CRISPR, animals, and FDA oversight: Building a path to success

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Technological advances, such as genome editing and specifically CRISPR, offer exciting promise for the creation of products that address public health concerns, such as disease transmission and a sustainable food supply and enable production of human therapeutics, such as organs and tissues for xenotransplantation or recombinant human proteins to treat disease. The Food and Drug Administration recognizes the need for such innovative solutions and plays a key role in bringing safe and effective animal biotechnology products to the marketplace. In this article, we (the Food and Drug Administration/Center for Veterinary Medicine) describe the current state of the science, including advances in technology as well as scientific limitations and considerations for how researchers and commercial developers working to create intentional genomic alterations in animals can work within these limitations. We also describe our risk-based approach and how it strikes a balance between our regulatory responsibilities and the need to get innovative products to market efficiently. We continue to seek input from our stakeholders and hope to use this feedback to improve the transparency, predictability, and efficiency of our process. We think that working together, using appropriate science- and risk-based oversight, is the foundation to a successful path forward.

CRISPR | animals | FDA | CVM | genome editing

Last December 2019, scientists gathered at the National Academy of Sciences colloqium, "Life 2.0: The Promise and Challenge of a CRISPR Path to a Sustainable Planet," to present research and discuss breakthrough genome-editing technology with the potential to have wide-ranging societal benefits. The presentations and discussions addressed the great promise of genome editing, and CRISPR in particular, to provide solutions to myriad challenges.

The Food and Drug Administration's (FDA's) Center for Veterinary Medicine (CVM) has long recognized and supports the potential of genome editing in animals to deliver transformative solutions to challenges in both human and veterinary medicine, agriculture, and more. For example, researchers are using genome editing to create alterations that target diseases with a significant impact on agricultural production, such as African swine fever or bovine respiratory disease (1-3), that prevent serious human diseases such as dengue or malaria (4, 5), and that enable production of safer xenotransplantation products for humans with less potential for immune rejection (6-9). Genomic alterations also offer unique solutions to agricultural production challenges, such as the development of animals with increased food yield (10, 11) or animals with improved tolerance to certain environmental conditions, such as warmer weather conditions (12).

While we (the FDA/CVM) are enthusiastic about the possibilities, we also recognize that new technological advancements, like genome editing, and the products they help create need to meet the standards for safety and effectiveness. The research community and the industry that are using advanced techniques like CRISPR to develop intentional genomic alterations (IGAs) in animals share the enthusiasm for using existing and newer biotechnology techniques to produce innovative products. They are eager to move forward with the fewest hurdles possible to provide breakthrough solutions. This sense of excitement and urgency can lead to a view that regulation hampers progress and that regulators are unjustifiably cautious and risk-averse. We believe products created using new technologies should strike a careful balance between fostering innovation while ensuring the products work and are safe.

State of the Science

Among the reasons that regulation is necessary is the fastchanging state of the science. Science is rapidly evolving and technological capabilities now exist that we never imagined in the past. Genome-editing technology, such as CRISPR/Cas9, has revolutionized the ability to make targeted changes to an animal's genome. However, as with any new technology, there are limitations and, despite its use for over a decade, there are still a lot of unknowns. What is known is that error can occur, such as off-target alterations due to mistargeting by the guide RNA (gRNA) (13–15). Furthermore, genome editing at the target site is not always precise due to different modes of DNA repair machinery, including nonhomologous end-joining resulting in variable length indels. Indels can promote internal ribosomal entry, produce aberrant proteins, or induce exon skipping by disruption of the alternative splicing mechanism (16-18). Unintended on-target effects, such as large-scale deletions and complex genomic rearrangements, as well as unintended integration of donor plasmid and multiple template insertions, have also been observed in different cell types, including human embryos (19–29). These errors could result in loss of heterozygosity, genome instability, or the unintended activation/inactivation of genes. There has been tremendous work in the field to mitigate these unintended outcomes by optimizing experimental design [e.g., improved gRNAs (30–35), limiting Cas nuclease exposure (36-38)], engineering new genome-editing systems with improved nuclease fidelity, or developing alternatives to DNA cleavage-induced editing (39-41). Furthermore, researchers are

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also enabling better detection of these events through the development of novel, unbiased detection methods (42, 43).

Researchers have used several Cas9 proteins and variants with improved on-target specificity, such as SaCas9 (44, 45), CjCas9 (46), eSpCas9 (47), HFCas9 (48), HypaCas9 (49), and Sniper Cas9 (50). They have also generated a variety of CRISPR systems, such as Cas12a (Cpf1) (51), Cas13 (52), CAST (CRISPR-associated transposase) (53), or Cascade (54) to overcome the limitations of the CRISPR/Cas9 system. And they recently have used prime-editing (55) or base-editing systems (56, 57) to make single nucleotide changes without generating double-stranded DNA breaks. Researchers are also developing new variants of base editors with reduced off-target activities (58–62); recent studies suggest that some base editors result in off-target RNA, in addition to DNA, editing (63, 64), and off-target alterations in a gRNA-dependent but also in a random gRNA-independent manner (64, 65).

Various off-target detection methods are in development, and each has its own strengths and weaknesses (43). Researchers have developed several bioinformatics-based tools (66-73) to rapidly and efficiently predict potential off-target sites, which can be subsequently validated via methods such as PCR or sequencing. The major limitation associated with such targeted methods is that the criteria for selecting for off-targets can introduce bias and some errors may get overlooked. Unbiased biochemical and cell-based methods, such as GUIDE-seq (74), HTGTS (75), BLESS (76), IDLV (77), CIRCLE-seq (78), SITEseq (79), Digenome-seq (80), DISCOVER-seq (81), and CHANGE-seq (82), have been developed to assess off-target alterations at a genome-wide level. The limitations of these methods include complex protocols, applicability across cell types, and low sensitivity, among others. Whole-genome sequencing is also an effective unbiased method to detect alterations, including structural variants; however, it requires suitable controls (e.g., a high-quality reference genome or unedited controls for comparison) and when sequencing depth is low, the detection of low frequency (in bulk cell populations) and large or complex alterations can be challenging (64, 83-85).

For the detection of unintended on-target effects, a comprehensive on-target analysis, using methods such as long-range PCR or long-read sequencing, could identify large-scale unintended on-target effects that may go undetected using conventional methods, such as short-range PCR. Additional methods are also under development, such as UDiTas (86), to measure large deletions, inversions, and translocations.

Moving Beyond the Bench to a Commercial Setting

The specificity of the CRISPR/Cas system and other genomeediting tools will continuously improve over time with the rapidly growing body of knowledge in the field. In addition to the discovery of higher-fidelity nucleases, improvements include development of measurements and standards (e.g., standardized off-target detection methods, controls, and so forth), such as the effort led by the National Institute of Standards and Technology Genome Editing Consortium*, which are important for the characterization of potential commercial IGA products developed using genome editing. As such improvements are still under development, commercial developers ("developers") can employ careful experimental design (e.g., selection of a highfidelity nuclease, inclusion of proper controls, adequate characterization methods, and so forth) to mitigate any potential unintended effects.

In contrast to genome editing in somatic cells, IGAs made in the germline of animals will be passed on to their offspring along with any unintended on- and off-target alterations, whether beneficial or detrimental. While it is important for developers to identify unintended effects and be alert to their potential risks, the presence of unintended effects in a genome-edited animal does not mean that the IGA is necessarily unsafe or should not enter the market.

Both phenotypic and genotypic characterization of IGAs and their potential unintended effects are important because genetic changes can impact safety. Asking certain questions can help to determine whether any unintended alteration results in such an impact. For example, where is it located? Is it in a region with known biological importance or function that could have an impact on animal safety? Are there any identified biological or physiological impacts on animal health (e.g., differences in morbidity/mortality, disease prevalence/susceptibility, routine health observations, and so forth, between animals with the alteration and comparator animals)? Developers rely on phenotypic characterization not only to ensure that they have successfully produced the intended trait for commercialization, but also to evaluate any unintentional effects of the IGA and the impact of any unintended alterations. For example, some CRISPR/Cas9-mediated myostatin-deficient animals exhibit the intended double-muscling phenotype but also exhibit unintended effects, such as stillbirth, early-stage death, spinal deformity, and abnormal fat, sugar, and protein metabolism (87-89). While it might seem that detrimental changes to the genome would result in a product that is not viable for the commercial market or would obviously impact animal health and well-being, changes that impact safety are not always so evident. For example, genetic changes in animals at certain receptors may increase susceptibility to other viruses, e.g., genetic alteration in the chemokine receptor CCR5 intended to yield protection against HIV infection may increase the risk of developing West Nile virus infection (90, 91). Tumor suppressor genes may be affected by CRISPR/Cas, as shown with p53, increasing the potential risk for cancer (92, 93). There also are other factors to consider aside from animal safety concerns, such as whether the IGA or any unintended alterations impact gene/protein expression, resulting in a change in the composition or nutritional content of food from the animals (if the animals will be used as food). For example, IGAs and any unintended alterations that result in changes to the composition of milk could impact the health of humans, and in particular infants. Identification of potential hazards is facilitated by the combination of both genotypic and phenotypic analyses, offering focus for the characterization of the resulting type expressed by the genetic alteration in the animal and its potential contribution to animal or human risk.

Science-Based, Risk-Appropriate Regulation

We are committed to pursuing an approach that strikes a careful balance between sufficient oversight to ensure products are safe and achieve their intended effect and minimizing regulatory burden. The goals of this approach are to protect consumers, enable developers to bring innovative products to market, and expend the FDA's limited resources prudently. In practice, what a risk-based approach means is that where the risk posed by the potential hazard(s) resulting from an IGA is low, we do not expect developers of those products to submit and obtain FDA approval of an application in order to market their product. Our assessment of the potential risk profile of a product is not based simply on the technology used (e.g., genome editing or recombinant DNA technology) or the size or type of the intended genomic alteration (e.g., single base pair changes versus large deletions; insertions versus deletions) but rather also on factors, such as the intended use, characteristics of the IGA, preexisting knowledge regarding safe use, and animal containment level. Furthermore, the FDA does not regulate based on whether a product is a genetically modified organism (GMO).

^{*83} Fed. Reg. 1335, 1335-36 (January 11, 2018).

Agricultural products containing foreign DNA and called GMO are ubiquitous[†] and all of those we are aware of on the market are safe. People and animals have been consuming them for decades. Since these foods were introduced in the 1990s, research (94) has shown that they are just as safe as non-GMO foods. Moreover, altering animals with techniques that result in incorporation of "foreign" DNA in the animal's genome, while admitting some additional risk, allows for a greater range of alterations that can produce the most innovative and beneficial qualities, such as disease resistance.

Regardless of the technology used to create the IGA, we evaluate based on risk. Where the risk is lowest, we do not expect developers to come to the FDA prior to marketing either with an approval application or with any risk data or even a notification. These types of IGAs include those in highly contained laboratory animals intended for research, such as mice and rats. The FDA believes that these IGAs are either already adequately regulated or that they pose negligible risk because the animals containing them are not likely to end up in the food supply or to get out into the environment. For those products that do not fit into this lowest risk category, the FDA/CVM may not expect developers to submit an application for approval in order to market their product if we review product risk data and conclude that the product is, in fact, low risk. Such products currently include IGAs in animals of foodproducing species intended for use as models of human disease and could potentially include IGAs in animals that are for use as food.

For those products that may pose greater risks and that we, therefore, expect to go through the FDA approval process, the FDA/CVM is committed to streamlining that process so that it functions efficiently and transparently, thereby enabling developers to have a roadmap of the FDA/CVM's data and information submission expectations. Clarity about the process will help IGA sponsors to make product development plans well in advance and to prepare high-quality FDA/CVM submissions that allow the approval process to operate most efficiently without the delays resulting from incomplete submissions.

Among the steps we have taken to support this goal is establishment of the Veterinary Innovation Program (VIP; https:// www.fda.gov/animal-veterinary/animals-intentional-genomicalterations/vip-veterinary-innovation-program). The VIP is available for developers of certain innovative products, including most IGAs in animals. It offers benefits, including a dedicated review team, the ability to stop and restart the review clock, pre- and post-review feedback, hands-on assistance, and senior management involvement. The goal of the VIP is to facilitate innovative animal product advancements by providing greater certainty in the regulatory process and supporting an efficient and predictable pathway to approval. We understand that for first time sponsors, who are often small start-up companies or academically based research initiatives, the approval process can be difficult to understand and plan for; the VIP is intended to help them through the process. As of the date of writing, the FDA/CVM has 25 products enrolled in the program and this number is continuing to grow.

FDA/CVM's Steps to Building a Path to Success

We intend to publish updated guidance for industry in keeping with our goal of greater transparency. We plan to make a number of changes in response to the feedback we have already received and continue to receive from academic researchers, small biotech companies, and other stakeholders, many of whom are currently developing IGAs in animals. In the meantime, we are continuing to engage with product developers early and often about their IGA products and how they can prepare for the approval process so they can successfully achieve product approval in the least amount of time possible.

One way we are engaging with stakeholders is through a series of outreach meetings. While we had hoped to hold in-person meetings in the spring/summer of this year, due to the COVID-19 pandemic we are planning to hold meetings later, on-line. Several stakeholders suggested that they would find case-study examples helpful to understanding how the FDA's regulatory program works in practice and the data the FDA would expect for hypothetical but representative products, so we have prepared several case studies of hypothetical products that we walk through in a webinar (https://www.fda.gov/animal-veterinary/animalsintentional-genomic-alterations/fda-cvm-animal-biotechnologywebinar-developers). We plan to collect feedback from the webinar and, depending on interest, follow the webinar with a series of small meetings to address the received feedback. We will also use the feedback we receive to revise the approach described in the case studies, as well as to inform our approach for existing and future guidance documents.

While we are planning to make changes that respond to comments and make the regulatory process more efficient, significantly, the statutory standards for approval and for environmental review will remain the same. IGAs in animals must be safe for the animal, safe for consumption (where relevant), and effective (i.e., the IGA does what the developer claims it will do), and the FDA/CVM must assess whether potential environmental impacts of an approval are significant, in accordance with the National Environmental Policy Act. However, the type and amount of data required to meet these standards may vary based on a product's risks. For example, if an IGA is in an animal of a food-producing species but will not be marketed for food use, the data expectations relating to food safety will be less than for an IGA in an animal that will be consumed.

Conclusions

The FDA/CVM, those developing IGAs in animals, and consumers each may have a different perspective. Ultimately, we believe that we share the same end goal: The availability of innovative products that can improve human and animal health, animal well-being, and food production and quality. Appropriate, science-based, and risk-based regulation is key to realizing this goal and building a path to success. We are eager to hear from those developing these products about the innovative solutions they are creating to address the challenges we face.

Data Availability. There are no data underlying this work.

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- S. Shanthalingam et al., Precise gene editing paves the way for derivation of Mannheimia haemolytica leukotoxin-resistant cattle. Proc. Natl. Acad. Sci. U.S.A. 113, 13186–13190 (2016).
- M. V. Borca, L. G. Holinka, K. A. Berggren, D. P. Gladue, CRISPR-Cas9, a tool to efficiently increase the development of recombinant African swine fever viruses. *Sci. Rep.* 8, 3154 (2018).
- 3. S. G. Lillico et al., Mammalian interspecies substitution of immune modulatory alleles by genome editing. *Sci. Rep.* 6, 21645 (2016).
- A. Buchman et al., Broad dengue neutralization in mosquitoes expressing an engineered antibody. PLoS Pathog. 16, e1008103 (2020).
- Y. Dong, M. L. Simões, E. Marois, G. Dimopoulos, CRISPR/Cas9-mediated gene knockout of Anopheles gambiae FREP1 suppresses malaria parasite infection. *PLoS Pathog.* 14, e1006898 (2018).
- K. Fischer et al., Viable pigs after simultaneous inactivation of porcine MHC class I and three xenoreactive antigen genes GGTA1, CMAH and B4GALNT2. Xenotransplantation 27, e12560 (2020).
- L. Li et al., Establishment of gene-edited pigs expressing human blood-coagulation factor VII and albumin for bioartificial liver use. J. Gastroenterol. Hepatol. 34, 1851–1859 (2019).

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^tFor example, in 2018, 94% of the soybeans and 92% of the corn planted in the United States were genetically engineered (https://www.ers.usda.gov/data-products/adoption-of-genetically-engineered-crops-in-the-us.aspx).

- D. Niu et al., Inactivation of porcine endogenous retrovirus in pigs using CRISPR-Cas9. Science 357, 1303–1307 (2017).
- 9. K. Fischer et al., Efficient production of multi-modified pigs for xenotransplantation by 'combineering', gene stacking and gene editing. *Sci. Rep.* **6**, 29081 (2016).
- S. J. Du et al., Growth enhancement in transgenic Atlantic salmon by the use of an "all fish" chimeric growth hormone gene construct. *Biotechnology (N. Y.)* 10, 176–181 (1992).
- 11. C. Proudfoot et al., Genome edited sheep and cattle. Transgenic Res. 24, 147–153 (2015).
- S. Dikmen et al., The SLICK hair locus derived from Senepol cattle confers thermotolerance to intensively managed lactating Holstein cows. J. Dairy Sci. 97, 5508–5520 (2014).
- E. McGrath et al., Targeting specificity of APOBEC-based cytosine base editor in human iPSCs determined by whole genome sequencing. Nat. Commun. 10, 5353 (2019).
- Y. Fu et al., High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells. Nat. Biotechnol. 31. 822–826 (2013).
- P. D. Hsu et al., DNA targeting specificity of RNA-guided Cas9 nucleases. Nat. Biotechnol. 31, 827–832 (2013).
- R. Tuladhar et al., CRISPR-Cas9-based mutagenesis frequently provokes on-target mRNA misregulation. Nat. Commun. 10, 4056 (2019).
- H. Mou et al., CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. Genome Biol. 18, 108 (2017).
- S. Lalonde et al., Frameshift indels introduced by genome editing can lead to in-frame exon skipping. PLoS One 12, e0178700 (2017).
- E. Rayner et al., CRISPR-Cas9 causes chromosomal instability and rearrangements in cancer cell lines, detectable by cytogenetic methods. CRISPR J. 2, 406–416 (2019).
- M. Kosicki, K. Tomberg, A. Bradley, Repair of double-strand breaks induced by CRISPR-Cas9 leads to large deletions and complex rearrangements. *Nat. Biotechnol.* 36, 765–771 (2018).
- G. Cullot et al., CRISPR-Cas9 genome editing induces megabase-scale chromosomal truncations. Nat. Commun. 10, 1136 (2019).
- 22. B. V. Skryabin *et al.*, Pervasive head-to-tail insertions of DNA templates mask desired CRISPR-Cas9-mediated genome editing events. *Sci. Adv.* **6**, eaax2941 (2020).
- K. S. Hanlon et al., High levels of AAV vector integration into CRISPR-induced DNA breaks. Nat. Commun. 10, 4439 (2019).
- A. L. Norris et al., Template plasmid integration in germline genome-edited cattle. Nat. Biotechnol. 38, 163–164 (2020).
- A. Rezza et al., Unexpected genomic rearrangements at targeted loci associated with CRISPR/Cas9-mediated knock-in. Sci. Rep. 9, 3486 (2019).
- A. E. Young et al., Genomic and phenotypic analyses of six offspring of a genomeedited hornless bull. Nat. Biotechnol. 38, 225–232 (2020).
- G. Alanis-Lobato et al., Frequent loss-of-heterozygosity in CRISPR-Cas9-edited early human embryos. bioRxiv:10.1101/2020.06.05.135913 (5 June 2020).
- D. Liang et al., Frequent gene conversion in human embryos induced by double strand breaks. bioRxiv:10.1101/2020.06.19.162214 (20 June 2020).
- M. V. Zuccaro et al., Reading frame restoration at the EYS locus, and allele-specific chromosome removal after Cas9 cleavage in human embryos. *bioRxiv*:10.1101/ 2020.06.17.149237 (18 June 2020).
- C. R. Cromwell et al., Incorporation of bridged nucleic acids into CRISPR RNAs improves Cas9 endonuclease specificity. Nat. Commun. 9, 1448 (2018).
- D. D. Kocak *et al.*, Increasing the specificity of CRISPR systems with engineered RNA secondary structures. *Nat. Biotechnol.* 37, 657–666 (2019).
- R. Graf, X. Li, V. T. Chu, K. Rajewsky, sgRNA sequence motifs blocking efficient CRISPR/ Cas9-mediated gene editing. *Cell Rep.* 26, 1098–1103.e3 (2019).
- T. Scott, R. Urak, C. Soemardy, K. V. Morris, Improved Cas9 activity by specific modifications of the tracrRNA. Sci. Rep. 9, 16104 (2019).
- Y. Fu, J. D. Sander, D. Reyon, V. M. Cascio, J. K. Joung, Improving CRISPR-Cas nuclease specificity using truncated guide RNAs. *Nat. Biotechnol.* 32, 279–284 (2014).
- S. B. Moon, D. Y. Kim, J. H. Ko, J. S. Kim, Y. S. Kim, Improving CRISPR genome editing by engineering guide RNAs. *Trends Biotechnol.* 37, 870–881 (2019).
- S. Kim, D. Kim, S. W. Cho, J. Kim, J. S. Kim, Highly efficient RNA-guided genome editing in human cells via delivery of purified Cas9 ribonucleoproteins. *Genome Res.* 24, 1012–1019 (2014).
- 37. X. Liang et al., Rapid and highly efficient mammalian cell engineering via Cas9 protein transfection. J. Biotechnol. 208, 44–53 (2015).
- J. Cao et al., An easy and efficient inducible CRISPR/Cas9 platform with improved specificity for multiple gene targeting. Nucleic Acids Res. 44, e149 (2016).
- J. A. Doudna, The promise and challenge of therapeutic genome editing. Nature 578, 229–236 (2020).
- H. Manghwar, K. Lindsey, X. Zhang, S. Jin, CRISPR/Cas system: Recent advances and future prospects for genome editing. *Trends Plant Sci.* 24, 1102–1125 (2019).
- S. Q. Tsai, J. K. Joung, Defining and improving the genome-wide specificities of CRISPR-Cas9 nucleases. Nat. Rev. Genet. 17, 300–312 (2016).
- S. B. Moon, D. Y. Kim, J.-H. Ko, Y.-S. Kim, Recent advances in the CRISPR genome editing tool set. *Exp. Mol. Med.* 51, 1–11 (2019).
- H. Manghwar et al., CRISPR/Cas systems in genome editing: Methodologies and tools for sgRNA design, off-target evaluation, and strategies to mitigate off-target effects. Adv. Sci. (Weinh.) 7, 1902312 (2020).

- Y. Tan et al., Rationally engineered Staphylococcus aureus Cas9 nucleases with high genome-wide specificity. Proc. Natl. Acad. Sci. U.S.A. 116, 20969–20976 (2019).
- F. A. Ran et al., in vivo genome editing using Staphylococcus aureus Cas9. Nature 520, 186–191 (2015).
- E. Kim et al., In vivo genome editing with a small Cas9 orthologue derived from Campylobacter jejuni. Nat. Commun. 8, 14500 (2017).
- I. M. Slaymaker *et al.*, Rationally engineered Cas9 nucleases with improved specificity. *Science* 351, 84–88 (2016).
- B. P. Kleinstiver et al., High-fidelity CRISPR-Cas9 nucleases with no detectable genome-wide off-target effects. Nature 529, 490–495 (2016).
- J. S. Chen et al., Enhanced proofreading governs CRISPR-Cas9 targeting accuracy. Nature 550, 407–410 (2017).
- J. K. Lee *et al.*, Directed evolution of CRISPR-Cas9 to increase its specificity. *Nat. Commun.* 9, 3048 (2018).
- B. Zetsche et al., Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR-Cas system. Cell 163, 759–771 (2015).
- 52. O. O. Abudayyeh et al., RNA targeting with CRISPR-Cas13. Nature 550, 280-284 (2017).
- 53. J. Strecker et al., RNA-guided DNA insertion with CRISPR-associated transposases. *Science* **365**, 48–53 (2019).
- S. E. Klompe, P. L. H. Vo, T. S. Halpin-Healy, S. H. Sternberg, Transposon-encoded CRISPR-Cas systems direct RNA-guided DNA integration. *Nature* 571, 219–225 (2019).
- A. V. Anzalone et al., Search-and-replace genome editing without double-strand breaks or donor DNA. Nature 576, 149–157 (2019).
- G. T. Hess, J. Tycko, D. Yao, M. C. Bassik, Methods and applications of CRISPRmediated base editing in eukaryotic genomes. *Mol. Cell* 68, 26–43 (2017).
- H. A. Rees, D. R. Liu, Base editing: Precision chemistry on the genome and transcriptome of living cells. Nat. Rev. Genet. 19, 770–788 (2018).
- Y. Yu et al., Cytosine base editors with minimized unguided DNA and RNA off-target events and high on-target activity. Nat. Commun. 11, 2052 (2020).
- N. M. Gaudelli et al., Directed evolution of adenine base editors with increased activity and therapeutic application. Nat. Biotechnol. 38, 892–900 (2020).
- J. Grünewald et al., CRISPR DNA base editors with reduced RNA off-target and selfediting activities. Nat. Biotechnol. 37, 1041–1048 (2019).
- C. Zhou et al., Off-target RNA mutation induced by DNA base editing and its elimination by mutagenesis. Nature 571, 275–278 (2019).
- B. W. Thuronyi et al., Continuous evolution of base editors with expanded target compatibility and improved activity. Nat. Biotechnol. 37, 1070–1079 (2019).
- J. Grünewald et al., Transcriptome-wide off-target RNA editing induced by CRISPRguided DNA base editors. *Nature* 569, 433–437 (2019).
- E. Zuo et al., Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. Science 364, 289–292 (2019).
- S. Jin et al., Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. Science 364, 292–295 (2019).
- S. Bae, J. Park, J. S. Kim, Cas-OFFinder: A fast and versatile algorithm that searches for potential off-target sites of Cas9 RNA-guided endonucleases. *Bioinformatics* 30, 1473–1475 (2014).
- J. Listgarten *et al.*, Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. *Nat. Biomed. Eng.* 2, 38–47 (2018).
- A. McKenna, J. Shendure, FlashFry: A fast and flexible tool for large-scale CRISPR target design. *BMC Biol.* 16, 74 (2018).
- S. Xie, B. Shen, C. Zhang, X. Huang, Y. Zhang, sgRNAcas9: A software package for designing CRISPR sgRNA and evaluating potential off-target cleavage sites. *PLoS One* 9, e100448 (2014).
- F. Alkan, A. Wenzel, C. Anthon, J. H. Havgaard, J. Gorodkin, CRISPR-Cas9 off-targeting assessment with nucleic acid duplex energy parameters. *Genome Biol.* 19, 177 (2018).
- K. Labun et al., CHOPCHOP v3: Expanding the CRISPR web toolbox beyond genome editing. Nucleic Acids Res. 47, W171–W174 (2019).
- M. Haeussler et al., Evaluation of off-target and on-target scoring algorithms and integration into the guide RNA selection tool CRISPOR. Genome Biol. 17, 148 (2016).
- F. Heigwer, G. Kerr, M. Boutros, E-CRISP: Fast CRISPR target site identification. Nat. Methods 11, 122–123 (2014).
- S. Q. Tsai et al., GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nat. Biotechnol. 33, 187–197 (2015).
- R. L. Frock et al., Genome-wide detection of DNA double-stranded breaks induced by engineered nucleases. Nat. Biotechnol. 33, 179–186 (2015).
- N. Crosetto et al., Nucleotide-resolution DNA double-strand break mapping by nextgeneration sequencing. Nat. Methods 10, 361–365 (2013).
- X. Wang et al., Unbiased detection of off-target cleavage by CRISPR-Cas9 and TALENs using integrase-defective lentiviral vectors. Nat. Biotechnol. 33, 175–178 (2015).
- S. Q. Tsai et al., CIRCLE-seq: A highly sensitive in vitro screen for genome-wide CRISPRcas9 nuclease off-targets. Nat. Methods 14, 607–614 (2017).
- P. Cameron et al., Mapping the genomic landscape of CRISPR-Cas9 cleavage. Nat. Methods 14, 600–606 (2017).
- D. Kim et al., Digenome-seq: Genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. Nat. Methods 12, 237–243 (2015).
- B. Wienert, S. K. Wyman, C. D. Yeh, B. R. Conklin, J. E. Corn, CRISPR off-target detection with DISCOVER-seq. *Nat. Protoc.* 15, 1775–1799 (2020).
- C. R. Lazzarotto et al., CHANGE-seq reveals genetic and epigenetic effects on CRISPR-Cas9 genome-wide activity. Nat. Biotechnol., 10.1038/s41587-020-0555-7 (2020).

AGRICULTURAL SCIENCES

- 83. Y. Dong et al., Genome-wide off-target analysis in CRISPR-Cas9 modified mice and their offspring. G3 (Bethesda) 9, 3645-3651 (2019).
- 84. V. Iyer et al., No unexpected CRISPR-Cas9 off-target activity revealed by trio sequencing of gene-edited mice. PLoS Genet. 14, e1007503 (2018).
- 85. H. K. Lee, H. E. Smith, C. Liu, M. Willi, L. Hennighausen, Cytosine base editor 4 but not adenine base editor generates off-target mutations in mouse embryos. Commun. Biol. 3, 19 (2020).
- 86. G. Giannoukos et al., UDiTaS™, a genome editing detection method for indels and genome rearrangements. BMC Genomics 19, 212 (2018).
- 87. Y.-C. Yeh et al., Using CRISPR/Cas9-mediated gene editing to further explore growth and trade-off effects in myostatin-mutated F4 medaka (Oryzias latipes). Sci. Rep. 7, 11435 (2017).
- 88. R. Guo et al., Generation and evaluation of Myostatin knock-out rabbits and goats using CRISPR/Cas9 system. Sci. Rep. 6, 29855 (2016).
- 89. Z. He et al., Use of CRISPR/Cas9 technology efficiently targetted goat myostatin through zygotes microinjection resulting in double-muscled phenotype in goats. Biosci. Rep. 38, BSR20180742 (2018).
- 90. W. G. Glass et al., Chemokine receptor CCR5 promotes leukocyte trafficking to the brain and survival in West Nile virus infection. J. Exp. Med. 202, 1087-1098 (2005).
- 91. W. G. Glass et al., CCR5 deficiency increases risk of symptomatic West Nile virus infection. J. Exp. Med. 203, 35-40 (2006).
- 92. R. J. Ihry et al., p53 inhibits CRISPR-Cas9 engineering in human pluripotent stem cells. Nat. Med. 24, 939-946 (2018).
- 93. E. Haapaniemi, S. Botla, J. Persson, B. Schmierer, J. Taipale, CRISPR-Cas9 genome editing induces a p53-mediated DNA damage response. Nat. Med. 24, 927-930 (2018).
- 94. National Academies of Science, Engineering, and Medicine, Genetically Engineered Crops: Experiences and Prospects (National Academies Press, Washington, DC, 2016).

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