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2016年度中国玉米生物学研究进展

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摘 要：近年来,我国在玉米生物学领域的研究水平不断提升,开始在国际主流学术期刊发表具有重要影响力的研究论文。2016年,我国在104个"SCI"收录的期刊发表研究论文338篇,其中,在5年平均影响因子超过5.0的期刊发表论文46篇。在玉米子粒发育遗传调控、玉米抗非生物胁迫基因挖掘和功能研究、玉米抗生物胁迫基因挖掘及功能分析、玉米重要农艺性状基因/QTLs发掘、玉米转录组蛋白质和代谢组研究、玉米栽培生理学研究以及玉米遗传育种新方法与新技术等方面取得了重要进展。

关键词：玉米;遗传育种;生物学
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Research Progress on the Maize Biology in China in 2016

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Abstract: In recent years, there are an increasing number of scientists participating in maize basic research in our country, which results in an improved overall quality of research in the field of maize biology. The progresses of maize biology research in China well demonstrated by starting to have high impact research articles published in top international academic journals. Over the past year, 338 research articles were published in 104 journals of SCI(Science Citation Index), with 46 of them having relatively high impact factor(IF>5). In summary, important progresses had been made in the following directions: the genetics regulation of kernel development, the gene discovery for abiotic stresses, the gene discovery for biotic stresses, QTL gene cloning for important agronomic traits, the omics research(transcriptomics, proteomics and metabolomics), physiologies for maize cultivation, new technologies for maize genetic studies and breeding.

Key words: Maize; Genetics and breeding; Biology

我国玉米的基础研究可以追溯到上个世纪40~50年代,我国老一辈的科学家取得了重大的研究成果,李竞雄先生1948年在《Science》期刊上发表玉米遗传学的研究成果[1]。改革开放以来,我国玉米研究队伍不断壮大,特别是本世纪初,我国玉米在基础研究方面得到重要进展,在"SCI"期刊收录上开始发表有重要影响的研究论文。2010年,我国第一篇基因组学研究成果在国际主流期刊《Nature Genetics》上发表[2],随后,国内玉米研究机构几乎每年在《Nature Genetics》上有论文发表[3~5]。另外,在《PNAS》、《Genome Research》、《Nature Communications》等国际著名期刊也发表多篇重要的研究成果[6~10],得到了国际同行的广泛关注,国际影响力大大增强。国内玉米研究人员开始在主要期刊发表综述性文章[11,12]。2014年,在北京举办了第56届"国际玉米遗传学大会",聚集了国内外500多名参会人员,这也是该会议首次在亚洲地区召开(http://www.maizegdb.org/maize_meeting/),对我国在玉米基础研究有很大的推动作用。

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附 注：国家玉米改良中心对每年的玉米生物学研究进展进行综述。由于受到文献检索方法的限制,难免会有个别文献没有被检索到,为了更全面地收集文献,欢迎大家在文章公开发表后把文献信息或全文发到国家玉米改良中心公共邮箱。E-mail:maizecenter@cau.edu.cn

本文利用文献数据库NCBI、Web of Science进行研究论文检索，文献检索时间为论文的首次在线发表时间，时间范围界定在2016年1月1日至2016年12月31日，论文的通讯作者所在研究单位隶属于中国。对检索出的文献进行作者单位和在线发表时间进行逐一核实，最终汇总出我国玉米科研单位研究人员作为通讯作者在2016年度所发表的研究论文，统计分析结果表明，2016年，我国在104个“SCI”收录期刊发表论文338篇(表1)，其中，在《Nature Genetics》、《PNAS》、《Molecular Plant》等14个高影响力的期刊上发表论文46篇(表2)。研究内容涉及数量遗传学、功能基因组学、表观遗传学、蛋白质组学等多个领域。本文主要从7个方面对2016年的研究结果进行综述，主要有玉米子粒发育遗传调控研究、玉米抗非生物胁迫基因挖掘和功能研究、玉米抗生物胁迫基因挖掘及功能分析、玉米重要农艺性状基因/QTLs发掘、玉米组学研究、玉米栽培生理学研究、玉米遗传育种新方法与新技术。

1 玉米子粒发育遗传调控研究

子粒是玉米重要的器官，对玉米子粒的发育遗传学研究有助于开展玉米品质性状和产量性状的协同遗传改良。以*O2*(*opaque2*)基因的突变体*o2*为基础所选育的优质蛋白玉米(Quality Protein Maize，QPM)不但赖氨酸含量提高，而且子粒表现为硬质胚乳。对其深入的分子机理研究发现，其与27-kD *γ-zein*基因的转录和蛋白表达水平升高有关。研究发现，这种表达量的提升是由于27-kD *γ-zein*基因所在的区段发生了片段重复(duplication)[13]。除了调控27-kD *γ-zein*基因之外，*O2*基因还参与调控了淀粉合成途径的相关基因。利用转录组分析、EMSA和免疫共沉淀等一系列分子生物学技术，还发现了淀粉合成途径中两个关键基因*PPDKs*和淀粉合成酶Ⅲ(SSⅢ)直接受到O2和PBF(prolamine-box binding factor)两个转录因子的调控，SSIIa和SBE1间接受O2和PBF调控[14]。此外，还有研究表明，*O2*基因和另外一个转录因子家族成员ZmMADS47通过特定的互作协同调控醇溶蛋白基因的表达[15]。另一项研究表明，玉米子粒淀粉合成途径的相关基因受到转录因子ZmbZIP91的调控[16]。除了这些醇溶蛋白基因的表达调控之外，上海大学研究小组还对醇溶蛋白的组装机制进行了深入研究，其中，一个关键基因为*O10*，该基因编码的蛋白和22-kD以及16-kD醇溶蛋白直接互作来稳定储藏蛋白体的环状结构[17]。在子粒表观遗传研究方面，对组蛋白去乙酰化酶HDA101如何调控玉米子粒基因表达进行了深入分析[18]。以授粉后12 d的玉米B73和Mo17正反交胚乳为材料，分别对其进行了转录组测序和组蛋白修饰H3K4me3、H3K36me3抗体的染色质免疫共沉淀实验，在玉米胚乳中全基因组范围内鉴定到超过300个印记的H3K4me3和H3K36me3靶位点[19]。此外，在玉米子粒发育方面，通过正向和反向遗传学技术，获得了对玉米子粒发育比较重要的基因*UBL1*、*reas1*、*dek35*、*Emp16*、*ZmDof3*等，这些基因的突变均能够影响子粒的正常发育[20~24]。

2 玉米抗非生物胁迫基因挖掘和功能研究

玉米生产过程中主要遇到的非生物胁迫包括干旱胁迫、盐胁迫和高温胁迫，其中，干旱是影响玉米生产最重要的非生物胁迫，苗期严重干旱会导致缺苗，同时也会影响到株高、开花期等农艺性状。因此，克隆玉米的抗旱基因，研究玉米抗旱分子调控机理，对玉米抗旱性状的遗传改良具有重大意义。中国科学院植物研究所和中国农业大学国家玉米改良中心合作，利用全基因组关联分析，结合候选基因分析策略，对玉米苗期的抗旱QTLs(Quantitative Tait Loci)位点进行扫描，克隆了一个重要抗旱基因*ZmVPP1*，该基因编码一个定位于液泡膜上的质子泵-焦磷酸水解酶；基因结构分析发现，该基因启动子区域有366个核苷酸的大片段缺失，该片段含有3个MYB转录因子作用元件。过表达*ZmVPP1*基因能够显著提高玉米的抗旱性[25]。该基因家族的另外一个成员*ZmVPP5*也参与到了非生物胁迫的响应，在玉米和酵母中过表达*ZmVPP5*基因，转基因玉米植株和酵母细胞表现出对盐胁迫高度敏感，推测该基因可能作为一个拮抗因子或者负调控因子参与细胞对外界的逆境胁迫响应[26]。

ZmNAC84转录因子受到ABA的诱导表达，该表达也受到H_2O_2的调节。进一步分析发现，ZmNAC84也在ABA诱导的抗氧化防护过程中起重要作用，且ZmNAC的作用依赖于*ZmCCaMK*对其氨基酸的磷酸化作用，过表达该基因，可以提高烟草的抗旱性[27]。另外，一个蛋白磷酸酶基因家族成员*ZmPP2C-A10*也作为一个负调控因子参与了玉米逆境胁迫响应过程，在玉米中过表达该基因植株表现出对干旱敏感。分析发现，该基因5’非翻译区内质网胁迫响应元件的缺失能够增强玉米的抗旱性[28]。其他玉米中鉴定到的非生物逆境胁迫基因还有*AtLOS5*、*ZmABA8ox1b*、*ZmNAC55*、*ZmABA2*、*ZmWRKY4*、

ZmDBF3、*ZmHDZ4*、*ZmGOLS2*等[29~36]。通过转录组测序和生物信息学分析等方法,鉴定出大量玉米苗期抗逆候选基因[37~41]。这些基因的克隆及功能解析有助于对玉米响应干旱等非生物胁迫的分子机制的了解,为培育抗旱玉米提供新的思路。

表1　我国科研单位在不同期刊发表玉米研究相关文章数量统计(2016年)

Table 1　Numbers of published papers related to maize biology research in different journals by different institutes from China (2016)

期刊名称 Journal name	5年影响因子 Impact factor of five years	篇数 Number of articles	期刊名称 Journal name	5年影响因子 Impact factor of five years	篇数 Number of articles
Nature Genetics	32.197	1	J Agric Food Chem	2.912	1
Proc Natl Acad Sci U S A	10.285	3	Genomics	2.896	2
Plant Cell	9.88	1	Mol Genet Genomics	2.858	3
PLoS Pathog	7.758	1	Int J Syst Evol Microbiol	2.782	4
New Phytol	7.554	5	Molecules	2.749	1
PLoS Genet	7.481	2	BMC Biotechnol	2.748	1
Plant Physiol	7.367	9	Int J Biometeorol	2.649	1
Mol Ecol Resour	7.347	1	Virus Res	2.611	1
Molecular Plant	6.885	6	J Sep Sci	2.586	2
Plant J	6.468	5	Molecular Breeding	2.575	5
Plant Cell Environ	6.443	1	Protoplasma	2.546	1
Environ Sci Technol	6.396	1	Plant Biol (Stuttg)	2.488	2
J Exp Bot	6.229	8	Biochem Biophys Res Commun	2.575	2
Plant Biotechnol J	5.951	2	J Sci Food Agric	2.546	2
Sci Rep	5.525	17	Plant Growth Regulation	2.185	1
Plant Cell Physiol	4.847	2	Peer J	2.392	1
Anal Chim Acta	4.841	1	AoB Plants	2.164	1
Biochim Biophys Acta	4.805	1	Microbiologyopen	2.152	1
BMC Plant Biol	4.604	12	Transgenic Res	2.099	3
Front Plant Sci	4.461	29	Dev Genes Evol	2.078	1
Front Microbiol	4.36	1	Int J Phytoremediation	1.451	2
Sci Total Environ	4.317	1	Insect Sci	1.041	1
BMC Genomics	4.278	13	J Plant Res	2.039	1
Theor Appl Genet	4.115	7	Plant Molecular Biology Reporter	1.995	5
Ann Bot	4.088	1	Euphytica	1.866	6
J Environ Manage	4.049	1	J Econ Entomol	1.847	1
J Integr Plant Biol	3.993	7	Int J Genomics	1.841	1
J Proteomics	3.986	1	Science of Nature	2.071	1
Database (Oxford)	3.983	2	Genetica	1.686	1
Plant Sci	3.981	4	J Virol Methods	1.642	1
Toxins (Basel)	3.942	2	Indian J Microbiol	1.156	1
Front Genet	3.92	1	Journal of Plant Biochemistry and Biotechnology	1.15	1
Plant Mol Biol	3.874	3	Genet Mol Res	0.912	7
Physiol Plant	3.799	4	J Genet	1.2	4
J Environ Sci (China)	3.726	3	Maydica	0.695	4
Photosynth Res	3.6	1	Plant Disease	3.268	1
Planta	3.593	6	Field Crops Research	3.541	4
PLoS One	3.535	29	Phytochemistry	3.218	1
Genetics	3.49	2	Plant Cell Tissue And Organ Culture	2.286	1
Viruses	3.437	1	Environmental Science and Pollution Research	2.876	1
Plant Physiol Biochem	3.434	5	Journal of Plant biology	1.369	1
Journal of Agricultural and Food Chemistry	3.308	1	Crop Science	1.758	6
Phytopathology	3.248	1	Acta Physiologiae Plantarum	1.692	3
J Plant Physiol	3.241	1	Plant Breeding	1.629	2
Mycorrhiza	3.231	2	European Journal of Plant Pathology	1.698	2
Int J Biol Macromol	3.22	3	Agronomy Journal	1.86	3
Phytochemistry	3.218	1	European Food Research and Technology	1.778	1
Int J Mol Sci	3.213	4	Journal of Integrative Agriculture	0.867	11
G3 (Bethesda)	3.198	1	Annals of Microbiology	1.331	1
Plant Cell Rep	3.187	3	Genes & Genomics	0.697	1
Pest Manag Sci	3.116	1	Spanish journal of agricultural research	0.873	1
J Genet Genomics	3.013	3	Research Journal of Biotechnology	0.336	1
J Agric Food Chem	2.912	1	合　计		338

表2 我国17个科研单位在5年影响因子大于5.0的国际主流期刊发表的研究论文数量统计(2016年)

Table 2 Published papers in journals with high quality(IF>5.0) by 17 different institutes from China(2016)

单位名称 Institute	Nature Genetics	PNAS	Plant Cell	PLoS Pathog	Molecular Plant	New Phytol	PLoS Genet	Plant Physiol	Mol Ecol Resour	Plant J	Plant Cell Environ	Environ Sci Technol	J Exp Bot	Plant Biotechnol J	合 计 A combined
中国农业大学		1	1		1	2		3		1			3		12
华中农业大学					3	2		1	1						7
上海大学					1		2	1					1		5
中国农业科学院作物科学研究所					1					1			1	1	4
中国科学院上海植物生理生态研究所		2		1											3
山东大学								1		1					2
四川农业大学								1					1		2
南京农业大学								1						1	2
中国科学院遗传与发育生物学研究所										1					1
中国科学院植物研究所	1														1
武汉大学						1									1
中国科学院土壤科学研究所										1					1
中国科学院昆明植物研究所											1				1
中国科学院生态环境科学研究中心												1			1
中国科学院上海计算生物学研究所													1		1
中国农业科学院生物技术研究所													1		1
同济大学								1							1
合 计	1	3	1	1	6	5	2	9	1	5	1	1	8	2	46

3 玉米抗生物胁迫基因挖掘及功能分析

病害是玉米生产中重要的影响因子,除了能影响产量,部分病害还严重影响玉米品质。开展抗病等生物逆境胁迫响应基因及其分子机理研究具有重要意义。利用转录组和降解组测序技术对由水稻黑条纹矮化病毒RBSDV(Rice black-streaked dwarf virus)引起的玉米粗缩病进行了研究,详细阐明了玉米植株感染RBSDV病毒后的响应分子机制,并鉴定出了新的响应miRNA和功能基因[42]。玉米大斑病NCLB(Northern corn leaf blight)研究方面,利用重组自交系群体结合高密度SNP遗传图谱,获得了两个在多个环境条件稳定表达的抗病QTL位点,对这两个位点开发了可以用于抗病分子育种的分子标记[43]。玉米茎腐病研究方面,利用遗传背景一致的抗病、感病近等基因系为材料(抗病QTLs为*qRfg1*和*qRfg2*),研究了玉米接种禾谷镰孢菌(*Fusarium graminearum*)以后玉米响应病原菌的分子机理,共鉴定到了1 000多个差异表达基因,这些基因功能富集在了生长发育、光合作用等遗传调控途径,结果还分析了两个QTL在抗病过程中的功能[44]。利用荧光标记的禾谷镰孢菌研究了玉米茎腐病的发病过程,发现早期的镰孢菌主要在细胞间隙生长,通过激光显微切割技术对侵染中的镰孢菌的表达谱分析,揭示了禾谷镰孢菌新的致病机理[45]。

除了茎腐病的遗传学研究之外,茎腐病的生物学防治方面也取得一定进展,离体条件下,从7种生防菌棘孢木霉(Trichoderma asperellum)中筛选对茎腐病的致病菌禾谷镰孢菌(*Fusarium graminearum*)具有拮抗作用的菌株,获得了对该致病菌具有很好的防治效果的菌株ZJSX5003,防治效果能够达到71%,为防治玉米茎腐病提供了新的途径[46]。在玉米对生物胁迫的防御反应方面,全基因组关联分析研究发现,木质素生物合成途径两类基因在植物的过敏反应中起着重要作用,并提出了一个与Rp1形成蛋白复合体的抗病反应模型[47]。东方黏虫的口腔分泌物能够诱导玉米的防御反应,包括基因的转录水平、翻译水平和代谢水平等[48]。

4 玉米重要农艺性状基因/QTLs发掘

玉米重要农艺性状基因/QTLs的挖掘为优良等位基因发掘、分子标记辅助选择育种提供重要支撑。重要农艺性状有穗行数、行粒数、灌浆速率、耐密性、株型、雄性不育等。利用10个重组自交系群体,结合多个生态环境的表型鉴定,对玉米穗部性状的遗传结构进行了分析,结果发现了大量微效QTL位点,总效应能够解释55.2%~82%的表型变异,此外,利用候选基因关联分析的方法对4个新的QTLs进行了验证[49]。在子粒性状方面,利用回交导入群体、关联分析群体对粒重、粒长、粒宽以及子粒灌浆速率进行精细定位和候选基因分析[50,51]。控制子粒重量和宽度的主效QTL qKW7的候选基因*GRMZM2G114706*编码一个蛋白激酶[52];粒长主效QTL qKL1.07获得了候选基因*ZmCKX10*,编码细胞分裂素氧化酶基因[53]。在株型方面,利用4个重组自交系对不同种植密度条件下的6个叶片相关性状进行了QTL分析,结果在两个密度条件下均鉴定到的QTL数量是55个,37个QTL位点仅在高密度条件下表达[54]。

开花期方面,利用866份玉米大刍草渗入系群体系统研究了叶片数和开花期的关系,结果表明,地上、地下和总的叶片数分别受到不同的遗传调控通路,而且受到不同的人工驯化和改良。叶片数和开花期二者紧密相关,遗传调控上也存在很多的相似性。对已报道的开花期已知基因*ZCN8*、*dlf1*和*ZmCCT*在开花期和叶片数的遗传多效性进行了验证[55]。通过利用超大规模的NAM关联分析群体和自然群体对开花期进行了深入的遗传学基础解析,共有90个QTL位点在两个群体中被鉴定到,包括群体特异表达的以及群体共同表达的QTL。利用3个群体进行联合分析发现,有1 000个与开花期紧密关联的SNP标记,这些SNP标记集中分布在220个候选基因的附近区域。深入分析结果表明,SNP富集在两种区域类型,一种是SNP直接富集在候选基因区域,另外一种是SNP富集在基因上下游约5 Kb的位置上[56]。此外,苞叶数、株高和穗位高、根形态、雄穗大小等方面也鉴定到多个QTL位点[57~61]。控制玉米雄性核不育基因*IPE1*编码葡萄糖甲醇胆碱氧化还原酶(glucose-methanol-choline oxidoreductase),该基因与核不育基因*MS26*和*MS45*协同调控玉米花药外皮和花药外壁的发育[62]。这些位点对玉米重要农艺性状的遗传改良提供很好的候选基因。

5 玉米转录组、蛋白组和代谢组学研究

近几年来,玉米转录组、蛋白组和代谢组数据大幅增加,对玉米不同组织器官的不同生长发育阶段进行了越来越细的组学分析。过去一年里,我国不同的玉米研究团队利用转录组测序技术开展控制玉

米子粒淀粉含量的候选基因挖掘,对淀粉合成过程中的转录变化有了更为深入的认识[63]。此外,对授粉后不同时期的胚乳进行转录组测序,鉴定出11 000个基因发生了可变剪切,并对这些基因的功能进行了注释和分类[64]。胚是除了胚乳之外子粒中另外一个重要组织器官,对两个杂交种以及其相应的亲本成熟胚进行了转录组测序,通过杂交种和亲本之间的差异表达基因,分析了父、母本在转录组水平上对杂种优势的贡献[65]。除了子粒性状之外,转录组技术还应用在其他产量构成因子转录差异分析以及玉米的抗病性、低养分胁迫及抗旱响应、驯化等研究领域[66~79]。开展玉米蛋白组学的研究有助于加深对玉米生长发育规律的认识。目前,玉米蛋白组学研究主要集中在逆境胁迫条件下蛋白组富集程度或者降解程度,如干旱胁迫、低温胁迫、重金属胁迫以及玉米子粒蛋白合成等方面[80~85]。各种生物学发育过程需要不同蛋白之间相互作用来完成,上海同济大学的研究小组利用14 000个蛋白的注释和模式生物的信息建立了1个预测的蛋白互作网络数据库,数据库中包含了276万个互作,该数据库为开展玉米功能基因组学领域的科学家提供了很好的帮助,目前该数据库已经免费对外开放(http://comp-sysbio.org/ppim)[86]。利用重组自交系对玉米子粒的155个代谢组分进行了代谢组的QTL分析,鉴定出大量QTL位点,并对这些QTLs之间的上位性互作进行了鉴定,研究结果能够为玉米品质的遗传改良提供重要信息[87]。另外,玉米抗逆响应的代谢组研究方面也取得了一定进展[88~92]。

6 玉米栽培生理学研究

根部相关性状是玉米栽培生理学研究的一个重要关注点,良好的根部生长环境会极大促进玉米地上部分的生长和发育。根的生长发育过程需要其他植物的根系以及与土壤微生物进行相互作用。我国传统的间作套种就是很好地利用了不同作物根系之间的相互作用有利的一面。研究发现,禾本科作物玉米与豆科作物蚕豆的间作套种能够促进蚕豆根部结瘤,并增强蚕豆本身的固氮效果,这种效果的增强主要依赖于玉米根系的一种分泌物(染料木素);体外实验结果表明,这种化学分泌物能够促进豆科作物固氮途径相关基因的表达,进而促进了蚕豆固氮能力的提升[93]。进一步研究发现,蚕豆根部的分泌物也能够促进玉米根系的生长发育,此外,蚕豆和玉米的根系之间的这种相互促进生长的模式也受到营养元素磷的调控[94]。磷元素的缺乏严重影响到玉米、蚕豆等作物的根系发育,同时,磷元素也会与铵态氮和硝态氮进行相互作用一起调控禾本科与豆科作物的根系生理特性和形态特征[95]。除了以上营养元素能够调节根的生长发育,研究表明,玉米根本身内源的微生物也能够促进根的生长,根部存在大量的微生物种群,部分微生物能够帮助玉米根系更好地吸收土壤中的营养元素,提高土壤中的化学肥料的吸收利用效率[96]。北京市农林科学院玉米研究中心对国内抗逆能力强、适应范围广、推广面积大的优良玉米杂交种京科968根部组织内源益生菌分离及其拮抗实验表明,新鉴定到的内源益生菌类芽孢杆菌(*Paenibacillus sp* 5 L8)能够抗包括禾谷镰刀菌在内的7种植物致病菌[97]。通过离体培养和分子生物学鉴定,从玉米根系中分离到4种新的内源细菌,并根据16S rRNA基因序列的相似性对他们进行了归类[98~101]。玉米内源微生物的鉴定和功能分析能够为未来的微生物菌肥产品开发提供重要信息资源。

7 玉米遗传育种新方法与新技术

新方法和新技术是促进玉米遗传育种学科进步重要推动力。基因编辑技术是目前公认的开展农作物功能基因组学和分子设计育种研究的有效工具,目前该技术已经应用于多个作物的遗传改良。根据玉米基因特点,对CRISPR/Cas9技术(Clustered regularly interspaced short palindromic repeats)体系进行优化,通过原生质体和玉米幼胚的遗传转化方法,对玉米基因进行编辑,结果显示,多个细胞或转化体目标基因均能够被编辑,而且目标基因的突变形式有不同程度的碱基缺失,初步建立起了玉米基因组编辑体系[102,103]。通过对该技术体系的进一步优化,不但能够对多个基因同时开展编辑,而且编辑的效率可以进一步提升[104]。基因瞬时表达体系的建立对深入开展玉米功能基因组学的研究具有重要意义,利用黄瓜花叶病毒(Cucumber mosaic virus)建立了一套高效的病毒侵染玉米叶片进而实现目标基因瞬时表达的体系,通过表达两个目标基因的反义片段,能够使得目标基因的表达丰度分别降低到对照的75%和78%,而且这个体系能够实现对大多数玉米骨干自交系的侵染[105]。GWAS(Genome-wide Association Study)已经被广泛应用于多个物种QTLs挖掘,随着玉米各种组学数据的不断增多,新的计算方法的不断创新,GWAS将在重要农艺性状遗传解析方面扮演更为重要的角色。

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关于召开“2017年全国玉米遗传育种学术研讨会”的通知

为了加强我国玉米遗传育种行业的学术交流,促进我国玉米遗传育种学科和种业的全面发展,中国作物学会玉米专业委员会定于2017年7月14~17日,在四川省成都市望江宾馆召开“2017年全国玉米遗传育种学术研讨会”。会议由中国作物学会玉米专业委员会主办,四川省农业科学院作物研究所、四川农业大学玉米研究所共同承办,四川省作物学会协办。会议主办单位特邀中国工程院戴景瑞院士、荣廷昭院士、中国作物学会、农业部等有关领导出席。会议主办单位还邀请农业部种子局马志强处长、中国农业科学院万建民副院长、中国农业大学陈绍江教授、中国农业科学院黎裕研究员、四川农业大学潘光堂教授、四川省农业科学院杨俊品研究员等专家、学者分别就“玉米品种审定标准解读”、“水稻分子育种进展”、“玉米单倍体育种技术体系创新”、“玉米优异资源挖掘”、“西南山地玉米区生态育种的理论与实践”、“四川玉米育种的挑战与对策”做大会报告。现将会议有关事宜通知如下:

一、**会议时间** 2017年7月14~17日

二、**会议地点** 成都军区第四招待所,又名:望江宾馆(酒店总机服务电话:028-84790000),地址:四川省成都市锦江区下沙河铺街42号

三、**会议内容** 1.玉米遗传育种学术交流;2.农业部国家玉米良种重大科研协作攻关专题报告;3.玉米学科群、良种协作攻关新品种、新组合田间展示观摩

四、**会议日程** 7月14日(星期五)全天报到;7月15日(星期六)开幕式及大会报告;7月16日(星期日)上午分会场报告或专题交流,下午田间展示观摩;7月17日(星期一)代表离会

五、**会议费** 参会代表会议费:1 200元/人,报到时酒店统一受理;食宿会务组统一安排,费用自理;根据会议规定,不接送站。由于会议住宿酒店房间的限制,参会代表务必填写回执,会务组以收到回执信息先后为序安排房间,会议不接待没有回执的代表。

六、**住宿安排说明** 住宿标准:370元/间·天(宏达楼·标间/单间·单早);400元/间·天(宏达楼·标间/单间·双早);500元/间·天(五福楼·标间·单早);530元/间·天(五福楼·标间·双早)

请参会代表务必在回执中填写好住宿人数及需要房间类型。

七、**会议联系人** 四川省农科院作物所 杨俊品 研究员 13708099287

四川农大玉米研究所 高世斌 教 授 18615786279

2017年全国玉米遗传育种学术研讨会组委会