



**INTERNATIONAL SEED TESTING ASSOCIATION  
ASSOCIATION INTERNATIONALE D'ESSAIS DE SEMENCES  
INTERNATIONALE VEREINIGUNG FÜR SAATGUTPRÜFUNG**

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To all participants  
ISTA GMO Proficiency Test PT11

Bassersdorf, 08 July 2009

Dear Madam, dear Sir,

**Proficiency Test Results and Rating**

Please find enclosed your laboratory's test results and ratings for PT11.

**EXPERIMENTAL DESIGN**

Samples were either negative, i.e. did not contain any transgenic events, or positive, i.e. contained the transgenic events T45 and/or RF3. When preparing the positive samples, defined numbers of seeds were mixed with non-GM seeds.

The genetic purity was tested prior to the sample preparation. The genetic purity of the negative (based on 30,000 seeds) and positive material (based on 200 single seeds) was pre-tested prior to the sample preparation. The negative material was tested for the specified two events only; not all possible contaminants. Additionally the GM seed used to prepare the positive material (all spiked events) were tested for extractability and amplifiability using 35S-P PCR. All 35S-P PCR analysis gave positive results verifying DNA could be extracted and amplified from GM seed.

Each participating laboratory received 12 numbered oilseed rape/canola seed samples, containing approximately 3000 seeds (13.35g) based on the 1000 seed weight. Each sample set comprised twelve samples with four spiking levels of 0.4, 0.6, 1.2 or 2.0 % (number of seeds) GM seeds (c.f. table below).

**PT11 sample details**

<b>Spiking level</b>	<b>0%</b>	<b>0.4%</b>	<b>0.6%</b>	<b>1.2%</b>	<b>1.2%</b>	<b>2.0%</b>
<b>Event</b>	None	T45	RF3	T45	RF3	T45 + RF3
<b>Lot No.</b>	1, 2	3, 4	5, 6	7, 8	9, 10	11, 12
<b>Number of samples</b>	2	2	2	2	2	2
<b>Number of non-GM seeds</b>	3000	2988	2982	2964	2964	2940
<b>Number of GM seeds</b>	0	12	18	36	36	30 + 30

## EVALUATION

Sample sets were sent to 49 laboratories. 43 participants submitted their results, 12 provided qualitative results only.

### QUALITATIVE RATING

The rating for the presence/absence (qualitative) results is based on a percentage of misclassified samples out of the total of 12 samples. Misclassification may either be a false positive or a false negative result. Missing results for individual samples are evaluated as misclassification.

Rating	Misclassified samples	Misclassified samples absolute numbers	Number of laboratories
A	0% - 5%	0	41
B	>5% - 10%	1	1
C	>10% - 20%	2	0
BMP	>20%	>2	1

### QUANTITATIVE RATING

The quantitative rating is based on the quantification results for the ten positive samples and their reference value (samples with zero spiking level are not used in quantification rating). The reference value is either the number of GM seeds in percent, the mass of the GM seeds in percent or the median of the results reported by the participants in the unit '%DNA copies'. Which of the reference values is chosen is determined by the panel of experts appointed for each round, the guiding principle being:

Sub-sampling quantification: %number

Results reported in %number: %number

Results reported in %mass: %mass

Results reported in any other unit, such as number DNA copies: median

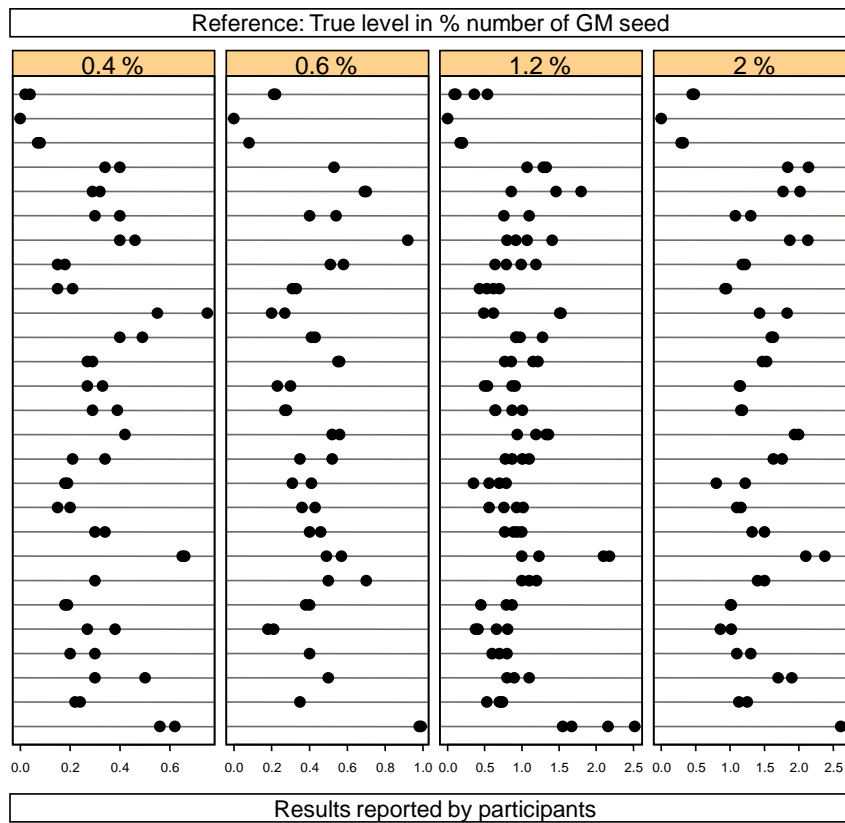
The ratings awarded in this round were as follows:

Rating	Number of laboratories
A	5
B	1
C	18
BMP	7

The reporting units used by participants were as follows:

Reporting unit	Number of laboratories
% number	10
% mass	11
% DNA copies	10

The spread of results obtained by individual participants at the four different spiking levels is shown in the following diagram.



If you require a more comprehensive explanation of the rating system, please refer to Seed Testing International, The ISTA News Bulletin No. 130 (quantitative rating) and No. 128 (qualitative rating) or contact the ISTA Secretariat.

Sincerely yours,

Dr. Norberto De Atrip  
TCOM Coordinator

Encls: mentioned