

Kyu Young Kang, Ph.D

Professor

Division of Applied Life Science (BK21 Program)
& Plant Molecular Biology and Biotechnology
Research Center, Gyeongsang National University,
Jinju, 660-701, South Korea
Tel: +82-55-772-1961 Fax: +82-55-772-1969
E-mail : kykang@gnu.ac.kr



Education & Experience

- Director of Bio-Vision Education Center, NURI (New University for Regional Innovation) (2005-2009)
- 'Proteomics'- editor (2006-present)
- Professor, Gyeongsang National University (1978-present)
- Post-Doc, University of Cambridge, UK (1988-1989)
- Ph.D., Plant Pathology, University of California, Riverside, USA (1979-1984)
- Dissertation Title: Biochemical studies on the mode of action of the fungicide metalaxyl
- M.S., Agricultural Chemistry, Seoul National University (1974-1976)
- B.S., Agricultural Chemistry, Seoul National University (1968-1972)

Research Areas

- Proteome Analysis of Rice-Rice Blast Fungus Interactions
- Isolation and Characterization of Pathogen Resistant Related Genes

Major research interests in my lab have been focused on rice-rice blast fungus interactions through 2-DE based proteome analysis. Proteome analysis can be applied to identify differentially expressed or modulated proteins after virulent or avirulent pathogen inoculation. Genes corresponding to the identified proteins were cloned into Gateway system and further being characterized. Differential proteome analyses during appressorium formation of rice blast fungus (*Magnaporthe grisea*) also revealed developmentally regulated protein expression. Secretome analysis from germinating conidia and appressorium is underway to unravel signal proteins which transduce to elicit resistant interactions. *In planta* appoplastic proteome analysis during rice-rice fungus interactions revealed that 40% proteins identified from pathogen and host has signal peptides. Integrative approaches utilizing DNA microarray, RT-PCR, proteome and transgenic rice plant are being carried out to unravel cross talks between host-pathogen interactions. Proteomic approaches combined with transgenic rice plants of overexpression or RNAi lines have been applied to understand gene functions involved in early germinating seeds modulated by several plant hormones and ROS related proteins which affect ROS production and root development using redox proteome.

Selected Publications

1. Kim SG, Kim ST, Wang Y, Yu S, Choi IS, Kim YC, Kim WT, Agrawal GK, Rakwal R, **Kang KY**. The RNase activity of rice probenazole-induced protein1 (PBZ1) plays a key role in cell death in plants. *Mol. Cells* 2011, 31: 25-31.
2. Kim SG, Kim ST, WangY, Kim SK, Lee CH, Kim KK, KimJK, Lee SY, **Kang KY**. Overexpression of rice isoflavone reductase-like gene(OsIRL) confers tolerance to reactive oxygen species. *Physiol Plant*. 2010, 138:1-9.
3. Lee TH, Kim YK, Pham TT, Song SI, Kim JK, **Kang KY**, An G, Jung KH, Galbraith DW, Kim M, Yoon UH, Nahm BH. RiceArrayNet: a database for correlating gene expression from transcriptome profiling, and its application to the analysisof coexpressed in rice. *Plant Physiol*. 2009, 151: 16-33.
4. Kim ST, Wang Y, Kang SY, Kim SG, Rakwal R, Kim YC, **Kang KY**. Developing Rice Embryo Proteomics Reveals Essential Role for Embryonic Proteins in Regulation of Seed Germination. *J Proteome Res*. 2009, 8: 3598-3605.
5. Kim ST, Kang YH, Wang Y, Wu J, Park ZY, Rakwal R, Agrawal GK, Lee SY, **Kang KY**. Secretome analysis of differentially induced proteins in rice suspension-cultured cells triggered by rice blast fungus and elicitor. *Proteomics* 2009, 9: 1302-1313.
6. Chen XY, Kim ST, Cho WK, Rim Y, Kim S, Kim SW, **Kang KY**, Park ZY, Kim JY. Proteomics of weakly bound cell wall proteins in rice calli. *J. Plant Physiol*. 2009, 166: 675-85.
7. Ryu YB, Curtis-Long MJ, Lee JW, Kim JH, Kim JY, **Kang KY**, Lee WS, Park KH. Characteristic of neuraminidase inhibitory xanthones from *Cudrania tricuspidata*. *Bioorg. Med. Chem*. 2009, 17: 2744-2750.
8. Kim ST, Kang SY, Wang Y, Kim SG, Hwang du H, **Kang KY**. Analysis of embryonic proteome modulation by GA and ABA from germinating rice seeds. *Proteomics* 2008, 8: 3577-3587.
9. Kim ST, Kim SG, Kang YH, Wang Y, Kim JY, Yi N, Kim JK, Rakwal R, Koh HJ, **Kang KY**. Proteomics analysis of rice lesion mimic mutant (spl1) reveals tightly localized probenazole-induced protein (PBZ1) in cells undergoing programmed cell death. *J Proteome Res*. 2008, 7: 1750-1760.
10. Kim ST, Yu S, Kang YH, Kim SG, Kim JY, Kim SH, **Kang KY**. The rice pathogen-related protein 10 (JIOsPR10) is induced by abiotic and biotic stresses and exhibits ribonuclease activity. *Plant Cell Rep*. 2008, 27: 593-603.
11. Kim SG, Kim ST, Kang SY, Wang Y, Kim W, **Kang KY**. Proteomic analysis of reactive oxygen species (ROS)-related proteins in rice roots. *Plant Cell Rep*. 2008, 27: 363-375.
12. Song YH, Song NY, Shin SY, Kim HJ, Yun DJ, Lim CO, Lee SY, **Kang KY**, Hong JC. Isolation of CONSTANS as a TGA4/OBF4 interacting protein. *Mol. Cells* 2008, 25: 559-565.
13. Hwang DH, Kim ST, Kim SG, **Kang KY**. Comprehensive analysis of the expression of twenty-seven beta-1, 3-glucanase genes in rice (*Oryza sativa* L.). *Mol. Cells* 2007, 23: 207-214.
14. Lee DG, Ahsan N, Lee SH, **Kang KY**, Bahk JD, Lee IJ, Lee BH. A proteomic approach in analyzing heat-responsive proteins in rice leaves. *Proteomics* 2007, 7: 3369-3383.
15. Koo SC, Yoon HW, Kim CY, Moon BC, Cheong YH, Han HJ, Lee SM, **Kang KY**, Kim MC, Lee SY, Chung WS, Cho MJ. Alternative splicing of the OsBWMK1 gene generates three transcript variants showing differential subcellular localizations. *Biochem. Biophys. Res. Commun*. 2007, 360: 188-193.

16. Kim ST, Yu S, Kim SG, Kim HJ, Kang SY, Hwang DH, Jang YS, **Kang KY**. Proteome analysis of rice blast fungus (*Magnaporthe grisea*) proteome during appressorium formation. *Proteomics* 2004, 4: 3579-3587.
17. Kim ST, Kim SG, Hwang DH, Kang SY, Kim HJ, Lee BH, Lee JJ, **Kang KY**. Proteomic analysis of pathogen-responsive proteins from rice leaves induced by rice blast fungus, *Magnaporthe grisea*. *Proteomics*. 2004, 4: 3569-3578.
18. Kim ST, Kim SG, Hwang DH, Kang SY, Koo SC, Cho MJ, **Kang KY**. Expression of a salt-induced protein (SALT) in suspension-cultured cells and leaves of rice following exposure to fungal elicitor and phytohormones. *Plant Cell Rep.* 2004, 23: 256-262.
19. Kim ST, Kim HS, Kim HJ, Kim SG, Kang SY, Lim DB, **Kang KY**. Prefractionation of protein samples for proteome analysis by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. *Mol. Cells* 2003, 16: 316-322.
20. Kim ST, Cho KS, Yu S, Kim SG, Hong JC, Han CD, Bae DW, Nam MH, **Kang KY**. Proteomic analysis of differentially expressed proteins induced by rice blast fungus and elicitor in suspension-cultured rice cells. *Proteomics* 2003, 3: 2368-2378.
21. Kim ST, Cho KS, Kim SG, Kang SY, **Kang KY**. A rice isoflavone reductase-like gene, OsIRL, is induced by rice blast fungal elicitor. *Mol. Cells* 2003, 16: 224-231.
22. Kang JG, Hur JH, Choi SJ, Choi GJ, Cho KY, Ten LN, Park KH, **Kang KY**. Antifungal activities of N-arylbenzenesulfonamides against phytopathogens and control efficacy on wheat leaf rust and cabbage club root diseases. *Biosci. Biotechnol. Biochem.* 2002, 66:2677-2682.
23. Kim ST, Cho KS, Jang YS, **Kang KY**. Two-dimensional electrophoretic analysis of rice proteins by polyethylene glycol fractionation for protein arrays. *Electrophoresis* 2001, 22, 2103-2109.