



Workshop and Training Program on Sampling and Detection Methods Applied to Transgenic Crops

November 17 – 19, 2011, NIN, Hyderabad, India



It Starts and Ends with Sampling

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Sampling

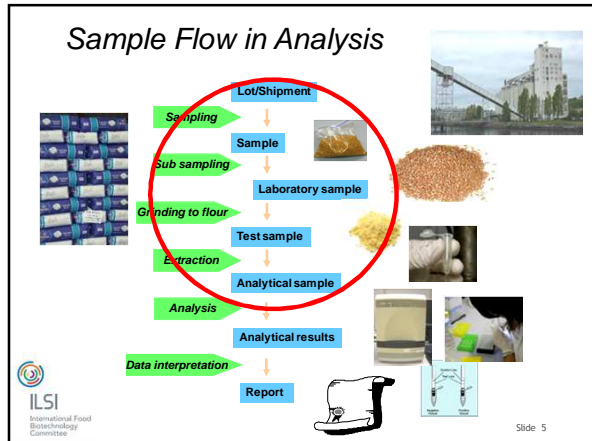
- Why sampling is necessary
- How do we Sample?
- Use of sampling approaches
- Conclusions

Why Sample?

- Much more cost effective than inspecting the entire lot
- 100% certainty requires inspection of every particle
- Testing is destructive
- Sampling precludes 100% certainty - no guarantees of “non-transgenic” or “transgenic-free”
- Design sampling to provide high levels of confidence that sample ‘represents’ bulk lot



Sample Flow in Analysis




Processing a sample


1. Take a sample of the seed, grain or food and send to the laboratory
2. Inspect the sample and record characteristics
3. Obtain a subsample (Laboratory sample)
4. Grind the sample (if seed/grain, or particulate food)
5. Obtain a subsample (Test sample)
 - Possibly re-grind the sample
6. Extract the analyte from the subsample
7. Measure the efficiency of extraction, and quality of extract
8. Obtain a subsample (Analytical sample)
9. Perform the analysis


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 **Step 1: Sampling the Lot**




Rules
ISO 6644:2002
ISO 15699:1999
Codex GAC/GL 50-2004


 **Taking a Grain Sample** 


ISO 24333/2009
Codex GAC/GL 50-2004
IWA on sampling



 **Step 2: Arrival at the laboratory**

- The handling of a sample once it arrives at the laboratory is a critical step.
- Samples must be followed in a record system to ensure they are handled appropriately.
 - High throughput laboratories typically have a computer system with database that tracks samples through the system
 - Low throughput laboratories typically do this by hand

 **The Laboratory Sample**



 **Step 3: Inspecting the Sample**



How much sample have you received ?

What is in the sample ?

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What's in your sample?



The first step is inspection of the sample commercial grain samples are often contaminated with other grain, which has led in a number of occasions to erroneous conclusions.



Step 4: Subsampling for Multiple Uses



A sample may be tested for multiple analytes, and a file (retain) sample may be required



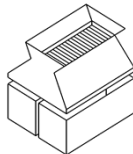
Subsampling



Boerner divider



Riffle multiple-slot divider

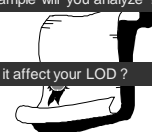


Step 5: Reducing the Laboratory Sample (by Grinding)



How much sample will you analyze ?

How does it affect your LOD ?



Grinding the Sample



Effect of Sample and Particle Size

- All samples consist of particles
 - Grain
 - Flour, meal
 - Molecules in solution (protein, DNA)
 - Containers
- A sample is a subset of particles from the bulk lot
- Sample size and particle size determine the number of particles in sample
- More particles are present in a sample of finer particles

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Sample Size and Particle Size

~~Zero~~ or Not Detected

Zero can only be tested by analyzing every seed !

Can be “not detected” by qualitative analysis;

- confidence depends on number and size of pools, and error rates

Can be “not detected” by quantitative analysis;

- no signal, but can be analytical method failure
- by false positive results depending on interpretation

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Enough seeds need to be tested to obtain a meaningful result.

If one transgenic seed is contained in a total of:	Testing a sample of 200 seeds yields a positive result:	Testing a sample of 1,000 seeds yields a positive result:	Testing a sample of 3,000 seeds yields a positive result:	Testing a sample of 10,000 seeds yields a positive result:
1,000 seeds	18% of the time	63% of the time	95% of the time	99.99% of the time
10,000 seeds	2% of the time	9.5% of the time	26% of the time	63% of the time
80,000 seeds	0.2% of the time	1.2% of the time	3.7% of the time	11.8% of the time
1,000,000 seeds	<0.1% of the time	<0.1% of the time	<0.1% of the time	3% of the time

LOD of the method must be taken into account
LOQ is important if quantification is required

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Threshold Testing

- Test to control distribution of grain
- Determine statistical probability that load is above or below threshold
- Use existing equipment and infrastructure
- Well established sampling protocols (e.g. USDA) to obtain a representative sample
- Rapid, protein strip tests
- Knowing the number of particles (seeds) in the sample allows estimation of maximum % transgenic

The Seed Pooling Test Strategy

(4 pools of 300 seeds, 95% LOC)

-	-	-	-	≤0.25%	SEED
+	+	-	-	≤0.77% 0.23% estimated	SEED
+	+	+	-	≤1.44% 0.46% estimated	SEED

0 of 4 pools positive - Seedcalc.xls

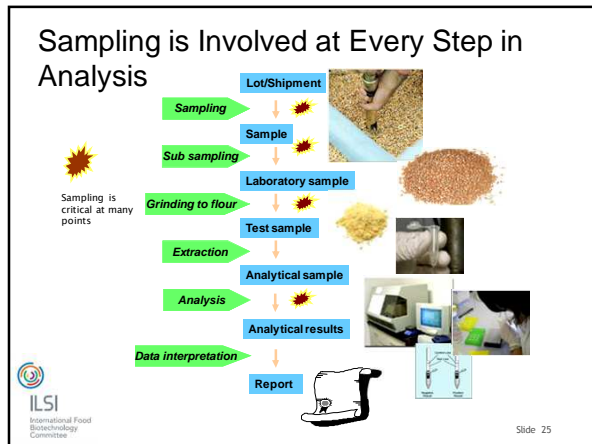
# of Seed Pools	4	Computed % in sample	0.00 %
# of Seeds per Pool	300		
Total Seeds Tested	1200	Measured properly on seed pools	
# Deviants Pools	0		
FPR% (AP Testing) or FNR% (Trait Purity Testing)	0.0	Desired Confidence Level	95 %
FNR% (AP Testing) or FPR% (Trait Purity Testing)	0.0		
Upper Bound of True % Impurity		0.25	
(95% confident that the lot impurity is below 0.25%)			
2-sided CI for True % Impurity		0.00 to 0.31	

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Sampling of DNA for analysis

- As the amount of DNA extracted from the sample becomes lower, sampling error becomes proportionally larger.
- 100 ng of DNA samples at a level of 0.1% (wt/wt) would produce GMO DNA estimates no better than 30% of the mean value, 95% of the time - a poor level of accuracy.....

The limits of GMO Detection.
Kay, S., & Van den Eede, G.
(2001) *Nature Biotech.*, 19, 405



Summary

- Sampling is the best way to get an estimate of the % transgenic in a lot
 - Improper sampling leads to false, imprecise and variable results
 - Representative samples are used
- Sample size is a balance between
 - Sensitivity
 - Cost
 - Probability of false negative results
- Sampling occurs throughout the analytical process



Thank you

Discussion