

**Name:** Meng Luo

**Rank:** Assistant Research Scientist (2004~now)

% Salary Budgeted: 100% research

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available

**Program Overview:**

To study the effects of drought stress and *Aspergillus* infection on corn and peanuts using functional genomics/microarray analysis of gene expression, and to develop drought tolerant corn inbred lines/germplasm and hybrids with reduced aflatoxin contamination, and to develop peanut EST/Microarray for identification of novel genes and development of DNA markers.

**Education:** Ph. D

**Employment:** Crop and Soil Sciences Department, the University of Georgia, Tifton, GA.

**Membership in Professional Societies:**

Member of the American Sigma Xi - the Scientific Research Society; Member of the American Phytopathological Society.

**Contributions to Research and Other Creative Activities**

Four of proceedings papers (since 2004)

- 1 . X.Q LIANG, **M. Luo**, B.Z. Guo. 2006. Resistance mechanisms to *Aspergillus flavus* infection and aflatoxin contamination in peanut. *Plant Pathology Journal* 5(1): 115-124.
- 2 . **Luo, M.**, X. Q. Liang, Dang, P., Holbrook, C. C., Bausher, M. G., Lee, R. D., Lynch, R.E., and Guo, B. Z. 2005. Microarray-based screening of differentially expressed genes in peanut in response to *Aspergillus parasiticus* infection and drought stress. *Plant Science* 169: 695-703.
- 3 . **Luo, M.**, Dang, P., Holbrook, C. C., Bausher, M. G., Lee, R. D., Lynch, R.E., and Guo, B. Z. 2005. Identification of transcripts involved in resistance responses to leaf spot disease caused by *Cercosporidium personatum* in peanut (*Arachis hypogaea* L.). *Phytopathology* 95:381-387.
- 4 . **Luo, M.**, Dang, P. He, G., Holbrook, C. C., Lee, R. D., Bausher, M.G Lynch, R. E. and Guo, B.Z. 2005. Generation and analysis of expression sequence tags (ESTs) for gene discovery and marker development for cultivated peanut. *Crop Science*, 45:346-353.

Eight of abstracts (since 2004)

1. Meng Luo, R.D. Lee, B.Z. Guo. A Microarray-based analysis of gene expression profiles of maize kernel during late development stages. *Plant and Animal Genome Conference XIV*, San Diego, CA, January 13-17, 2007.
2. Meng Luo, R.D. Lee, B.Z. Guo. Microarray as tool in understanding the resistance mechanisms of preharvest aflatoxin contamination in corn. The 6th Annual Fungal Genomics Workshop, 7th Annual Fumonisin Elimination Workshop, and 19th Annual Aflatoxin Elimination Workshop will be held October 16-18 in Fort Worth, Texas, 2006.
3. Meng Luo, R.D. Lee, B.Z. Guo. Microarray-based Pathways Analysis of Maize Kernels with Drought Tolerance and Low Aflatoxin Contamination. The 48<sup>th</sup> Annual Maize Genetics Conference, Pacific Grove, CA, March 9-12, 2006.

4. Meng Luo, R.D. Lee, B.Z. Guo. Transcriptional Profiles of Tex6 Maize Kernels in Response to Water Deficit during Late Developmental Stages. Plant and Animal Genome Conference XIV, San Diego, CA, January 14-18, 2006.
5. M. Luo, R.D. Lee, B.Z. Guo. Quantitative Expression Analysis of Adversity Resistance Genes in Corn Germplasm with Resistance to Preharvest Aflatoxin Contamination. Aflatoxin/Fumonisin Elimination and Fungal Genomics Workshop, Raleigh, NC. Oct. 24-26, 2005.
6. Luo, M., C. Corley Holbrook, R. Dewey Lee, Michael G. Bausher, Baozhu Guo. Identification of tolerant gene in a peanut genotype against *Aspergillus flavus* infection and drought stress. Plant and Animal Genome Conference XIII, San Diego, CA, January 15-19, 2005.
7. M. Luo, R. D. Lee, and B. Z. Guo. Gene Differential Expression of Corn Lines at the Late Development Stage under Drought Stress and *Aspergillus flavus* Infection. Aflatoxin/Fumonisin Elimination and Fungal Genomics Workshop, Fresno, CA. October 26-29, 2004.
8. Luo, M., Dang, P., Liang, X.Q., Holbrook, C.C. and Guo, B.Z. 2004. Identification of resistance related genes in peanut using microarray analysis. Plant and Animal Genome Conference XII, San Diego, CA, January 11-15, 2004.

#### **Sources of Grants/amounts (since 2004)**

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|------|---|
| 2006 | Sustainable dry-land corn production: Gene expression analysis of developing ears in response to drought-stress and select drought-tolerant corn germplasm. Funded (\$12,000) by Georgia Corn Commodity.  |
| 2006 | Pyramid and Develop Corn Germplasm and Inbred Lines Resistant to Preharvest Aflatoxin Contamination and Ear-feeding Insects. Funded (\$12,000) by Georgia Corn Commodity.   |
| 2005 | Development of Expressed Sequence Tag (EST)-based resource and tools: Genes, SSR and SNP Polymorphic Markers for Genetic Breeding and Improvement of Resistance to <i>Aspergillus</i> and Aflatoxin Contamination. Funded (\$83,000) by USDA Multi-Crop Aflatoxin Elimination Workshop. |
| 2005 | Breeding corn lines with resistance to preharvest aflatoxin contamination and understanding the interactions of drought stress and <i>Aspergillus flavus</i> aflatoxin using maize microarray. Funded (\$20,000) by USDA Multi-Crop Aflatoxin Elimination Workshop.                     |
| 2004 | Researches of EST and Microarray to identify genes and develop DNA markers related with important traits for peanuts. Funded (33,000) by USDA Multi-Crop Aflatoxin Elimination Workshop, Peanut Foundation, Georgia Agricultural Commodity Commission.                                  |

#### **Goals for the Next Five Years**

1. Keep going the study of resistance mechanism for pre-harvest aflatoxin contamination in corn kernel. To investigate differential gene expression profiles in pre-harvest corn kernel in response to environmental stress-drought/ high temperature and *Aspergillus flavus* infection by comparing the resistant and susceptible corn lines.
2. Keep going the research of gene probes development which will be used in corn germplasm assessment and molecular assistant selection in corn breeding. To help breeders to develop drought tolerance and low aflatoxin contamination varieties. This work includes: 1) probes are screened from known and unknown function genes which have differential expression between resistant and susceptible corn lines, or which are sensitive in response to the

environmental stresses or *Aspergillus flavus* infection. 2) Protocols are developed and optimized to fit the probes application in practical breeding research.

3. To explore and develop new technology which can be used in gene expression analysis of post-harvest corn seeds in response to *Aspergillus flavus* infection, a severe problem during the corn seeds storage.
4. To develop other areas in which the research can benefit Georgia agriculture and economy.