UN environment programme

CBD

Convention on Biological Diversity

Distr.
GENERAL

CBD/CP-DIOM/2023/1/1
1 August 2024

ENGLISH ONLY

INTERNATIONAL CONFERENCE ON GMO
ANALYSIS AND NEW GENOMIC TECHNIQUES
Berlin, 14–16 March 2023

REPORT OF THE INTERNATIONAL CONFERENCE ON GMO ANALYSIS AND NEW GENOMIC TECHNIQUES BERLIN, 14–16 MARCH 2023*

I. INTRODUCTION

1. In decision CP-10/11, the Conference of the Parties serving as the meeting of the Parties to the Cartagena Protocol on Biosafety recognized the need for capacity-building activities on new detection techniques. Further, Conference of Parties serving as the meeting of the Parties to the Cartagena Protocol on Biosafety encouraged Parties and international organizations to fund the capacity-building of personnel involved in the field of detection and identification of living modified organisms. Furthermore, the Conference of Parties serving as the meeting of the Parties to the Cartagena Protocol on Biosafety requested the Executive Secretary to further enhance capacity-building in the field of detection and identification of living modified organisms, including the convening, in cooperation with relevant organizations, subject to the availability of resources, of regional and subregional capacity-building activities, such as online training and face-to-face workshops.

2. Accordingly, with the financial support of the Government of Germany, the Secretariat co-organized the International Conference on Genetically Modified Organisms (GMO[1]) Analysis and New Genomic Techniques (NGT) with German Federal Institute for Risk Assessment (Bundesinstitut für Risikobewertung), Federal Office of Consumer Protection and Food Safety (Bundesamt für Verbraucherschutz und Lebensmittelsicherheit), German Federal Ministry of Food and Agriculture (Bundesministerium für Ernährung und Landwirtschaft), Julius Kühn Institute and European Commission, Joint Research Centre. The conference was held from 14 to 16 March 2023 in Berlin, Germany.

3. The Conference had a technical programme that was organized into seven sections:

i. Detection and identification of "classical" GMO and NGT products - Status and challenges;

ii. Detection of NGT products - Analytical methods;

iii. Requirements for the Identification of NGT products;

iv. Detection of "classical" GMOs - Analytical methods;

v. Regional networks: experiences gained in various regions;

vi. Global information sharing; and

* The present document is being issued without formal editing.

[1] The term "genetically modified organism" was used to align the terminology with researchers involved in the field. However, it should be noted that the term can be considered to be interchangeable with the term "living modified organism" as defined by the Cartagena Protocol on Biosafety in the context of the Conference.

vii. Alternative approaches for GMO traceability.

4. A poster session was also run in parallel to the oral presentations and a panel discussion took place following the seven technical sessions. An overview of the programme can be found in annex I.

5. Twenty-one participants from twenty-one Parties[2] attended the Conference. Three participants from three Parties[3] were unable to travel to the conference and participated online.

6. The conference webpage is available: https://www.bfr-akademie.de/gmo2023/.

II. OPENING OF CONFERENCE

7. The Conference opened at 13:30 on Tuesday 14 March 2023.

8. Opening remarks were provided by Mr. Andreas Hensel, President of the German Federal Institute for Risk Assessment; Ms. Silvia Bender, State Secretary of the German Federal Ministry of Food and Agriculture; Ms. Wadzanayi Mandivenyi, Head of the Biosafety Unit of the Secretariat of the Convention on Biological Diversity; Mr. Ralf Wilhelm, Head of Institute for Biosafety in Plant Biotechnology of the Julius Kühn Institute; Mr. Friedel Cramer, President of the Federal Office of Consumer Protection and Food Safety and Ms. Salla Saastamoinen, Deputy Director-General of the European Commission Joint Research Centre. The speakers reflected on the importance of the field of detection and identification for both agriculture and biodiversity.

9. Following the opening remarks, Mr. Hermann Broll provided the organization for the conference, which can be found in annex I.

III. SESSION 1: DETECTION AND IDENTIFICATION OF "CLASSICAL" GMO AND NGT PRODUCTS - STATUS AND CHALLENGES

10. In the first technical session of the Conference, presentations focused on the status and challenges for the detection and identification of "classical" GMO and NGT products. The aim of this session was to provide a background and current status of the field of detection and identification.

11. To provide a historical context, Mr. Guy Van Den Eede from the European Commission Joint Research Centre reflected on the achievements obtained by the field of detection and identification in the first presentation. In particular, the contributions of the European Network of GMO Laboratories of the European Commission and their work in global harmonization of detection methodologies, as well as on the "Global Conference on GMO Analysis", which was previously held in Como, Italy, from 24 to 27 June 2008, were highlighted.

12. Following this presentation, Mr. Emilio Rodríguez Cerezo from the European Commission Joint Research Centre provided an overview of new genomic techniques. The current status of research and development of NGT applications, including examples of crops, animals and microorganisms, was overviewed in the presentation from Mr. Cerezo.

13. Next, Mr. Malcom Burns from the LGC Group Limited (formerly Laboratory of the Government Chemist) provided a technical background on the detection and identification of LMOs and the detection of NGT products. In his presentation, Mr, Burns mentioned the harmonization of terminology, analytical challenges in the detection of small sequence alterations, the need to establish the origin of the mutation and the availability of suitable reference materials and databases.

14. In the final presentation for the first section, Ms. Alexandra Ribarits from the Austrian Agency for Health and Food Safety provided an overview of the identification of known and unknown LMOs and NGT

[2] Bosnia and Herzegovina, Burundi, Cameroon, China, Costa Rica, Ghana, Honduras, Italy, Latvia, Lebanon, Lesotho, Nigeria, Philippines, Serbia, South Africa, Sudan, Türkiye, United Kingdom of Great Britain and Northern Ireland, Uruguay, Venezuela and Zimbabwe.

[3] Belarus, Brazil and Sri Lanka.

products. During the presentation, reference materials and prior knowledge were also considered under these contexts for their importance for technical detection and identification. In addition, the role detection and identification have in organic agricultural practices was mentioned.

15. Following the presentations, participants in-person and virtually were given an opportunity to ask questions.

IV. SESSION 2: DETECTION OF NGT PRODUCTS – ANALYTICAL METHODS

16. The focus of Session 2 was the analytical methods for the detection of NGT products. The session aimed to explore and consider the analytical methods available to support the detection of NGT products.

17. First, Mr. Raymond Shillito from BASF provided an overview of the analytical methods available for the detection of NGT products, including considerations for their applicability and implementation. Challenges for distinguishing between NGT-induced and naturally occurring mutations were also described.

18. In the second presentation, Ms. Margit Ross from Corteva Agriscience provided an example of the detection of maize carrying a 4-kilobase deletion in the *waxy1* gene, which was induced using CRISPR-Cas9[4]. The presenter detailed the minimum performance criteria for detection, identifiability, practicability and applicability that would be required. Further, results were presented for the detection and identification of the genome-edited maize from starch.

19. Next, Marie-Alice Fraiture from Sciensano presented targeted approaches to detect single nucleotide variants in genome-edited plants. In the presentation, two examples from two projects were provided: the first was a digital droplet polymerase chain reaction (PCR) workflow and the second was a targeted high-throughput sequencing approach. In both examples, the tools detected the single nucleotide variants in plants and were suggested by the Ms. Fraiture to be tools that could support food and feed traceability.

20. In the final presentation for the second session, Dirk Schenke of Christian-Albrechts-Universität Kiel presented on next generation sequencing tracking of CRISPR-Cas-induced mutation in crops with complex genomes. In the example provided during the presentation, next generation sequencing was applied to detect changes at one locus in rapeseed (an allotetraploid). However, the presenter noted that identification might be challenging. It was suggested that in this case, whole genome sequencing might be required to find if a marker is present that could be used for identification of the line.

21. A question-and-answer period followed the presentations, allowing for attendees to pose questions and presenters to respond.

V. SESSION 3: REQUIREMENTS FOR THE IDENTIFICATION OF NGT PRODUCTS

22. Following the session related to the detection of NGT products, the third technical session focused on the requirements for the identification of NGT products.

23. In the first of two presentations, Mr. Sławomir Sawo from the Plant Breeding and Acclimatization Institute overviewed the challenges related to the detection and identification of NGT products. Mr. Sawo noted that unlike transgenesis, screening approaches based on genetic elements may not be able to be applied for organisms containing single nucleotide variations. Thus, the importance of prior knowledge for detecting and identifying NGT products was emphasized during the presentation.

24. In the second presentation, Mr. Patrick Guertler from the Bavarian Health and Food Safety Authority evaluated the methods that could be used for the identification of organisms containing single nucleotide variations. During the presentation, examples of quantitative and digital PCR methodologies were detailed for the detection of rapeseed, as well as a next-generation sequencing approach for tomatoes

[4] Clustered regularly interspaced short palindromic repeats (CRISPR); CRISPR associated protein 9 (Cas9)

with elevated gamma-aminobutyric acid. Mr. Guertler stressed the need for sufficient information on the genomic changes and the availability of reference materials.

25. Following the technical presentations, participants were given an opportunity to ask questions.

VI. SESSION 4: DETECTION OF "CLASSICAL" GMOS – ANALYTICAL METHODS

26. After the technical sessions related to the detection and identification of NGT products, the fourth session was dedicated to the analytic methods utilized for the detection of LMOs, including transgenic organisms.

27. In the first presentation, Mr. Frédéric Debode from the Walloon Agricultural Research Centre provided an update of the current status of PCR and sequencing-based techniques for detecting and identifying transgenic organisms. The presentation overviewed screening for transgenic organisms and the challenges faced due to the increased development of new LMOs. High-throughput sequencing approaches were also mentioned by Mr. Debode as a potential solution for these challenges, while also noting the difficulties related to complex or large genomes.

28. Next, Mr. Reona Takabatake from the Food and Nutrition Research Institute provided an update on the detection of living modified seeds and stacked events. In particular, Mr. Takabatake detailed an approach to enable the analysis of LMO content on a weight/weight basis irrespective of the presence of stacked events, the development of a loop-mediated isothermal amplification-based detection method using lateral flow DNA chromatography for LMO detection and the development of a PCR-mediated detection method targeting the right border of T-DNA for plants developed through the use of Agrobacterium-mediated transformation.

29. Following this presentation, Mr. Frank Narendja from Environment Agency Austria detailed routine analysis of LMOs in food and feed. In this, Mr. Narendja overviewed the screening process, followed by the identification of an LMO based on the screening result, and, if necessary, quantifying the LMO event present in the sample. Relevant International Organization for Standardization standards were also mentioned. Information on bioinformatics tools developed by the European Union Reference Laboratory for Genetically Modified Food and Feed were also shared. It was suggested that digital PCR and next-generation sequencing methodologies could be useful for control laboratories but may require further evaluation for their applicability in routine analysis and accreditation.

30. In the fourth presentation of this session, Mr. Fabrice Touzain from the Agency for Food, Environmental and Occupational Health & Safety presented on a bioinformatics and machine learning pipeline for the detection of known and unknown genetically modified bacteria. In the presentation, Mr. Touzain noted that the pipeline was able to detect exogenous and mutated coding sequences. It was suggested that the pipeline could be further applied to detect recent horizontal gene transfer events as well.

31. Following the four technical presentations, participants present in person and virtually were able to pose questions to the presenters.

VII. SESSION 5: REGIONAL NETWORKS – EXPERIENCES GAINED IN VARIOUS REGIONS

32. In the fifth technical session of the Conference, the presentations focused on the experiences gained from regional networks of laboratories and how regional networks of laboratories can support activities related to the detection and identification of LMOs.

33. The first presentation was provided by Mr. Dabing Zhang from Shanghai Jiao Tong University, who overviewed LMO analysis activities in China, including end-point PCR, real-time PCR, DNA arrays, next-generation sequencing and enzyme-linked immunosorbent assays. Mr. Dabing then further described novel analytical methodologies being developed and applied for LMO analysis, including microarray platforms, capillary arrays for visual detection, loop-mediated isothermal amplification techniques,

sequencing with enrichment strategies, multiplexed droplet digital PCR protocols and PCR methodologies integrating either Argonaute or Cas9.

34. For the second presentation of the session, Mr. Chris Viljoen from University of the Free State provided a presentation on the Southern African Network of GM Detection Laboratories and lessons learnt from capacity-building. Mr. Viljoen shared the history of the Network, noting that the Network was established between 13 members [5] in 2009 and received support from Regional Agricultural and Environmental Innovations-Africa and United National Environment Programme-Global Environment Facility for reinforcing projects. It was emphasized in the presentation that capacity-building was more effective in a supportive network, where important lessons could be shared and a reiterative approach to capacity-building could be taken.

35. Next, Ms. Luu Minh Cuc from the Agricultural Genetics Institute, Ministry of Agriculture and Rural Development of Viet Nam detailed the current status and challenges of the development of LMOs and LMO detection methods in Viet Nam. An overview of the LMO testing reference laboratories in Viet Nam was also provided and current challenges related to stacked events in food, mixtures of single events compared to stacked lines, unauthorized LMOs and detecting genome-edited organisms were also mentioned.

36. In the fourth presentation, Ms. Fabiola López Ramírez from the National Service of Agro-Alimentary Health, Safety and Quality of Mexico overviewed their activities and capacity related to the detection and identification of LMOs in Mexico. Ms. Ramírez mentioned that the National Reference Centre for the Detection of Genetically Modified Organisms has been involved in development of certified reference materials, participation in aptitude tests, detection of LMO material in honey, cooperation with the Joint Research Centre and capacity-building with Bolivarian Republic of Venezuela, Colombia, Cuba and Peru.

37. In the final presentation of this session, Mr. Austein McLoughlin of the Secretariat of the Convention on Biological Diversity shared information regarding the Network of Laboratories for the Detection and Identification of Living Modified Organisms, which is hosted on the Biosafety Clearing-House. Mr. McLoughlin emphasized the importance of the Network for supporting the programme of work on detection and identification of LMOs under the Cartagena Protocol on Biosafety and their role in developing Biosafety Technical Series 05: Training manual on the detection and identification of living modified organisms in the context of the Cartagena Protocol on Biosafety. Further, participants were also encouraged to join the Network.

38. After the technical session, a discussion was facilitated between the presenters from the questions posed by the participants.

VIII. SESSION 6: GLOBAL INFORMATION SHARING

39. The sixth session of the Conference focused on global information sharing and the technical databases available to support activities on LMO analysis.

40. In the first presentation of this session, Mr. McLoughlin provided a detailed overview of how the Biosafety Clearing-House supports global activities related to the detection and identification of LMOs. In the presentation, Mr. McLoughlin differentiated between the various types of records on the Biosafety Clearing-House, while emphasizing the particular scientific records that could provide valuable resources of technical information. In addition, the presenter demonstrated how to find scientific information and refine search results while using the Biosafety Clearing-House.

41. The second presenter, Ms. Laura Bonfini of the European Union Reference Laboratory for Genetically Modified Food and Feed of the Joint Research Centre explained the activities of the European

[5] Angola, Botswana, Democratic Republic of the Congo, Eswatini, Lesotho, Madagascar, Malawi, Mozambique, Namibia, South Africa, United Republic of Tanzania, Zambia and Zimbabwe

Union Reference Laboratory for Genetically Modified Food and Feed. Ms. Bonfini summarized the available resources, such as the GMOMETHODS databases and online bioinformatics tools (GMO-Matrix, GMO-Event finder, GMO-Screen, GMO-Amplicons), and how they can be utilized to support activities related to LMO analysis.

42. In the third presentation, Mr. Theo Prins of Wageningen University presented on the European GMO Initiative for a Unified Database System, which is an initiative between Federal Office of Consumer Protection and Food Safety and Wageningen Food Safety Research. During the presentation, Mr. Prins mentioned how the database was structured, how information is treated within the database, the Genetic Element Thesaurus and the tools available to support detection and identification of LMOs.

43. For the final presentation of the session, Ms. Sonia Herrero of Syngenta detailed the Detection Methods Database, which is supported by the members of CropLife International and comprises full descriptions of validated DNA methods based on PCR, and lists providers for protein-based detection methods for living modified crops produced by CropLife members. It was mentioned that links to certified reference materials are also included in the database. Further, Ms. Herrero also provided information on the BioTrade Status and AgbioInvestor GM Monitor databases as general resources related to the regulation of LMOs.

44. Following the four presentations, participants were encouraged to pose questions regarding global information sharing and the databases presented.

IX. SESSION 7: ALTERNATIVE APPROACHES FOR GMO TRACEABILITY

45. For the seventh session of the Conference, the presentations focused on alternative approaches for LMO traceability. The aim of this session was to complement the previous sessions regarding potential, novel strategies to support traceability in supply chains.

46. In the first of two presentations, Ms. Jenny Teufel from the Institute of Applied Ecology described a project exploring the traceability of LMO and NGT products, which was conducted in collaboration with the Oko Institute and the Environmental Agency Austria. Ms. Teufel described how other traceability systems, such as those utilized for “conflict minerals” and illegal timber, could be applied to LMOs and organisms produced through the use of new genomic techniques. The presenter detailed how such systems could be potentially implemented in a supply chain.

47. In the second presentation, Mr. Inácio Henrique Yano from the Brazilian Agricultural Research Corporation detailed a prototype tracking system for non-genetically modified soybeans using blockchain technology. Mr. Yano described that blockchain technology could provide a secure platform for storing digital ‘smart’ contracts, which prevents tampering and allows for auditing of all changes made to the stored information. Based on this, it was suggested that blockchain technology could be a novel system for traceability of LMOs in the supply chain as it could store URL or QR codes for obtaining PCR results or information on the particular commodity, such as the soybeans provided in the example.

48. Following the two presentations, participants were given an opportunity to ask questions to the presenters.

X. PANEL DISCUSSION

49. In the last session of the Conference, a panel discussion was held to exchange on the future detection and identification of LMOs, harmonization opportunities and capacity-building. The discussion was chaired by Ms. Ursula Vincent from the Joint Research Centre and Mr. Malcom Burns. Ms. Gretta Abou Sleymane from the American University of Science and Technology, Ms. Josephine Amedu from the National Biosafety Management Agency of Nigeria, Mr. Martin Lema from National University of Quilmes, Mr. Theo Prins and Mr. Guy Van Den Eede took part in the discussions.

50. During the exchange, the panellists agreed that international conferences, more frequent exchanges and international cooperation were necessary for advancing the field of detection and identification of

LMOs and the analysis of NGT products. The role of laboratory networks, such as the Southern African Network of GM Detection Laboratories, the Middle East and North Africa Network of GMO Laboratories and the Network of Laboratories for the Detection and Identification of Living Modified Organisms, was also highlighted as being important for method validation and harmonization, as well as information sharing. Further, there were calls for further capacity-building and development. Furthermore, the lack of access to and the high cost of technical infrastructure and consumables was acknowledged as a critical challenge for some countries.

XI. CLOSURE OF CONFERENCE

51. In closing statements, the organizing institutions and support staff at the conference were thanked for their role in facilitating the Conference.

52. The conference closed at 16:05 on Thursday, 16 March 2023.

XII. POST-CONFERENCE SURVEY

53. Following the conference, the participants were sent an online evaluation to provide feedback on the Conference. Fourteen participants responded to the survey. The results of the survey can be found in annex II.

54. Overall, the participants gave a rating of either “good” or “excellent” for the Conference and felt that the Conference met their expectations. Based on the average ratings, the participants suggested that they learned a significant amount about detection and identification of LMOs and the Biosafety Clearing-House. Sessions 1 (Detection and identification of ‘classical’ GMO and NGT products – Status and Challenges) and 4 (Detection of ‘classical’ GMOs – Analytical methods) were the highest rated sessions of the Conference.

55. In their written responses, some of the participants found that the conference was useful and timely considering new developments within the field of detection and identification of LMOs, as well within the context of new genomic techniques.

Annex I

OVERVIEW OF THE CONFERENCE PROGRAMME

Programme for the International Conference on GMO Analysis and New Genomic Techniques

14 March 2023	
	Opening
	Session 1: Detection and identification of "classical" GMO and NGT products – Status and challenges
15 March 2023	
	Session 2: Detection of NGT products - Analytical methods
	Session 3: Requirements for the Identification of NGT products
	Session 4: Detection of "classical" GMOs - Analytical methods
	Poster session
16 March 2023	
	Session 5: Regional networks: experiences gained in various regions
	Session 6: Global information sharing
	Session 7: Alternative approaches for GMO traceability
	Panel discussion: Future needs for detection, identification, harmonisation and capacity-building
	Closing

Annex II

RESULTS OF THE SURVEY

1. During the Conference, how much did you learn regarding the detection and identification of living modified organisms? (Scale: 1 is "none" and 5 "a significant amount")

Scale:	**1**	**2**	**3**	**4**	**5**
Number of responses:	0	0	1	4	9
Average:	4.57				

2. During the Conference, how much did you learn regarding the detection and identification of the products of new genomic techniques (NGT)? (Scale: 1 is "none" and 5 "a significant amount")

Scale:	**1**	**2**	**3**	**4**	**5**
Number of responses:	0	0	2	7	5
Average:	4.21				

3. During the Conference, how much did you learn regarding the Network of Laboratories for the Detection and Identification of LMOs? (Scale: 1 is "none" and 5 "a significant amount")

Scale:	**1**	**2**	**3**	**4**	**5**
Number of responses:	0	0	0	7	7
Average:	4.5				

4. During the Conference, how much did you learn regarding the Biosafety-Safety Clearing House (BCH)? (Scale: 1 is "none" and 5 "a significant amount")

Scale:	**1**	**2**	**3**	**4**	**5**
Number of responses:	0	0	0	7	7
Average:	4.5				

5. To what extent were your expectations regarding the Conference met?

	Did not meet expectation	Partly met expectations	Met expectations	Exceeded expectations
Number of responses	0	3	9	2

6. How relevant was the subject matter of the course to your job activities?

	Not relevant	Somewhat relevant	Very relevant
Number of responses	0	1	13

7. The objective of the Conference was clear

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	4	10

8. Organization of sessions

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	4	10

9. Balance and relevance of topics

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	1	5	8

10. Content of the Conference

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	1	6	7

11. Usefulness of Session 1 (Detection and identification of 'classical' GMO and NGT products – Status and Challenges).

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	5	9

12. Usefulness of Session 2 (Detection of NGT products – Analytical methods)

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	1	0	7	6

13. Usefulness of Session 3 (Requirements for identification of NGT products)

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	7	7

14. Usefulness of Session 4 (Detection of 'classical' GMOs – Analytical methods)

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	5	9

15. Usefulness of Session 5 (Regional networks: experiences gained in various regions)

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	1	8	5

16. Usefulness of Session 6 (Global information sharing)

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	7	7

17. Usefulness of Session 7 (Alternative approaches for GMO traceability)

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	1	0	0	3	4	6

18. Usefulness of Panel discussion

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	10	4

19. Overall assessment of the Conference

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	8	6

20. Time for distributing the invitations, agenda, relevant materials

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	5	9

21. Sufficient time for discussion and participation in sessions

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	1	8	5

22. Delivery time of travel arrangements and expenses

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	1	0	1	2	5	5

23. Duration of the Conference

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	2	6	6

24. Quality of Conference venue and facilities

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	6	8

25. Planning and overall organization of the Conference

	Not applicable	Very poor	Poor	Adequate	Good	Excellent
Number of responses	0	0	0	0	5	9