INTERNATIONAL SEED TESTING ASSOCIATION (ISTA)
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To all participants
ISTA GMO Proficiency Test
PT19

Bassersdorf, 21 July 2014

Dear Madam, dear Sir,

Proficiency Test Results and Rating

Please find enclosed your laboratory's test results and ratings for PT19.

Experimental Design

Samples were either negative, i.e. did not contain any transgenic events, or positive, i.e. contained the transgenic events MON89788, GTS40-3-2. When preparing the positive samples, defined numbers of seeds were mixed with non-GM seeds. The purity of both seed lots used in this PT round (GM and non-GM) was checked by PCR and confirmed as meeting the purity standard required, prior to sample preparation.

Each participating laboratory received a sample set made of 8 numbered soybean seed samples, containing approximately 1800 seeds based on the 1000 seed weight.

The sample sets comprised samples with spiking levels listed in the following table:

PT19 sample details

Spiking level	**0 %**	**0.11 %**	**0.555 %**	**1.455 %**
Event	None	MON89788	GTS40-3-2	MON89788, GTS40-3-2
Lot numbers	1, 2	3, 4	5, 6	7, 8
Number of samples	2	2	2	2
Number of non-GM seeds	1800	1798	1790	1774
Number of GM seeds	0	2	10	8+18=26

Evaluation

Sample sets were sent to 46 laboratories. 39 participants submitted their results, 8 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 samples. Misclassification may either be a false positive or a false negative result. Missing results for individual samples are considered as misclassification.

Rate	Misclassified samples	Misclassified samples absolute numbers	Number of laboratories
A	0% - 5%	0	34
B	>5% - 10%	-	-
C	>10% - 20%	1	4
BMP	>20%	>1	1

Quantitative rating

The quantitative rating is based on the quantification results for the 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 of the results

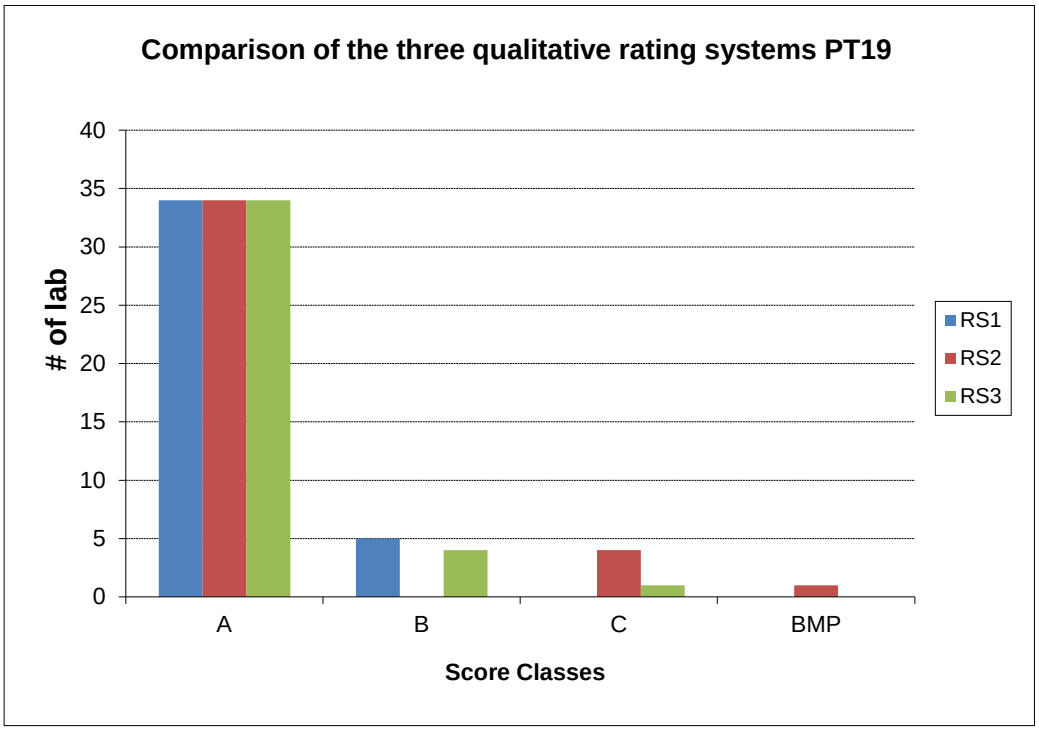
Important Note:
For this PT round, a change in the procedure has been made in order to better take into account recognized standards regarding the precision of a quantitative result. Therefore, in the definition of the Reference intra-laboratory standard-deviation used in the computation of the z-scores, we have introduced the following change (using the same notations as in the reference document in ISTA News Bulletin No. 130):
If (reference lab stdev)/(true level) is lower than 0.25, use 0.25 x (true level) as the Reference intra-laboratory standard deviation.

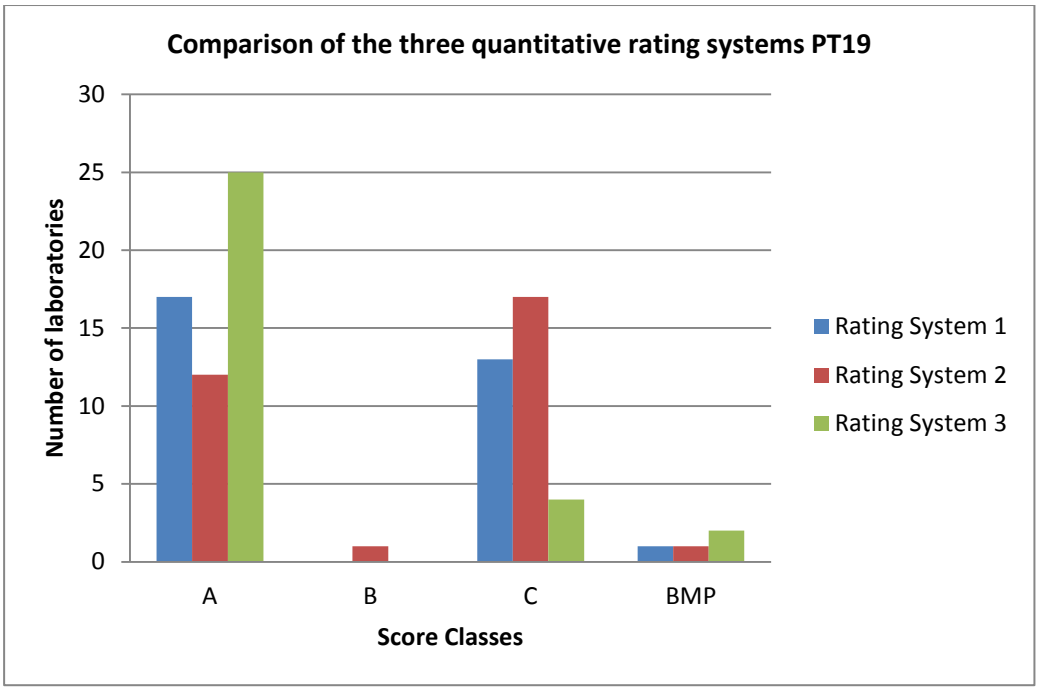
The ratings awarded in this round were as follows:

Rate	Number of laboratories
A	19
B	1
C	11
BMP	-

The reporting units used by participants were as follows:

Reporting unit	Number of laboratories
% number	7
% mass	21
% DNA copies	3





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.

Yours sincerely,

Nadine Ettel
TCOM Coordinator

Enclose: mentioned