Aflatoxin

Managing the Menace

What is Aflatoxin?

Aflatoxin is a prominent class of mycotoxins (toxic chemical compounds that are produced by fungi.)

Aflatoxin Facts

- Product of fungal growth
  - o *Aspergillus flavus, Aspergillus parasiticus*
  - o Occurs naturally in agricultural environments
- Invisible (microscopic)
- 4 types
  - B_1, B_2, G_1, G_2
  - B_1 is most toxic and typically the most prevalent

Aflatoxin Facts

- Food and Agricultural Organization estimates 25% of the World's crops are contaminated by mycotoxins
  - ubiquitous
- Aflatoxin contaminates a range of important crops
  - Maize, peanut, cotton, rice, nuts, chiles, spices

http://www.icrisat.org/what-we-do/satrends/may2007.htm

Why do we care?

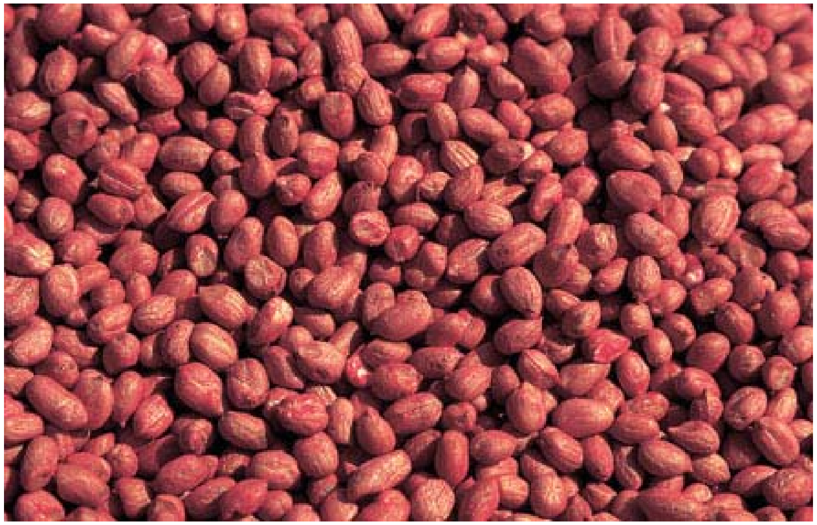
- Aflatoxin is a Class 1 carcinogen - liver cancer
- Peanuts are a high risk crop for aflatoxin.
- The US Industry has made extensive investments to minimize aflatoxin in the edible market.
- Let’s recognize these efforts, and keep pushing to deliver the highest quality peanuts to the world
- Developing countries, this is a much different story

Aflatoxin & Control Points

- Extensive pre-harvest, harvest, and post-harvest
- Highlight a few

Control Points – Pre Harvest

- Seed



ARTICLES

nature genetics

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The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut

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Cultivated peanut (*Arachis hypogaea*) is an allotetraploid with closely related subgenomes of a total size of ~2.7 Gb. This makes the assembly of chromosomal pseudomolecules very challenging. As a foundation to understanding the genome of cultivated peanut, we report the genome sequences of its diploid ancestors (*Arachis duranensis* and *Arachis ipaensis*). We show that these genomes are similar to cultivated peanut's A and B subgenomes and use them to identify candidate disease resistance genes, to guide tetraploid transcript assemblies and to detect genetic exchange between cultivated peanut's subgenomes. On the basis of remarkably high DNA identity of the *A. ipaensis* genome and the B subgenome of cultivated peanut and biogeographic evidence, we conclude that *A. ipaensis* may be a direct descendant of the same population that contributed the B subgenome to cultivated peanut.

Peanut (also called groundnut; *A. hypogaea* L.) is a grain legume and oilseed, which is widely cultivated in tropical and subtropical regions (annual production of ~46 million tons). It has a key role in human nutrition. In Africa and Asia, more peanut is grown than any other grain legume (including soy bean) (FAOSTAT 2015; see URLs). The *Arachis* genus is endemic to South America and is composed mostly of diploid species ($2n = 2x = 20$). *A. hypogaea* is an allotetraploid (AABB-type genome; $2n = 4x = 40$), probably derived from a single recent hybridization event between two diploid species and polyploidization[1–6]. Chromosomes are of mostly similar size and are metacentric, but strong chromosomal centromeric banding and one pair of small chromosomes distinguish the A from the B subgenome. Cytogenetic, phylogeographic and molecular evidence indicate *A. duranensis* Krapov. & W.C. Greg. and *A. ipaensis* Krapov. & W.C. Greg. as the donors of the A and B subgenomes, respectively[3,5,7–11].

The peanut subgenomes are closely related[5,12]. This, together with a total genome size of ~2.7 Gb and an estimated repetitive content of 64% (ref. 13), makes the assembly of the peanut genome sequence very challenging. However, the A and B subgenomes appear to have undergone relatively few changes since polyploidization: genomic *in situ* hybridization (GISH), using genomic DNA from the diploid species as probes, clearly distinguishes A and B chromosomes and does not show large A-B mosaics[7,8]. Also, the genome size of *A. hypogaea* is close to the sum of those for *A. duranensis* and *A. ipaensis* (1.25 and 1.56 Gb, respectively[14]), indicating that there has been no large change in genome size since polyploidy. Most notably, observations of progeny derived from crosses between cultivated peanut and an artificially induced allotetraploid *A. ipaensis* K30076 × *A. duranensis* V14167 ($2n = 4x = 40$)[15] strongly support the close relationships between the diploid genomes and the corresponding

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Control Points – Pre Harvest

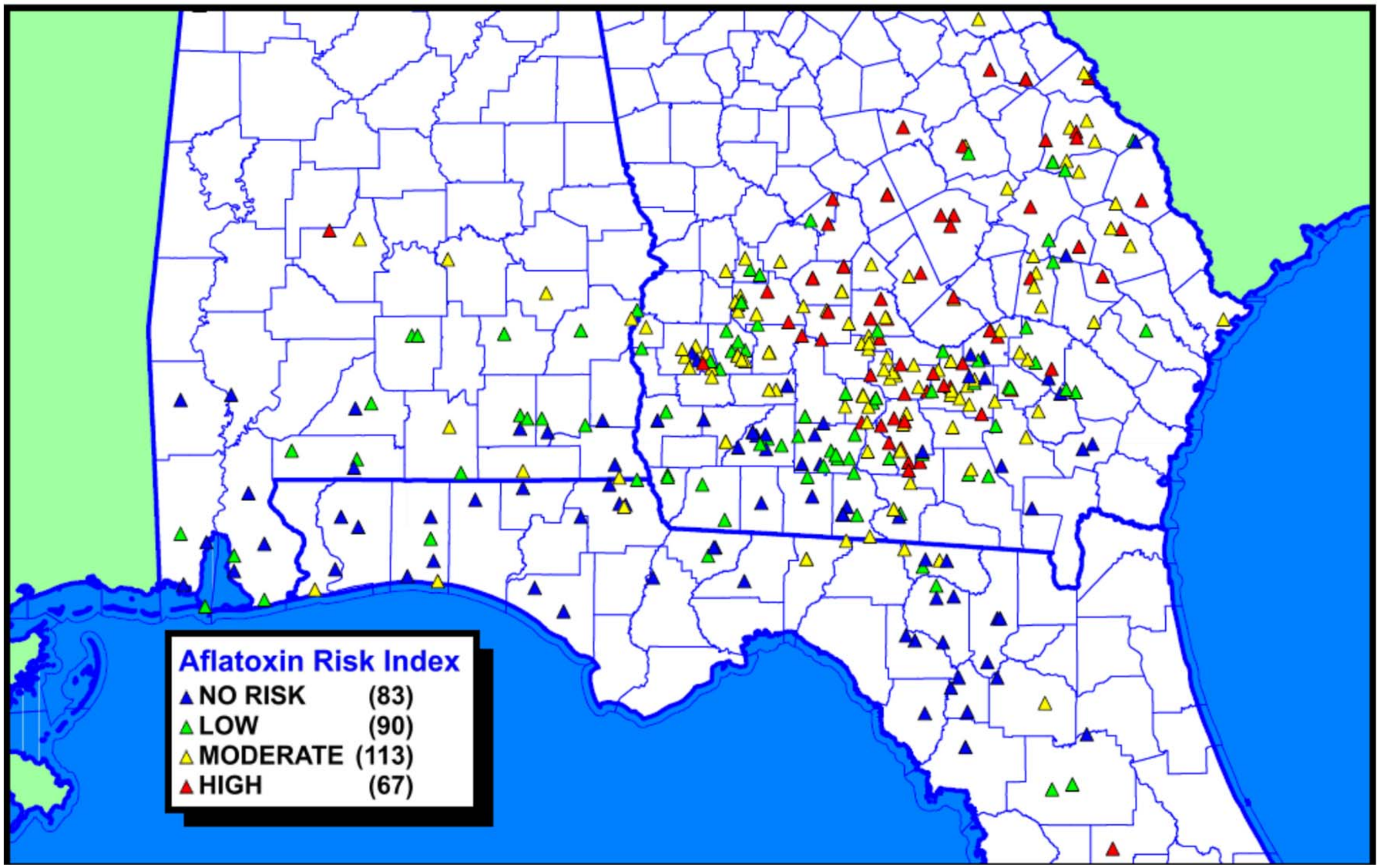
- Good agricultural practices, rotations, inputs, irrigation, etc.

Control Points – Pre Harvest

- Risk is amplified by late season heat & drought

Control Points – Pre Harvest

- We cant control the weather, but we can understand risks



Control Points – Harvest

- timing

Control Points – Harvest

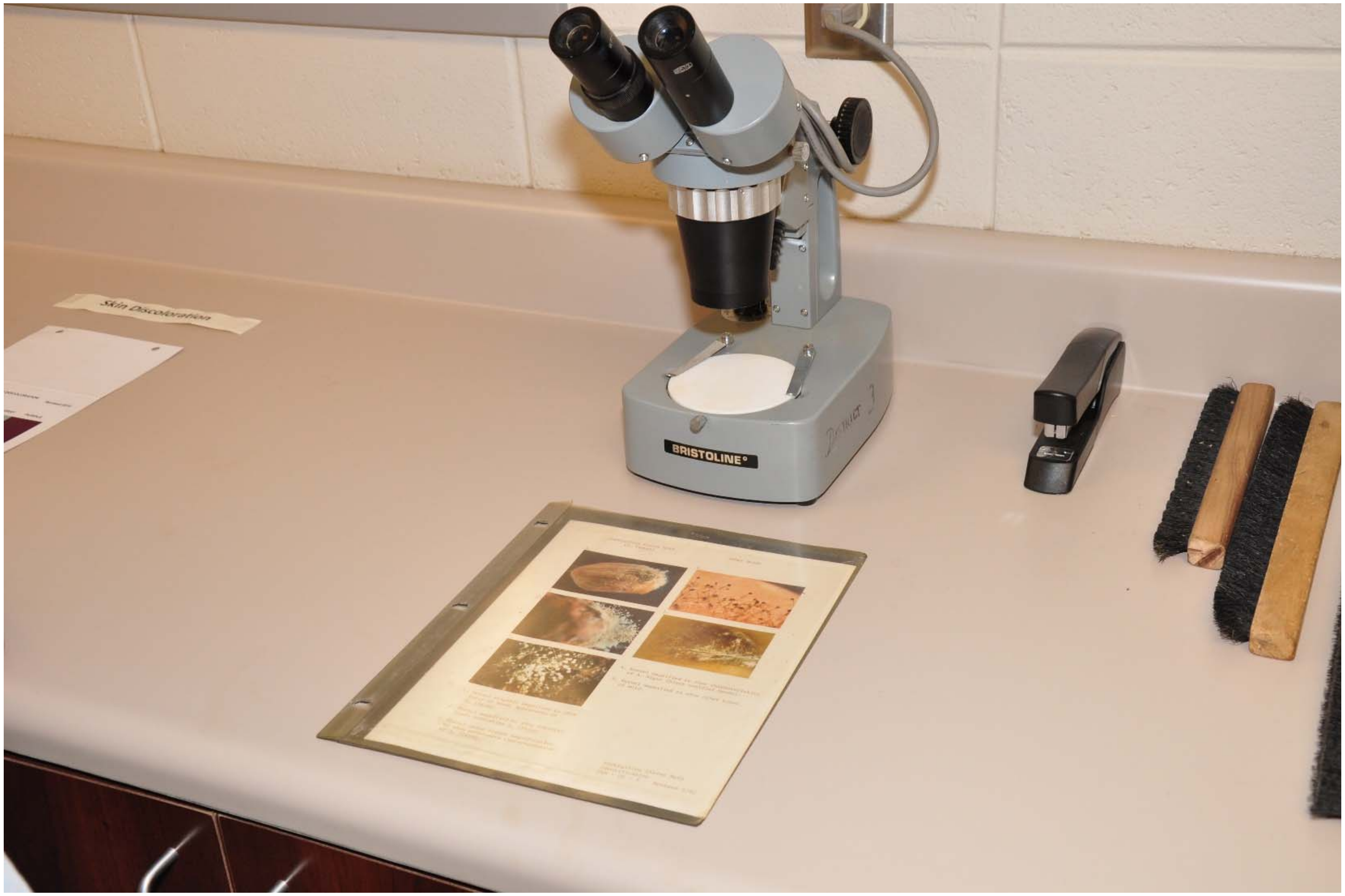
- Dry corners

Control Points – Harvest

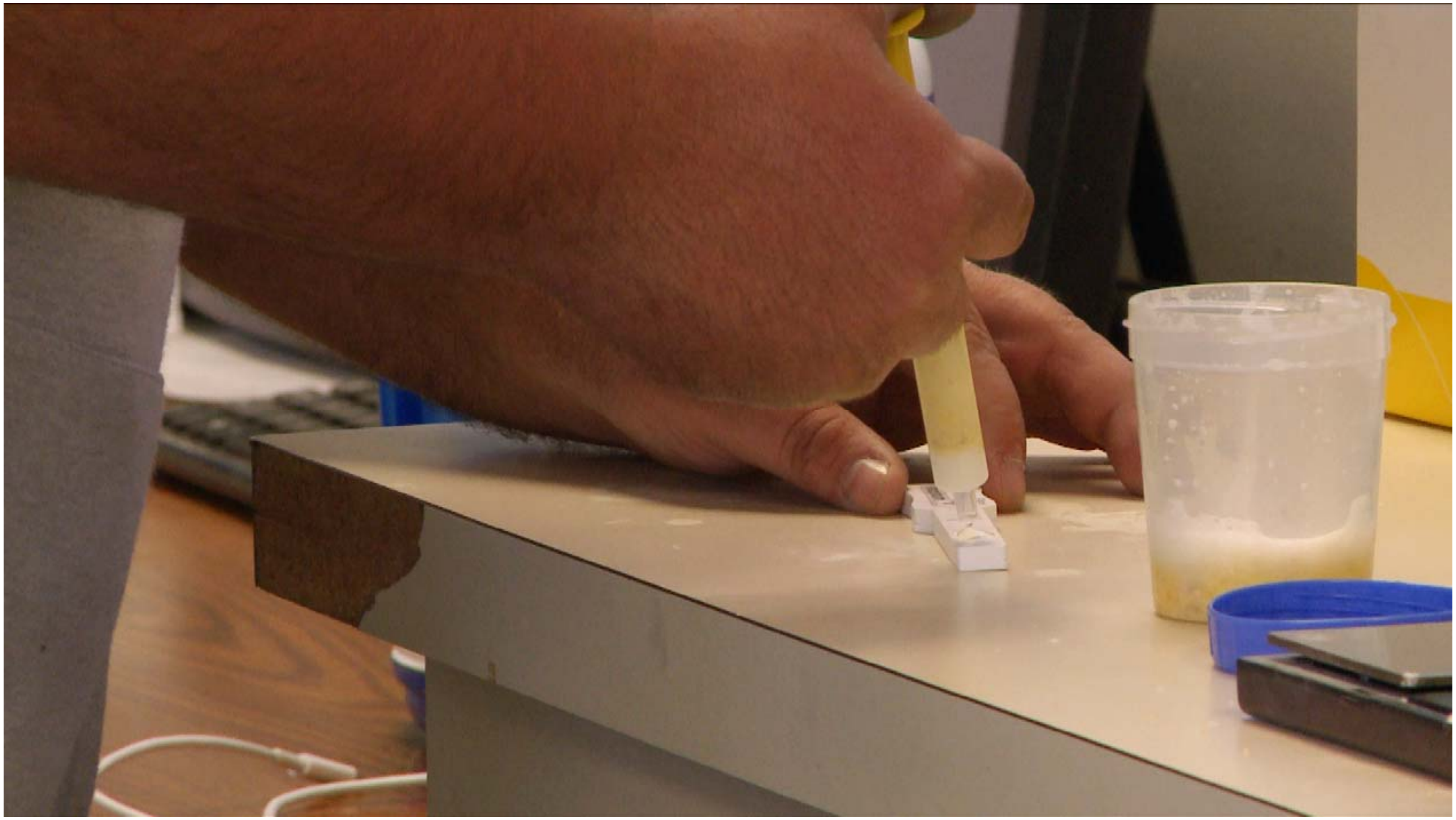
Control Points – Post Harvest

- D

Control Points – Post Harvest



Control Points – Post Harvest



Control Points – Post Harvest

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- Sheller is targeting high risk kernels, size, density, visual damage, etc.
- Positive lot identification and sampled by FSIS

Sampling & Testing

- Shelled lots being considered for the edible market are sampled & tested for aflatoxin per USDA AMS regulations.

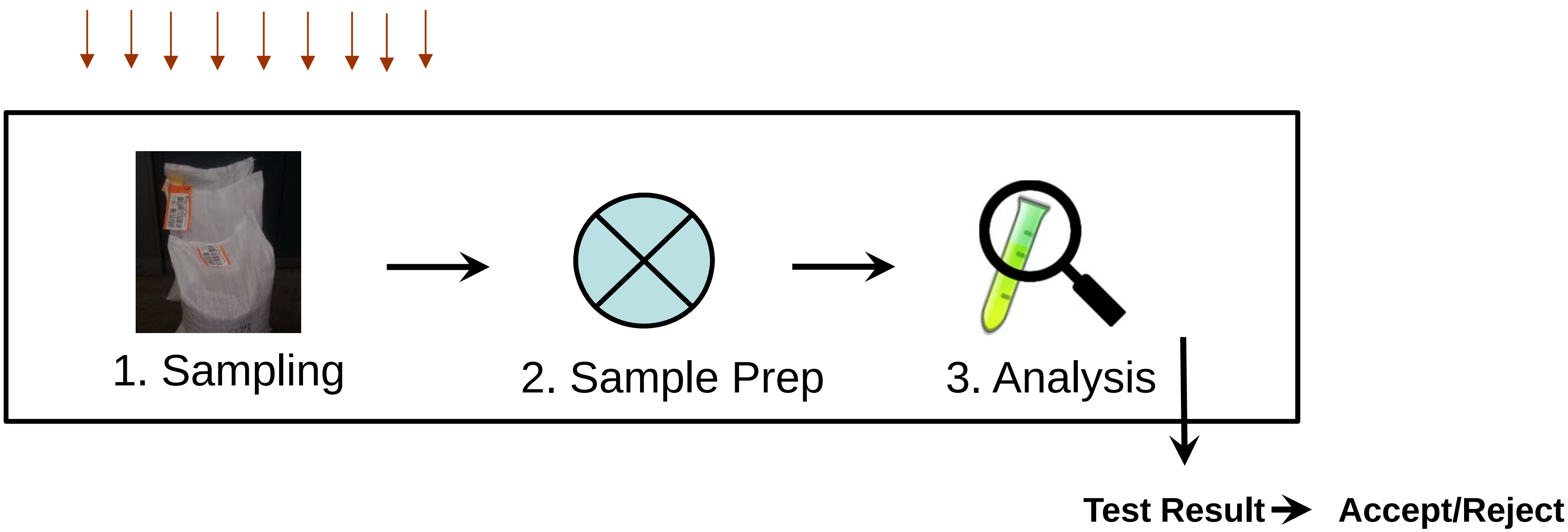
- Providing an accurate, unbiased, time efficient and cost effective sampling & testing system is critical.

Key Facts

- kernel to kernel contaminate
- typically, a very small frequency of ‘bad’ kernels among a much larger frequency of ‘good’ kernels
- often, bad kernels are highly contaminated
- resulting in a highly positively skewed distribution
  - median, much lower than the mean
  - large sampling variation that must be understood

Sampling & Testing

Commercial Lot



**Slide adapted from that of Dr. Tom Whitaker

Control Points – Post Harvest

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- manufacturer handles with care, roaster, sorting, etc.

Control Points – Post Harvest

- Finished product must meet FDA limits for aflatoxin

Control Points – Throughout

- Documentation

Implications

- The US Peanut Industry has invested heavily over the past 50+ years to minimize aflatoxin in the edible market
- Incremental progress on many fronts
- Major supply and economic considerations