has been proposed. Rice plant architecture, a collection of the important agronomic traits that determine its grain production, is mainly affected by factors including tillering (tiller number and tiller angle), plant height, and panicle morphology. To elucidate molecular mechanisms that control rice plant architecture, we have identified several related mutants and isolated their corresponding genes. Among them, the *MONOCULM1* (*MOC1*) gene was characterized as an essential regulator involved in tiller bud initiation and outgrowth; the *DWARF27* (*D27*) gene acts as a new component involved in the biosynthesis of strigolactones and controls rice tiller number by regulating the outgrowth of tiller buds; the *LA1* gene plays an important role as a negative regulator of polar auxin transport (PAT) and loss of function of *LA1* enhances PAT greatly and thus alters the endogenous IAA distribution in shoots; the *SMALL PANICLE* (*SP*) gene encodes a transporter that regulates the panicle size. Most importantly, we recently cloned and characterized an important quantitative trait locus gene, *Ideal Plant Architecture 1* (*IPA1*), which profoundly affects rice plant architecture and substantially enhances rice grain yield. *IPA1* encodes SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 14 (OsSPL14) and is regulated by *miRNA156* in vivo. Our results demonstrated that a point mutation in *IPA1*/*OsSPL14* perturbs *miRNA156*-directed regulation of *IPA1*/*OsSPL14*, generating an ideal rice plant that exhibits a reduced tiller number, increased lodging resistance, and enhanced grain yield. Our studies demonstrate that the application of these genes will facilitate the breeding of new elite varieties by modifying the tiller number, tiller angle, plant height, and panicle morphology.

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Biomarkers: At the Intersection Between Nutrition, Human Health, and Agriculture

Mary Ann Lila. North Carolina State University, 600 Laureate Way North Carolina Research Campus Kannapolis, North Carolina, 28081 USA. Email: mlila@ncsu.edu

LILA, MARY ANN[1], Luther, Michael[2]
[1]Plants for Human Health Institute, North Carolina State University, 600 Laureate Way, North Carolina Research Campus, Kannapolis, NC 28081
[2]David H Murdock Research Institute, 150 Research Campus Dr., North Carolina Research Campus, Kannapolis, NC 28081

Biomarkers are the critical indicators requisite for the objective evaluation of high-value traits and responses in plant, animal, and human research. They signal biological events or provide measures of exposure, composition, response, or susceptibility. In the wake of new biotechnologies including genomics, proteomics, metabolomics, glycomics, imaging, and meta-analysis, biomarkers have redefined the quest for evidence-based approaches to human health and wellness. Sensitive, cutting-edge technology platforms coupled with high-performance computing and data analysis are now available to monitor, with an unprecedented degree of precision, biomarkers of potent therapeutically active phytochemicals in plants or of disease susceptibility, diagnosis, or treatment response in animal and human systems. By integrating our analyses of these complex and previously unintelligible or intractable biomarkers and the wealth of insights acquired by probing genomic/epigenetic and metabolomic status, science can now, for the first time, begin to interpret how functional foods and phytopharmaceuticals interface with human pathophysiology at the molecular level to protect or enhance health and metabolism. Many of the same approaches applied to pharmacogenetic and pharmacogenomic responses for drug therapies can now be adapted for the plant and food arenas. Specific research outcomes targeting antimalarial, anti-diabetic, neuroprotective, and other bioactive natural products and their relevant biomarkers (both in the plant and in the patient, at cellular or whole-organism levels) all converge on the same conclusions: generic treatments are not solutions when health outcomes hinge on the metabolic variations of the individual.

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Bioactive Secondary Metabolites from Higher Fungi in China

Ji-Kai Liu. State Key Laboratory of Phytochemistry and Plant Resources in West China, State Key Laboratory of Phytochemistry and Plant Resources in West China, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650204, China. Email: jkliu@mail.kib.ac.cn

LIU, JI-KAI
State Key Laboratory of Phytochemistry and Plant Resources in West China, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650204, China

China is extraordinarily rich in higher fungi. To date, about 10,000 species of fungi have been reported from the vast territory of China. Among them, nearly 6,000 species, belonging to about 1,200 genera, are higher fungi. Higher fungi in bio-resources belong to the very productive biological sources which produce a large and diverse variety of secondary metabolites. We have been interested in the biologically active substances present in untapped and diverse source of higher fungi from China. In order to search for naturally occurring bioactive metabolites from higher fungi, we have investigated the chemical constituents of more than 100 higher fungi in China since the last 10 yr. More than 300 novel terpenoids, phenolics, and nitrogen-containing compounds were isolated from basidiomycetes and ascomycetes (*Albatrellus confluens*, *Albatrellus dispansus*, *Boletus edulis*, *Boletopsis grisea*, *Boreostereum vibrans*, *Cortinarius tenuipes*, *Cortinarius vibratilis*, *Craterellus odoratus*, *Daldinia concentrica*, *Engleromyces gotzii*, *Hexagonia speciosa*, *Hydnum repandum*, *Hygrophorus eburnesus*, *Lactarius deliciosus*, *Lactarius hirtipes*, *Lactarius mitissimus*, *Lactarius rufus*, *Polyporus ellisii*, *Russula cyanoxantha*, *Russula foetens, Russula lepida*, *Russula nigricans*, *Sarcodon leavagatum*, *Sarcodon scabrosus*, *Shiraia bambusicola*, *Suillus granulatus*, *Thelephora aurantiotincta*, *Thelephora ganbajun*, *Tremella aurantilba*, *Tricholomopsis rutilans*, *Trogia* sp., *Tylopilus plumbeoviolaceus*, *Xylaria euglossa*, etc.). Some of them showed very interesting pharmacological activities. The isolation, structural elucidation, and biological activity of the new compounds are discussed. Supported by the National Basic Research Program of China (973 Program, 2009CB522300), the National Natural Science Foundation of China (30830113). Selected references: 1. N-containing Compounds of Macromycetes, *Ji-Kai Liu**, *Chem. Rev.* 2005, 105:2723–2744; 2. Natural terphenyls, development since 1877, *Ji-Kai Liu**, *Chem. Rev.* 2006, 106:2209–2223; 3. A lipase inhibitor with an unusual fused beta-lactone produced by cultures of the basidiomycete *Boreostereum vibrans*. Dong-Ze Liu, Fei Wang, Tou-Gen Liao, Jian-Guo Tang, Wolfgang Steglich, Hua-Jie Zhu, and *Ji-Kai Liu**, *Org. Lett.* 2006, 8:5749–5752; 4. Induced daldinin A, B, C with a new skeleton from cultures of the ascomycete *Daldinia concentrica*, Hong-Jun Shao, Xiang-Dong Qin, Ze-Jun Dong, Hong-Bin Zhang, *Ji-Kai Liu**, *J. Antibiot.* 2008, 61:115–119; 5. Rare merosesquiterpenoids from basidiomycete *Craterellus odoratus* and their inhibition of 11b-hydroxysteroid dehydrogenases, Ling Zhang, Yu Shen, Fei Wang, Ying Leng, *Ji-Kai Liu**, *Phytochemistry* 2010, 71:100–103; 6. Speciosins A–K, oxygenated cyclohexanoids from the basidiomycete *Hexagonia speciosa*, Meng-Yuan Jiang, Ling Zhang, Rong Liu, Ze-Jun Dong, *Ji-Kai Liu**, *J. Nat. Prod.* 2009, 72:1405–1409

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Understanding and Harnessing Enhancer—promoter Interactions and Insulation Systems for Precisely Engineering Gene Function and Agronomic Traits in Plants

Zongrang Liu. USDA-ARs Appalachian Fruit Research Station, 2217 Wiltshire Road, Kearneysville, WV 25430. Email: zongrang.liu@ars.usda.gov

Singer[1]*, Stacy[1], Hily[1]*, Jean-Michel[2], Yang[1,2], Yazhou[3], LIU1, ZONGRANG[4]
[1]1USDA-ARS Appalachian Fruit Research Station, 2217 Wiltshire Road, Kearneysville, WV25430, USA. *Current address: Department of Plant Pathology, New York State Agricultural Experiment Station, Cornell University, NY, 14456, USA
[2]1USDA-ARS Appalachian Fruit Research Station, 2217 Wiltshire Road, Kearneysville, WV25430, USA. *Current address: Department of Plant Pathology, New York State Agricultural Experiment Station, Cornell University, NY, 14456, USA
[3](1) USDA-ARS Appalsachian Fruit Research Station, 2217 Wiltshire Road, Kearneysville, WV25430, USA. (2) College of Life Sciences, Northwestern A&F University, Yangling, Shaanxi 712100, P.R. China
[4]1USDA-ARS Appalachian Fruit Research Station, 2217 Wiltshire Road, Kearneysville, WV25430, USA

Plant biotechnology provides a powerful tool for both basic research and agronomic trait improvement in a variety of crops through engineering gene expression. Often, this requires the simultaneous insertion of multiple, tandemly arranged genes that are controlled by distinct promoters. However, the presence of multiple promoter and enhancer elements within a single transgene cassette might, due to the inherent orientation-independent nature of enhancers, provoke enhancer–promoter or promoter–promoter cross-talk, which could inevitably alter the specificity and strength of discrete promoters in transgenic plants and consequently affect the outcome of the engineered traits. We found that both tissue-specific and constitutive enhancer elements can effectively activate adjacent promoters in non-targeted tissues. The detailed analyses revealed that enhancer-mediated gene activation occurred through the non-specific activation of gene transcription at multiple sites. Using this system, we developed an assay strategy for the identification of enhancer-blocking insulators. Our study showed that at least two of the DNA fragments tested had insulating activity. Potential applications of these insulators for eliminating the enhancer–promoter interaction and crosstalk within a composite transgene cassette