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CRISPR/Cas 基因编辑系统在水稻中的研究进展

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摘要:基因编辑是一种能对特定基因进行修饰的基因工程技术,能快速对靶点基因编辑,是高效捕获目的基因、快速研究目标基因功能的重要手段,在基因功能研究和作物育种等方面有着重要意义和广阔的应用前景。基因编辑利用特异的 DNA 结合元件和切割元件开展编辑工作,然而该技术最需注意的是特异性和脱靶率问题,不同时期的基因编辑技术也针对上述 2 个问题进行改良,目前应用最为广泛的是 CRISPR/Cas9,Cas12a 由于其特异性高且脱靶率大大降低也受到越来越多的关注。本文对基因编辑的技术发展及特点、CRISPR/Cas9 和 Cas12a 的技术优势进行介绍,并对这 2 种技术在水稻产量、抗性 & 品质中的研究进展进行综述,同时对拓展 CRISPR/Cas 基因编辑技术在水稻中的应用提出展望,为基因功能鉴定及遗传改良提供参考。

关键词:基因编辑;Cas9;Cas12a;水稻;性状改良

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基因编辑(gene editing)是一种能对特定基因进行修饰的基因工程技术^[1-2],该技术利用工程核酸酶切割目标基因组产生 DNA 双链断裂(DSB),进而激活细胞内源性 DNA 修复机制从而产生包括插入、缺失及基因片段替换等新的基因突变类型^[3-5]。

1996 年出现的锌指核酸酶(ZFN)为基因编辑技术的发展奠定了基础^[6-7],利用该技术首次于 2002 年果蝇染色体上实现基因定点突变^[8]。随后转录激活样效应因子核酸酶(TALENs)^[9]及由 RNA 介导的 Cas9 蛋白相关的成簇规则间隔短回文重复序列(CRISPR)相继被发现^[10-11],特别是 CRISPR/Cas9 于 2013 年开始应用于植物基因组编辑,被 Science 列入 2013 年十大科学进展^[10]。此外,用于切割双链 DNA 的 CRISPR/Cas12a(Cpf1)^[12-13]及在

crRNA 指导下切割 ssRNA 的 CRISPR/Cas13 (C2c2)^[14]于 2015 年和 2016 年相继被发现(图 1)。

基因编辑利用特异的 DNA 结合元件和切割元件开展编辑工作,然而该技术最需注意的是特异性和脱靶率问题,基因编辑技术的更迭对这 2 个方面的改善也各不相同(表 1)。ZFNs 是第一个应用于基因定点编辑的技术,然而其 ZFN 剪切 DNA 形成同源二聚体的同时,可能会产生异源二聚体引起脱靶且难以实现多靶点编辑等问题,严重阻碍了其应用^[15-16];TALENs 技术是 1 个 TALE 基序识别 1 个碱基对,因此多个串联的 TALE 基序与其识别的碱基对呈一一对应关系,大大提高了编辑特异性并降低脱靶率,但其编辑效率较低,且难以进行多基因编辑^[17-20];CRISPR/Cas9 技术在 sgRNA 的指导下与靶点结合,并利用 HNH 和 RuvC 对外源 DNA 进行切割,其编辑效率大大提高,且可以对多基因同时编辑,然而其缺点是靶向目标 DNA 序列容易出现错配,存在脱靶率高、编辑特异性低等缺陷^[4,16,21-22];Cas12a 可以在 crRNA 引导下识别 PAM,识别到正确序列才会形成封闭的 R 环,因此编辑准确性相对 Cas9 有了较大提高,其脱靶率也有所降低^[12-13,23]。

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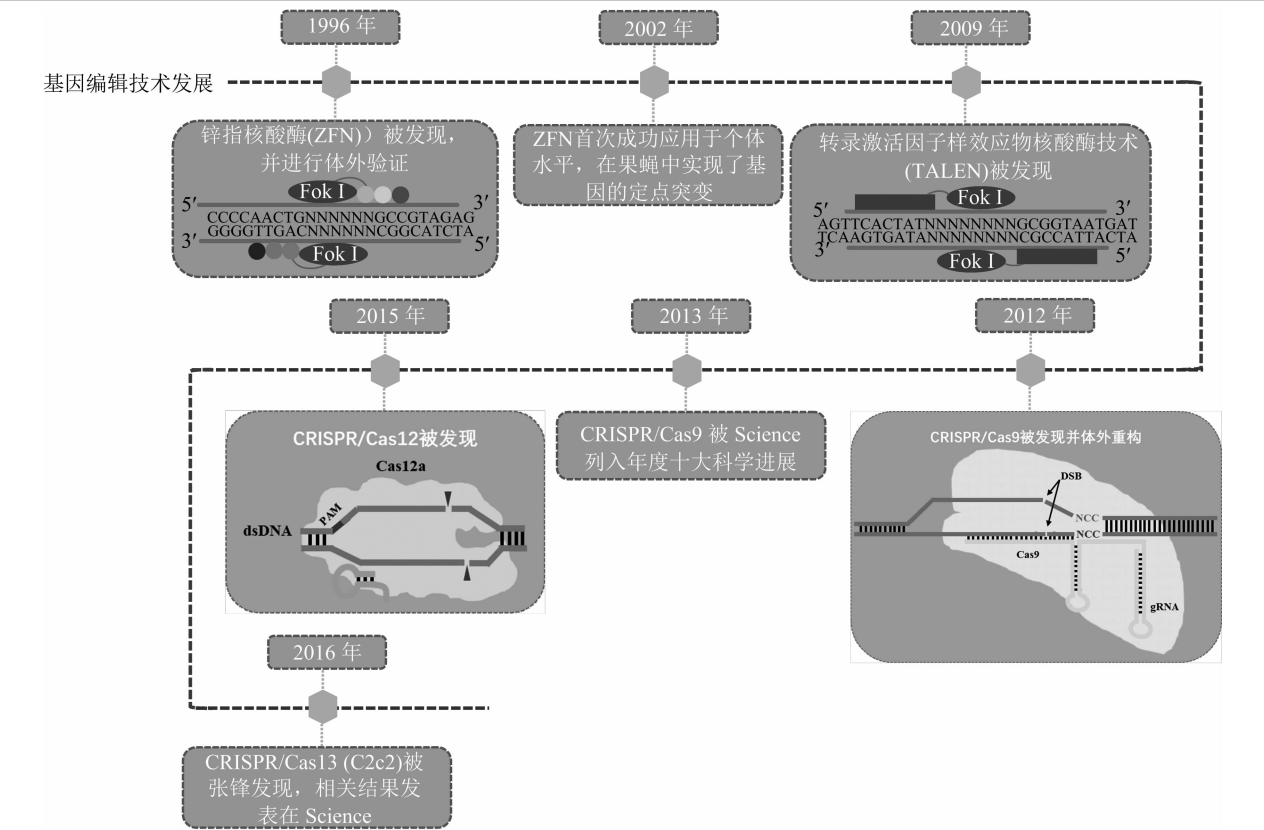


图1 基因编辑技术的发展简介

表 1 基因编辑技术对比汇总

基因编辑技术	目标识别效率	组成成分	识别模式	编辑效率 (%)	脱靶率 (%)
ZFNs	高	锌指结构域,非特异的 FokI 核酸酶结构域	蛋白 - DNA	<30	0.01
TALENs	最高	TALE DNA 结合结构域,非特异的 FokI 核酸酶结构域	蛋白 - DNA	100	0
Cas9	高	crRNA, tracrRNA, Cas9 蛋白	RNA - DNA	<80	0.04 ~ 0.60
Cas12a	很高	crRNA, CpfI 蛋白	RNA - DNA	90	0.40
参考文献	[24]	[10,13,25 - 26]	[10,13,25 - 26]	[27 - 32]	[33 - 36]

CRISPR/Cas9 及 Cas12a 是目前基因编辑技术中应用最为广泛的 2 种技术,在水稻产量、品质、生物胁迫及非生物胁迫性状关键基因的分子遗传功能解析和目标性状的精准改良上已成熟应用(表 2)。

2 CRISPR/Cas 在水稻中的研究进展

2.1 产量性状

水稻产量由单株穗数、每穗粒数、粒型及粒重等多个性状综合组成^[112-113]。目前已有 29 个产量相关基因被编辑,其中 4 个基因对产量起正调控作用,其他 25 个基因均作为负调控因子发挥作用。Li 等对每穗粒数 *Gn1a*、粒型 *DEP1*、粒重 *GS3* 及理想株型基因 *IPA1* 定点突变, *gn1a*、*dep1* 和 *gs3* 的 T2 突变

体出现穗粒数增加、粒型变大,成功提高了产量^[37]。其他研究分别对 *Gn1a&DEP1*、*GS3&DEP1*、*GS3*、*GS2/GRF4* 及 *SPL16/qGW8* 等开展基因编辑,在穗粒数、粒型、粒重等性状上调控产量,改善农艺性状同时提高产量^[39,42,44,47-48]。开展多基因同时编辑也可快速调控产量,Xu 等同时对负调控粒重、粒型基因 *GS3*、*GW2*、*GW5* 及 *TGW6* 进行编辑,快速改良突变体粒重及产量^[41]。Zhou 等同时编辑 *GS3*、*Gn1a* 及 *GW2*,相关突变体出现籽粒变大、穗粒数增多从而提高水稻产量^[38]。Zeng 等同时编辑 *PIN5b*、*GS3* 和 *MYB30*,突变体兼顾了高产和耐冷性^[43]。非产量调控基因突变也会提高产量,Miao 等获得 ABA 受体突变体 *pyll/4/6*,通过增加 31% 籽粒数量从而提高产量^[57],除此之外,对 *FWL4*、*SD1* (*OsGA20ox2*)

表 2 基因编辑技术在水稻产量、抗性及品质中的应用汇总

性状	调控性状	基因名称	调控方式	基因登录号	编辑方式	参考文献
产量	每穗粒数	<i>Gn1a</i>	负调控	Os01g0197700	Cas9	[37–39]
		<i>Gn1a</i>	负调控	Os01g0197700	Cas12	[40]
		<i>CKX4</i>	负调控	Os01g0940000	Cas12	[40]
		<i>CKX11</i>	负调控	Os08g0460600	Cas12	[40]
		<i>CKX9</i>	负调控	Os05g0374200	Cas12	[40]
	粒重、粒型	<i>GS3</i>	负调控	Os03g0407400	Cas9	[37–38,41–44]
		<i>GW5</i>	负调控	Os05g0187500	Cas9	[41]
	粒型	<i>DEP1</i>	负调控	Os09g0441900	Cas9、Cas12	[37,39,42,45–46]
		<i>GW2</i>	负调控	Os02g0244100	Cas9	[38,41]
		<i>GS2/GRF4</i>	负调控	Os02g0701300	Cas9	[47]
		<i>TGW6</i>	负调控	Os06g0623700	Cas9	[41]
		<i>SPL16/qGW8</i>	负调控	Os08g0531600	Cas9	[48]
		<i>CKX5</i>	负调控	Os01g0775400	Cas12	[40]
		<i>CKX7</i>	负调控	Os02g0220100	Cas12	[40]
		<i>IPA1</i>	负调控	Os08g0509600	Cas9	[37]
		<i>PIN5b</i>	负调控	Os08g0529000	Cas9	[43]
		<i>FWL4</i>	负调控	Os03g0829900	Cas9	[49]
	蔗糖转运	<i>SWEET11</i>	正调控	Os08g0535200	Cas9	[50]
	株高	<i>SD1/GA20ox2</i>	负调控	Os01g0883800	Cas9	[51–52]
		<i>CAO1</i>	负调控	Os10g0567400	Cas12	[32,53]
	花器官发育	<i>DEP</i>	正调控	Os07g0108900	Cas12	[54]
	芒伸长、气孔密度	<i>EPFL9</i>	负调控	Os01g0824500	Cas12	[55–56]
	外卷叶	<i>ROC5</i>	负调控	Os02g0674800	Cas12	[45–46,54]
	ABA 受体	<i>PYL1</i>	负调控	Os01g0827800	Cas9	[57]
		<i>PYL4</i>	负调控	Os03g0297600	Cas9	[57]
		<i>PYL6</i>	负调控	Os05g0473000	Cas9	[57]
		<i>PYL9</i>	负调控	Os06g0562200	Cas9	[58]
		<i>MYB30</i>	负调控	Os02g0624300	Cas9	[43]
	NBS–LRR 蛋白	<i>RGA1</i>	正调控	Os05g0333200	Cas9	[42]
	干旱、低温胁迫	<i>PDS</i>	负调控	Os03g0184000	Cas12	[45,54]
品质	直链淀粉含量	<i>Wx</i>	正调控	Os06g0133000	Cas9	[59–62]
		<i>Wxb</i>	负调控	Os06g0133000	Cas9	[63]
		<i>SBEIIb</i>	正调控	Os02g0528200	Cas9	[64]
	蛋白含量、直链淀粉含量	<i>AAP6/10</i>	负调控	Os01g0878700	Cas9	[65]
				Os02g0722400	Cas9	[65]
	油酸浓度	<i>FAD2</i>	负调控	Os02g0716500	Cas9	[66]
	淀粉含量	<i>ISA</i>	正调控	Os08g0520900	Cas9	[67]
	植酸含量	<i>ITPK</i>	正调控	Os03g0726200 等	Cas9	[68]
	β -胡萝卜素	<i>Or</i>	负调控	Os06g0187000	Cas9	[69]
	香味	<i>BADH2</i>	负调控	Os08g0424500	Cas9	[70–71]
	粒形	<i>GS9</i>	负调控	Os09g0448500	Cas9	[72]
		<i>GL3.2</i>	正调控	Os03g0417700	Cas9	[71]
	干旱、低温胁迫	<i>PDS</i>	负调控	Os03g0184000	Cas12	[73]
	抗性相关	<i>BEL</i>	负调控	Os03g0760200	Cas12	[73]

表 2(续)

性状	调控性状	基因名称	调控方式	基因登录号	编辑方式	参考文献
生物胁迫	稻瘟病抗性	<i>ERF922</i>	负调控	Os01g0752500	Cas9	[74]
		<i>SEC3A</i>	负调控	Os03g0625700	Cas9	[75]
		<i>ALB1/RSY1</i>	负调控	—	Cas9	[76]
		<i>Pi21</i>	负调控	Os04g0401000	Cas9	[77–78]
	白叶枯病抗性	<i>SWEET13</i>	负调控	Os12g0476200	Cas9	[79]
		<i>SWEET11/8N3</i>	负调控	Os08g0535200	Cas9	[80]
		<i>SWEET14</i>	负调控	Os11g0508600	Cas9	[81]
		<i>Xa13/SWEET11</i>	负调控	Os08g0535200	Cas9/Cas12	[82–83]
	稻曲病抗性	<i>USTA/UoSLT2</i>	负调控	—	Cas9	[84]
	生物胁迫相关	<i>MPKs</i>	负调节	Os10g0533600 等	Cas9	[85–86]
非生物胁迫	ABA 响应/干旱胁迫	<i>SAPK2</i>	正调控	Os07g0622000	Cas9	[87]
		<i>ERA1</i>	负调控	Os01g0737800	Cas9	[88]
		<i>PYL9</i>	负调控	Os06g0562200	Cas9	[58]
	干旱、低温胁迫	<i>PDS</i>	负调控	Os03g0184000	Cas12	[83,89]
	半卷叶	<i>SRL1</i>	负调控	Os07g0102300	Cas9	[90]
		<i>SRL2</i>	负调控	Os03g0308200	Cas9	[90]
	盐胁迫	<i>RAV2</i>	正调控	Os01g0141000	Cas9	[91]
		<i>RR22</i>	负调控	Os06g0183100	Cas9	[92]
		<i>OTS1</i>	正调控	Os06g0487900	Cas9	[93]
		<i>DST</i>	负调控	Os03g0786400	Cas9	[94]
		<i>PQT3</i>	负调控	Os10g0431000	Cas9	[95]
		<i>EPSPS</i>	负调控	Os06g0133900	Cas9	[96]
	抗性相关				Cas12	[83]
		<i>FTIP1e</i>	负调控	Os07g0483500	Cas9	[97]
		<i>ALS</i>	负调控	Os02g0510200	Cas9、Cas12	[83,97–103]
		<i>MKK5</i>	正调控	Os06g0191300	Cas12	[104]
		<i>NRAMP</i>	负调控	Os07g0258400	Cas12	[83]
		<i>RLKs</i>	正调控	Os02g0176100 等	Cas12	[105]
		<i>BELs</i>	正调控	Os03g0760000 等	Cas12	[105]
		<i>MIR535</i>	负调控	osa – MIR535	Cas9	[106]
	镉积累	<i>Nramp5</i>	负调控	Os07g0257200	Cas9	[107–108]
	开花期,成熟期	<i>Hd2/4</i>	负调控	Os07g0695100/	Cas9	[109]
				Os07g0261200		
	低温胁迫	<i>Ann3</i>	正调控	Os05g0382600	Cas9	[110]
	衰老	<i>SAP</i>	正调控	AB734097	Cas9	[111]

及 *PYL9* 进行定点突变也可不同程度提高产量^[49,51–52,58]。然而产量正调控基因如 *RGAI*、*SWEET11* 被编辑后会分别引起植株极端矮化及灌浆功能受损,从而减产^[42,50]。

CRISPR/Cas12a 在水稻产量调控中应用也日渐增多,Malzahn 等对粒长基因 *DEP1* 和叶片卷曲度基因 *ROC5* 进行敲除提高产量。对水稻 *PDS*、*DEP* 和 *ROC5* 基因所有靶点进行突变,能同时改良农艺性

状及抗性^[45,54],而将叶绿素 a 加氧酶基因 *CAOI* 靶向敲入水稻中,突变体的产量及品质降低^[32,53],Zheng 等同时利用 Cas9 和 Cas12a 对细胞分裂素家族基因 *OsCKX1–11* 进行编辑,获得了农艺性状及产量均有提升的单基因及多基因突变体,Cas9 的编辑效率为 26.9%~90.0%,有 8 个基因的编辑效率高于 50.0%,而 Cas12a 的编辑效率为 36.8%~100%且 9 个基因的编辑效率高于 60%,Cas12a 的

多基因编辑效率高于 Cas9 (91.7% > 54.5%)^[40]。上述研究表明,对负调控基因进行定点突变后可快速获得目标性状改善的编辑系,然而有些基因突变后会对其他性状产生不利影响,因此多重基因编辑技术的应用为多个性状同时改良提供了方案和可行性,在开展基因编辑时 Cas12a 的编辑效率及稳定性均高于 Cas9。

2.2 品质性状

稻米品质是水稻商业价值的核心卖点,受到多个基因综合调控,已有大量基因被证实直接或间接调控稻米品质,可用于定向改良直链淀粉含量、蛋白、香味等性状。目前有 13 个品质基因被编辑,其中 4 个基因(*ISA*、*ITPK*、*GL3.2* 和 *BEL*)正调控稻米品质,其他基因负调控稻米品质。*Wx* 基因的基因编辑位置差异对稻米品质影响不同,对 *Wx* 基因功能位点进行突变,可以将直链淀粉含量降至与糯稻相似,在不影响产量前提下改良稻米品质^[59-61];对 *Wx^b* 基因启动子转录因子结合位点进行突变,获得新的 *Wx* 等位基因并获得直链淀粉含量不同程度降低的突变体,改良了稻米品质^[62]。*fad2* 突变体的油酸浓度提高,*gs9* 突变体的粒型、垩白及外观等品质显著改善,*or* 突变体籽粒 β -胡萝卜素含量显著提高,*isa* 突变体总淀粉含量下调,*ZmPsy* 和 *SSU-crtl* 突变体水稻的籽粒类胡萝卜素含量提高,*badh2* 突变体籽粒产生香味,均可改良稻米品质^[66-67,69-70,72,114]。多基因同时突变可综合提升水稻性状,如 *app6/10* 双突变体的直链淀粉、蛋白及谷蛋白含量均下调^[65];细胞色素 P450 家族基因(*Os03g0603100*、*Os03g0568400* 和 *GL3.2*)和香味基因 *BADH2* 同时突变后改良稻米香味并提高产量^[71]; *PDS* 和 *BELs* 同时突变稳定提高水稻产量和品质^[73]。对正调控基因进行突变,有助于理解基因在稻米品质改良中的作用,敲除 *Wx^b* 第一内含子、*SBEIIb* 进行精准敲除,突变体直链淀粉含量上调,且引起营养特性改变^[63-64]。Jiang 等突变 *ITPK1-6*,降低籽粒植酸含量然而却提高无机磷含量,不利于水稻生长繁殖,证实该基因对水稻正常生长发育的重要性^[68]。对负调控稻米品质基因的敲除加速了优质水稻品种选育的进程,与其他产量性状相关基因同时编辑,有望在保证产量的同时提高品质。

2.3 生物胁迫

水稻生长过程对生物胁迫的抗性也可利用基因编辑方法改良,对抗性相关基因 *MPK1*、*MPK2*、

MPK5 和 *MPK6* 的敲除能够提高抗病性^[85-86]。*ERF922*、*SEC3A*、*ALB1*、*RSY1* 和 *Pi21* 敲除后,突变体对稻瘟病的抗性提高,同时农艺性状也得到改良^[74-78]。*SWEET13* 和 *SWEET14* 敲除后突变体对白叶枯病菌的抗性提高,且 *SWEET14* 突变体无产量损失^[79,81]。对 *SWEET11/8N3/Xa13* 编码区及启动子区定点突变,也能提高水稻对白叶枯病的抗性^[80,82]。Liang 等对稻曲病相关基因 *USTA* 和 *UvSLT2* 进行编辑,显著提高了水稻对稻曲病抗性^[84]。利用 Cas12a 低水平同源性核酸酶 *MAD7* 对水稻基因 *EPSPS*、*NRAMP*、*PDS*、*Xa13* 及 *ALS* 等进行多重基因敲除,同步提升了突变体的品质、除草剂及白叶枯病抗性^[83]。Wang 等利用 Cas12a 对受体样激酶(*OsRLK*)相关基因(*OsRLK-798*、*OsRLK-799*、*OsRLK-802* 和 *OsRLK-803*)及 CYP81A 家族基因(*OsBEL-230*、*OsBEL-240*、*OsBEL-250* 和 *OsBEL-260*)开展多重基因编辑,获得了阳性植株,相关突变体调控了水稻的抗逆性^[105]。

对水稻负调控抗性基因进行敲除或替换可快速改善目标性状,提升水稻抗性,然而有些编辑以损失产量为代价^[109],而有些编辑在不损害甚至优化农艺性状前提下同步改善水稻品质^[77-78,81,90,95],因此在进行水稻抗性改良时需要考虑基因对水稻的综合影响,从而制定相应编辑策略。

2.4 非生物胁迫

水稻生长发育过程中会受到多种非生物胁迫的影响,如干旱、低温、盐、除草剂等,相关基因的大量挖掘促进了基因编辑在水稻非生物胁迫中的应用,目前有 24 个相关基因被编辑,其中 8 个基因起正调控作用,即 *Ann3*、*OTS1*、*RAV2*、*SAPK2*、*BELs*、*MKK5*、*RLKs* 和 *SAP*。在水稻抗旱性方面,*PYL9*、*ERA1*、*PDS*、半卷叶基因(*SRL1* 和 *SRL2*)和 *MIR535* 的基因突变会增强突变体的抗旱性^[58,88-90,106]。而敲除 *SAPK2* 和 *SAP* 基因后,突变体对干旱胁迫和活性氧更敏感,农艺性状显著下降^[87,111]。在水稻响应盐胁迫方面,敲除水稻中的 *RR22*、*DST* 及 *PQT3* 基因,可显著提高耐盐性且不影响农艺性状^[92,94-95],但对 *OTS1* 编码区及 *RAV2* 启动子的 GT-1 元件突变后,其耐盐性下降^[91,93]。在水稻抗除草剂方面,通过将 *EPSPS*、*ALS* 突变基因敲入,或点突变野生型基因(*ALS*、*FTIP1e*)均能使水稻获得除草剂抗性^[96-103]。

除此之外,敲除 *Nramp5* 能降低 Cd 的积累且不影响产量^[107-108]; *Ann3* 敲除后对低温的耐受性降

低^[110];敲除 *MKK5* 后,突变体抗逆性降低^[104];同时突变抽穗基因 *Hd2*、*Hd4* 和 *Hd5* 后突变体开花期及成熟期提前有助于逃避胁迫^[109],然而农艺性状受到较大影响,因此在应用时可进行单基因编辑,从而消除对产量的损害。

3 CRISPR/Cas 的技术展望

基因编辑技术为生命科学带来重大进展,然而几种技术的脱靶率及特异性问题仍需重点关注。研究人员优化了相关技术,开发了 DB-PACE 法从而降低基因编辑工具酶的脱靶效应,大大提高 TALEN 核酸酶的 DNA 结合能力和切割特异性^[115];开发出提高 Cas9 基因编辑和碱基编辑特异性的选择性核输出抑制剂(SINE)^[116];Sheng 利用脐介导 CRISPR/Cas12a 系统,通过互补碱基配对引起的邻近效应来加速整个激活链的形成,从而提高 Cas12a 系统的特异性^[117]。除此之外,CRISPR 系统的 sgRNA 的优化、PAM 修饰、crRNA 优化及 Cas 蛋白突变体挖掘也会进一步提高编辑范围及特异性并降低脱靶率^[12,46,104,118-120]。此外 Cas12a 蛋白表现出对低温敏感的特征,目前 Cas12a 突变体是解决该问题的主要方式,而引起低温敏感的分子机制尚不明确。上述问题的解决,将大大提高基因编辑水平,对目标基因进行定向编辑,产生无外源 DNA 插入的新品种,从而加快育种速度、缩短育种年限。

水稻产量、抗性和品质相关基因的挖掘及分子机理解析,有助于更全面了解基因功能,目前基因编辑主要集中在编码区,有少量研究是编辑启动子的转录结合位点实现性状调控的。已有研究表明,DNA 结构本身,如拓扑异构结构等也会影响基因表达水平^[121],因此,未来也可能作为基因编辑靶点,增加目标性状精准改良的可能性。随着人工智能的发展,AlphaFold 等技术对蛋白预测精准度提高,越来越多的蛋白结构被预测,对目标基因的模拟突变有助于挖掘关键碱基序列,可进行靶向预测,实现新的目标性状的改良已经成为可能。相信随着基因编辑技术的不断完善、生物信息学和人工智能的不断发展,水稻育种将会迅猛发展。

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肠道微生物对鸡免疫功能的影响综述

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摘要:鸡肠道微生物群是一个庞大又复杂的生态系统,其内的基因可能比宿主自身多 100 倍,鸡肠道微生物在机体内参与营养物质的吸收与消化,维持肠道内稳态有利于机体健康生长,同时也是维持机体内环境稳态的先天性防御屏障。由此可见,鸡肠道微生物的聚集可对其机体各系统产生深远的影响,尤其是肠道免疫系统,即天然免疫(innate immunity)和适应性免疫(adaptive immunity)。鸡肉是人类高效生产蛋白质的主要提供者之一,因此鸡肠道健康问题的解决迫在眉睫。另外,当前抗生素在国内外全面禁用,因此深入了解肠道微生物对家禽免疫的影响十分重要。本文主要阐述了肠道微生物对鸡免疫功能的影响,包括肠道微生物的建立、影响鸡肠道微生物的因素、肠道微生物群的环境因素以及家禽的免疫系统等,并进一步从肠道微生物对各种免疫细胞的调节作用和代谢产物(短链脂肪酸、胆汁酸及色氨酸)等肠道微生物代谢物对机体免疫细胞的调控作用及作用机制等方面阐述肠道微生物对鸡免疫功能的影响。旨在为未来研究疾病易感性、疫苗应答、家禽健康和生产力等方面提供参考。

关键词:鸡;肠道微生物;肠道免疫系统;免疫细胞;代谢产物

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肠道是机体与外界环境接触最密切的组织,其不仅仅是消化器官,还是体内最大的免疫器官。肠道中存在着一个由庞大而复杂的微生物群组成的微生态系统,研究表明这一微生态系统中每一种微

生物都有 2 000 个基因,组成了 200 万个基因,这比鸡的估计基因数量(大约 17 000 个)多 100 倍^[1]。研究表明,与哺乳动物相比,鸡肠道较短,食物在其中的保留时间不超过 3.5 h,因此鸡肠道微生物群的微生物多样性与其他动物相比较低^[2]。Wei 等通过对鸡肠道微生物进行宏基因组数据分析共发现 900 个种水平的分类操作单元(OTUs),13 个门和 117 个属,其中:门类以厚壁菌门(70%)、拟杆菌门(12.3%)和变形菌门(9.3%)为主,占总微生物 90% 以上,主要是厌氧菌;而属类以梭状芽孢杆菌属、反胃球菌属、乳杆菌属和拟杆菌属为主^[3]。

肠道微生物受到日龄、日粮和饲养环境等的影响,并与宿主形成共生关系。近年来,随着高通量

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