the scope and refocusing the document with a view towards the elaboration of guidance that would be useful to detect DNA/protein generally.

ICGMA supports the development of Codex texts that are science based and respond appropriately to the protection of consumers' health and facilitation of fair trade practices in food. In this regard, we propose that the Guidance should relate to detection of DNA/protein in all food products (not specifically or exclusively those derived from r-DNA technology) and focus on the use of DNA and protein detection platforms that can be broadly applied to many areas of the food supply chain, such as pathogens, allergens, toxins and other contaminants as well as DNA/protein from r-DNA derived foods.

In addition, a guidance with a broader scope better responds to recommendations made in the 2002 FAO/WHO Evaluation of Codex to devote resources to standards more horizontal in nature.

Again, we appreciate the work that has been developed to date and the opportunity to comment on its progress. Further, we commit to working within the Codex system to assist in development of a relevant, scientifically-based system for detection of protein and/or DNA in all food and feed matrices.

ILSI

On behalf of the International Life Sciences Institute (ILSI), I would like to submit the following comments for consideration by the Codex Committee on Methods of Analysis and Sampling.

Together with AACC International, governmental and other non-governmental organizations, ILSI has participated in and/or organized 13 training workshops covering the scientific issues surrounding sampling and the application of methods such as PCR and antibody-based assays for the detection of products of modern biotechnology. More than 650 members of local governments, academia and industry from about 20 countries have taken part in these workshops. In addition, ILSI has supported the attendance of experts to such workshops as both participants and instructors.

The existing Codex Guidelines contain principles for method adoption, and they have been developed primarily for chemico- and physico-analytical testing methods. It is important to recognize that methods used for the detection of specific DNA sequences and proteins in food are of a biological nature (biomolecular) and in addition to addressing what unique testing principles may need to be applied for these

[1] ICGMA, a recognized NGO before the Codex Alimentarius Commission, represents the interests of national and regional associations who collaborate with all sectors of the consumer packaged goods industry. ICGMA promotes the harmonization of scientific standards and policies concerned with health, safety, packaging, and labeling of foods, beverages, and other consumer packaged goods. ICGMA also works to facilitate international trade in these sectors by elimination or preventing artificial barriers to trade.

methods, this biomolecular class of methods may also have significant relevance beyond the detection and identification of foods derived from biotechnology.

ILSI IFBiC recognizes that biomolecular methods are applicable not only for the detection of products of modern biotechnology, but also for food safety and control processes and can be broadly applied to areas of the food supply chain such as detection of pathogens and of adulteration. As such, CCMAS may find it beneficial to expand the scope of this work item beyond foods derived from modern biotechnology to include other analytical areas in the Codex Guidelines. The evidence demonstrates that the types of biomolecular methods applied to products of modern biotechnology are widely applicable, and that there is an excellent scientific basis for CCMAS to broaden the scope of the work proposed to cover methods for establishing the presence of all specific DNA sequences and/or specific proteins in food.

In addition to expanding the scope of the work item, ILSI brings to the attention of the Committee, that the present Codex and IUPAC guidelines are insufficient to cover the detection of materials via biomolecular methods. The approval by the Commission of new work at CCMAS on the Guidelines on the Criteria (taking into consideration the concerns expressed at the session regarding the scope) offers an excellent opportunity to update the Codex guidelines to consider and include guidelines for a broad range of biomolecular methods.

Use of Biomolecular Methods in Food Testing

PCR methods are being used for routine examination and control purposes in various areas of the food chain for the determination of species contamination, and/or the presence of DNA that may indicate the presence of a particular allergen, pathogens or other contaminant. In addition, antibody-based methods have been extensively used in quality control in the food supply chain for decades. Examples of such uses can be found in the literature (see selected references attached). Due to the limited information regarding the performance of such methods measured against Codex Criteria (see Codex Alimentarius Procedural Manual), most of them must presently be considered type IV methods.

While it is important not to duplicate the work of other organizations in the same area, many countries (and especially developing countries) consider such biomolecular methods important and are looking to Codex for technical guidance. In addition, there is a need to facilitate harmonization at the international level to prevent barriers to trade (Bridges 2007). The International Organization for Standardization (ISO) also is addressing biomolecular methods and has formed a specific Subcommittee (TC 34/SC 16) to address method standardization. The intended scope of the SC (as resolved at its first meeting) is “Standardisation of biomolecular testing methods applied to: foods; feeds; seeds and other propagules of food and feed crops.”

ILSI

ILSI is a nonprofit, worldwide foundation established in 1978 to advance the understanding of scientific issues relating to nutrition, food safety, toxicology, risk assessment, and the environment by bringing together scientists from academia, government, industry, and the public sector to solve problems with broad implications for the well-being of the general public. ILSI receives financial support from industry, government, and foundations.

ILSI is affiliated with the World Health Organization as a nongovernmental organization and has specialized consultative status with the Food and Agriculture Organization of the United Nations. Thus, it is as a nongovernmental organization that we respectfully submit these comments.