



## 吴为人

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### 学术兼职

浙江大学农业与生物技术学院客座教授、博士生导师

福建省遗传学会理事长

中国遗传学会理事

中国作物学会分子育种分会理事

《分子植物育种》执行主编

《遗传》副主编

《科学通报》编委

### 荣誉称号

新世纪“百千万人才工程”国家级人选

享受国务院政府特殊津贴专家

福建省教学名师

### 研究领域和方向

分子数量遗传学: 数量性状基因座 (QTL) 定位和克隆

分子遗传学与分子生物学: 分子标记开发; 分子遗传图谱构建; 基因克隆和功能分析

基因组学与生物信息学: 转录组分析 (基因芯片, 深度测序); 基因组进化

植物分子育种: 分子标记辅助育种; 基因工程

## 科研课题

(仅列出近5年承担的课题)

一个水稻苗期低温失绿基因*cisc(t)*的克隆与功能分析, 国家自然科学基金项目(31071399), 2011-2013

水稻营养生长与花器官发育多效基因*DDF1*的克隆与功能分析, 国家自然科学基金项目(30970175), 2010-2012; 教育部博士点基金, 2009-2011

烟草SSR标记开发及应用, 中国烟草总公司云南省公司科技项目, 2010-2011

水稻高叶绿素含量基因、单侧卷叶基因和包穗基因的克隆与功能验证, 国家转基因重大专项(2009ZX08009-109B), 2009-2011

福建特色烤烟新品种选育研究, 分子标记辅助育种, 福建省烟草专卖局科技项目, 2008-2012

松树内含子多态性标记开发及其在遗传作图中的应用, 国家自然科学基金项目(30771750), 2008-2010

水稻DNA指纹检测体系的建立与应用, 福建省科技重大专项“粮食作物育种技术研究”专题二“水稻分子植物育种研究与应用”(2008NZ02-02)子专题四, 2008-2010

植物与微生物互作的跨基因组多基因遗传体系的研究, 国家自然科学基金项目(30671123), 2007-2009

水稻雌雄蕊发育关键基因*PSD2*的克隆与功能分析, 国家自然科学基金项目(30671122), 2007-2009

烟草遗传群体建立与分子标记遗传连锁图谱构建, 中国烟草总公司项目, 2007-2010

主要农作物骨干亲本遗传构成和利用效应的基础研究, 973计划项目(2006CB101708), 2007-2012

植物ILP标记的大规模开发与数据库建设, 863计划“十一五”专题项目(2006AA10Z1E2), 2006-2010

水稻花器官发育关键基因及其作用网络的研究, 863计划“十一五”专题项目(2006AA10Z128), 2006-2010

## 发表论文

(仅列出SCI收录的论文; \*号表示通讯作者)

Zheng Y, Zheng W, Lin F, Zhang Y, Yi Y, Wang B, Lu G, Wang Z, Wu W\*. *AVR1-CO39* is a predominant locus governing the broad avirulence of *Magnaporthe grisea* strain 2539 on cultivated rice (*Oryza sativa* L.). *Molecular Plant Microbe Interaction*, 2011, 24(1): 13-17

Chen X, Zhang G, Wu W\*. Investigation and utilization of intron length polymorphisms in conifers. *New Forests*, 2010, DOI 10.1007/s11056-010-9229-5

Duan Y, Diao Z, Liu H, Cai M, Wang F, Lan T, Wu W\*. Molecular cloning and functional characterization of *OsJAG* gene based on a complete-deletion mutant in rice (*Oryza sativa* L.). *Plant Molecular Biology*, 2010, 74: 605-615

Lan T, Wang B, Ling Q, Xu C, Tong Z, Liang K, Duan Y, Jin J, Wu W\*. Fine mapping of *cisc(t)*, a gene for cold-induced seedling chlorosis, and identification of its candidate in rice. *Chinese Science Bulletin*, 2010, 55: 3149-3153

Tang J, Yan J, Ma X, Teng W, Wu W et al. Dissection of the genetic basis of heterosis in an elite maize hybrid by QTL mapping in an immortalized  $F_2$  population. *Theoretical and Applied Genetics*, 2010, 120: 333-340

Zhao X, Yang L, Zheng Y, Xu Z, Wu W\*. Subspecies-specific intron length polymorphism markers reveal clear genetic differentiation in common wild rice (*Oryza rufipogon* L.) in relation to the domestication of cultivated rice (*O. sativa* L.). *Journal of Genetics and Genomics*, 2009, 36: 435-442

Zheng Y, Zhang G, Lin F, Wang Z, Jin G, Yang L, Wang Y, Chen X, Xu Z, Zhao X, Wang H, Lu J, Lu G, Wu W\*. Development of microsatellite markers and construction of genetic map in rice blast pathogen *Magnaporthe grisea*. *Fungal Genetics & Biology*, 2008, 45: 1340-1347

Huang D, Wu W, Abrams SR, Cutler AJ. The relationship of drought-related gene expression in *Arabidopsis thaliana* to hormonal and environmental factors. *Journal of Experimental Botany*, 2008, 59: 2991-3007

Wen Y, Wu W\*. Experimental designs and statistical methods for mapping quantitative trait loci underlying triploid endosperm traits without maternal genetic variation. *Journal of Heredity*, 2008, 99(5): 546-551

Yang J, Wu W, Zhu J. Mapping interspecific genetic architecture in a host-parasite interaction system. *Genetics*, 2008, 178: 1737-1743

Yang L, Jin G, Zhao X, Zheng Y, Xu Z, Wu W\*. PIP: a database of potential intron polymorphism markers. *Bioinformatics*, 2007, 23: 2174-2177

Wen Y, Wu W\*. Interval mapping of quantitative trait loci underlying triploid endosperm traits using  $F_3$  seeds. *Journal of Genetics and Genomics*, 2007, 34(5): 429-436

Huang D, Jaradat MR, Wu W et al. Structural analogs of ABA reveal novel features of ABA perception and signaling in *Arabidopsis*. *Plant Journal*, 2007, 50: 414-428

Wang X, Zhu H, Jin G, Liu H, Wu W\*, Zhu Jun. Genome-scale identification and analysis of LEA genes in rice (*Oryza sativa* L.). *Plant Science*, 2007, 172: 414-420

Tang J, Ma X, Teng W, Yan J, Wu W, Dai J, Li J. Detection of quantitative trait loci and heterotic loci for plant height using an immortalized  $F_2$  population in maize. *Chinese Science Bulletin*, 2007, 52(4): 477-483

- Wu W\*, Huang B. Strategy for the mapping of interactive genes using bulked segregant analysis method and Mapmaker/Exp software. Chinese Science Bulletin, 2006, 51(21): 2619-2623
- Wen Y, Wu W\*. Methods for mapping QTLs underlying endosperm traits based on random hybridization design. Chinese Science Bulletin, 2006, 51(16): 1976-1981
- Wang X, Zhao X, Zhu J, Wu W\*. Genome-wide investigation of intron length polymorphisms and their potential as molecular markers in rice (*Oryza sativa* L.). DNA Research, 2005, 12: 417-427
- Wang X, Wu W\*, Jin Gulei, Zhu Jun. Genome-wide identification of R genes and exploitation of candidate RGA markers in rice. Chinese Science Bulletin, 2005, 50(11):1120-1125
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- Huang D, Wu W, Lu L. Microdissection and molecular manipulation of single chromosomes in woody fruit trees with small chromosomes using pomelo (*Citrus grandis*) as a model: II. cloning of resistance-gene analogs from single chromosomes. Theoretical and Applied Genetics, 2004, 108: 1371-1377
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- Wu W\*, Li W, Tang D et al. Time-related mapping of quantitative trait loci underlying tiller number in rice. Genetics, 1999, 151: 297-303
- Wu W\*, Li W. Joint mapping of quantitative trait loci using  $F_2$  populations. Theoretical and Applied Genetics, 1996, 93: 1156-1160
- Wu W\*, Li W. Model fitting and model testing in the method of joint mapping of quantitative trait loci. Theoretical and Applied Genetics, 1996, 92: 477-482
- Wu W\*, Li W. A new approach for mapping quantitative trait loci using complete genetic marker linkage maps. Theoretical and Applied Genetics, 1994, 89: 535-539

#### 出版论著

方宣钧, 吴为人, 唐纪良. 《世纪之交863计划生物高技术丛书·作物DNA标记辅助育种》, 科学出版社, 2001

#### 获奖成果

水稻分子标记辅助选择技术体系的建立与应用, 福建省科学技术奖二等奖(2006; 排名第一)

用PCR技术快速鉴定sorghum属, 福建省科学技术奖三等奖(2006; 排名第四)

细胞工程应用于水稻遗传育种的研究, 福建省科学技术奖二等奖(2001; 排名第五)