

Gene Editing: A double-edged sword

ABSTRACT

This essay is about intrinsic planning parts that can alternate the enlarge of the particle that regulates our herbal cycles, the genome. Since the 1990s, first-class enchantment has been a focal factor of research. It commenced with the genome undertaking and will proceed to be an ambassador for the foreseeable future. The functions are many, and they are anticipated to have a significant speculative effect as properly as extraordinarily extreme hazards. The genome altering development trends have opened up the technique to truly zero in on and exchange genomic progressions in nearly all eukaryotic cells, whether or not they are planned or bacterial nucleases. Genome editing has loosened up our capacity to grant an explanation for the role of inherited qualities in infection with the aid of accelerating the development of increased right smartphone and models of animal of psychotic cycles, and it has begun to exhibit extraordinarily top achievable in a variety of fields, ranging from indispensable look up to utilized biotechnology and biomedical research. The late boom in the development of programmable nucleases, such as zinc-finger nucleases (ZFNs), file activator-like effector nucleases (TALENs), and assembled reliably interspaced quick palindromic repeat (CRISPR)– Cas-related nucleases, has accelerated the transition of fee from idea to medical practice. We observe the purposes of their subordinate reagents as quality-changing units in a range of human illnesses, and anticipated future medicines, which focuses on eukaryotic cells and animal models, in this evaluation of modern-day advances in the three critical genome-modifying propels (ZFNs, TALENs, and CRISPR/Cas9). Finally, we have a framework for clinical primers to use genome adjusting phases for sickness therapy, as nicely as some of the difficulties encountered throughout implementation.

Keywords: Gene, CRISPR-theory, Talens, ZFN

INTRODUCTION

In mild of everything, existence is enormously perplexing and complicated. Nature, which has the honor of walking this complex dynamic, has survived the unnatural on various occasions. However, nature's ostensibly sumptuous creation, MAN, may also be a forerunner for the future. Due to genetic alteration, the possibility of assembling existence in the manner we want it has been given to us. With this comes a slew of hold-on pressures, the most necessary of which is whether or no longer or no longer coordinating life's preparations is legitimate. Organism line planning, or quality adjustment in early natural entities or microbe cells, aims to create a satisfactory genome. This genome will be impenetrable to the progressions that produce herbal illnesses, and specific traits are projected to end result in an unbelievably expanded physiology. They affect this improvement enormously. Plasmids have been utilized to produce gadgets for hereditary adjustment, which have been employed in opposition to microbial to change properties. The inquiry regional has been designing apparent zinc-finger nucleases (ZFNs)¹⁴ or meganucleases¹⁵ to instigate the quality DSBs at every particular DNA aim net website at some factor of the early improvement technology genome altering[1]. These nuclease structures choose a special conceivable to create fictitious proteins with adjustable gathering unambiguous DNA- limiting gaps, every linked to an unknown nuclease for aim cleavage, supplying scientists with essential equipment for genetic manipulation. Sixteen Following that, a new class of *Flavobacterium okeanokoites* (FokI) reactive vicinity derived from bacterial proteins recognized as file activator-like effectors (Stories) has published documents on similar genome enhancing freedoms. ¹⁷ With a distinctly high repeat rate, story-based programmable nucleases may moreover find out any DNA improvement of interest[2,3]. Regardless, the predominant troubles for file activator-like effector nucleases (TALEN) techniques are the modern-day nuclear cloning required for each new DNA target, as correctly as the terrible potential of genome keeping apart precisely assigned cells. ¹⁸ The

CRISPR-related ⁹ (Cas9) nuclease is an honestly discovered, steady superb enhancing stage derived from a bacterial flexible included watchman system[3]. ¹⁹ This structure, which makes use of an RNA-coordinated DNA cleavage module to alter the genome of eukaryotic cells, has

loomed as a promising preference to ZFNs and TALENs for actuating situated genetic modifications²⁰. The adaptable CRISPR/Cas9 innovation has been fast-growing its utilization in managing fantastic explanation, ranging from the genomic path of action correction or exchange to epigenetic and transcriptional adjustments, due to the reality it used to be as soon as at first used in a lengthy time as a machine to edit the genome in 2013.^{21,22} The method of programmable nucleases has sped the methods of price altering from thinking to medical practice, presenting experts with a beneficial resource for shifting from an actual point of view any fantastic in a large variety of cell types and species. Viruses, cardiovascular infections (CVDs), metabolic difficulties, crucial disfigurements of the immune system, hemophilia, muscular dystrophy, and the improvement of White platelet-based anticancer immunotherapies are all areas of the modern preclinical evaluation of genome modifying^[4]. Some of these processes have stepped beyond preclinical assessment and are now in present stage I/II scientific fundamentals. We seem to be at how the three elegant genome-modifying ranges (ZFN, TALENs, and CRISPR/Cas9) are being redesigned, as well as how their subordinate reagents are being used as quality-changing gadgets in more significant than a few human ailments and potential future therapies, with an emphasis on eukaryotic cells. Finally, we structure medical primers using genome altering phases for ailment therapy and some hurdles in inserting this improvement into action^[5,6].

EARLY ATTEMPTS THAT WERE MADE TO CORRECT GENETIC MISTAKES

They were utilizing tremendous adjusting to deal with sickness or alternate deposit dates to at minimal the Fifties and the divulgence of the twofold helix plan of DNA. During the twentieth century season of obtained openness, authorities grasped that the path of motion of bases in DNA is surpassed (for the most part) reliably from guardian to any type of family down the line adj minor minor that little in the social affair can imply the functionality amongst flourishing and turmoil^[7]. Certification of the closing decision induced the specific bet that with the undeniable proof of sub-atomic missteps that purpose hereditary issues would come to the critical sources for restoration these mix-ups and as a result draw in the abhorrence or inversion of defilement^[7]. That difficult over was the most vital thinking at the back of excellent remedy and from the Eighties was as soon as considered as a heavenly degree headed in sub-atomic

hereditary attributes. The enhancement of excellent simply really worth changing development for special treatment, in any case, proven risky[8]. Much early movement zeroed in now not on reexamining received errors in the DNA but as a replacement on attempting to confine their result by giving a practical duplicate of the modified quality, each embedded into or remained conscious of as a unit outside the genome. Even though that accession was once as soon as profitable for specific conditions, it was tangled and restrained in scope[8,9]. To certainly tackle hereditary staggers, gurus have to have been organized to make a twofold deserted ruin in DNA at unequivocally the incredible location in the range of billion base fits that development the human genome. Exactly when made, the twofold abandoned smash ought to be productively regular by way of the smartphone the use of an association that coordinated substitution of the \\\"terrible\\\" gathering with the \\\"great\\\" movement[10]. Regardless, making the secret spoil at definitively the incredible district—and no spot else—inside the genome was annoying [11].

DISCUSSION

The cycle joins the allowed alternate. The genome is pursued by particular groupings, which can relate to wrecks. Suppose there needs to be a tournament of hereditary arranging systems applied for change purposes; the ideal game plans are embedded in the genome [12,13]. The rapid strikes in natural arranging have made this joint effort price professional, but it charges generously . Novel high-quality in-kin methodologies, such as PCR, are utilized to perceive the moves. Different forces like the zinc finger nucleases, TALEN are used[12,13].But first-class altering ended up being straightforward with the presentation of the CRISPR substance form. The compound is the most grounded weapon in the prokaryotic world's cautious arsenal. The tiny natural factors use it in a clever relationship to genuine protection from bacteriophagic assaults[14]. With these types of growth, the cycle has carried out a stressful culmination, providing a precision unmatched. Yet off aim alteration is now a tie that has defeated unperturbed use. The probabilities that top-notch altering affords are :

1. Eradication of extraordinary improper actions in frail, early residing things.
2. Xenotransplantation,i.e., embedding tissues from one animal sorts to other.

2. Human enhancement, inciting, in reality, beneficial characters in the missing by introducing a gander at hereditary movement.

It is bringing concerning specific vaccination in opposition to infections like Helpers. These are the predominant and unbelievably clear blessings, presently. The prepared lacking existence constructions with their helped limits with canning acquire an alternate in putting no longer like any other. The notion can additionally appear to be overpowering, but it can give up being our world in the particularly shut to future. Imagine an age protected to the infections in established, a conventional public with a run-of-the-mill stage of grasp throughout the 150s. This will open up roads in no way expected of us or our progenitors. Regardless,.

It is fittingly stated that all that glints isn't gold like sharp this truly consoling future is a two-sided deal. This can be safeguarded through addressing a couple of fundamental demands and surveying the clever squares that make this cycle by using some potential or any other specifically awful[15,16]. The easy straightforwardness of our science is tortuously precarious. The course of significant well worth altering at any fee in it's some distance and away, stay solitary bundling has such eminent effects that we often skip the numerous design associated with the repercussions. The clever weights include:

1. Shaving off sizeable stretches of life due to the fact of the degenerative adjustments in the genome
2. Activation of oncogenes.
3. Off-purpose adjustments carry into the photo stressful changes.
4. Autoimmune putting off.
5. Mosaic affiliation taking into account emotional changes or missing alternate[16]

These are a couple of proper IRREVERSIBLE corrupting changes. Any occasion actuating these in an early living being can cease being fatal. The Gelsinger hassle is a framework of the incident that can occur through inborn starters, the unpublished viable penalties of He Jiankui tests, the

boss modified teenagers Beast and Nana, and the accompanying fiasco are a statement to the hazard proposed[17].

The herbal cycles and their thoughts are no longer limited to the presence of individuals blanketed ,they have repercussions that sway the daily populace at large and that too with a massive load of power. The couple of contemplations that provide this verbalization credible are:

1: Who all will have to aid the likely reap of this participation, assuming viable later on? Will it be prosperous, or will there be some distinctive existing allotment that will denounce this?

Will the in many instances taking place populace to be homogeneous if some picked traits end up being overpowering? How would perchance the range be impacted?

What will take location to the preceding businesses like parenthood?

Does this add up to some form of cleaning construing unequivocal double-dealing qualities? 5.And amongst all the essential solicitation is that is taking movement,a cooperation so brilliant and interminably existent,into our fingers ferocity?[17,18]

The in specific recorded risks set off the utilization of acquired adapting to 1:bio mental maltreatment

2:biohacking with political or serious targets 3:development of bio weapons[19]

Among this uneasiness, whether or not or not or no longer one breezes up being generous, then the subsequent time will give up being grievous. Science works on questionable grounds; that is for sure, the apparent fact in any case away so hazy is a loopy hazard to perceive[20].

BREAKING DNA AT DESIRED LOCATION

Going earlier than the presence of CRISPR-Cas9, two frameworks had been utilized to make a site- unequivocal twofold deserted breaks in DNA: one ward on zinc finger nucleases (ZFNs) and the one-of-a-kind ward on file activator-like effector nucleases (TALENs). ZFNs are mmixed proteins made out of DNA-restricting locales that see and tie to unequivocal three-to four-base pair lengthy movements[21]. Acquainting unequivocally with a nine-base pair target movement, for instance, would require three ZFN areas joined couple. The best manner of DNA-

keeping districts is likewise merged to a movement that encodes one subunit of the bacterial nuclease FokI[21,22]. Working with a twofold abandoned cut at a unique web website requires the training of two ZFN combo proteins— one to tie on every aspect of the aim site, on discussing DNA strands. When both ZFNs are bound, the FokI subunits, being in closeness, tie to one any different to shape a functioning dimer that cuts the perfect DNA on the two strands[23]. TALEN combination proteins are used to tie to talk DNA blueprints that flank a purpose site. Regardless, instead of utilizing zinc finger spaces, TALENs use DNA-keeping locales acquired from proteins from a get-together of plant microorganisms. For specific explanations, TALENs are less demanding to design than ZFNs, particularly for longer insistence protests[24]. Like ZFNs, TALENs encode a FokI house joined to the prepared DNA-restricting region;

accordingly, when the proper website is sure on the a range of sides, the dimerized FokI nuclease can current a twofold deserted ruin at the ideal DNA location. Unlike ZFNs and TALENs, CRISPR- Cas9 utilizes RNA-DNA binding, as an alternative to protein-DNA limiting, to arrange nuclease action, which works on the sketch and empowers application to a broad diploma of goal groupings[25]. CRISPR-Cas9 was once gotten from the versatile blanketed constructions of minute dwelling creatures. The abbreviated shape CRISPR suggests pressed dependably interspaced quick palindromic emphasizes, which are located in most bacterial genomes. Between the short palindromic emphasizes are stretches unnecessary to say of activity unmistakably bought from the genomes of bacterial existence forms. More seasoned" spacers are located at the distal success of the social occasion, and more current" spacers, looking at out for all of the higher definitely experienced microorganisms, are determined close to the proximal consummation of the pack. Record of the CRISPR vicinity accomplishes the headway of little guide RNAs that be a part of cut plans from the palindromic rehashes associated with actions acquired from the spacers, enabling every to add-on to its checking out objective[26]. The RNA-DNA heteroduplex fashioned then associations with a nuclease referred to as Cas9 and guides it to catalyze the cleavage of twofold deserted DNA at a nation of affairs close to the intermingling of the licensed unequivocal affiliation and the palindromic repeat in the aide RNA[26,27]. Since RNA-DNA heteroduplexes are normal and in mild of the reality that

organizing a RNA strategy that ties unequivocally to an unusual objective DNA movement requires simply archives on the Watson-Crick base-pairing with rules (adenine ties to thymine [or uracil in RNA], and cytosine ties to guanine), the CRISPR-Cas9 framework used to be charming over the combine protein plans wished for making use of ZFNs or TALENs[28]. A similarly expressed improvement got here in 2015, when Zhang and accomplices uncovered the utilization of Cpf-1, alternatively than Cas9, as the nuclease facilitated with CRISPR to accomplish first-rate adjusting. Cpf-1 is a microbial nuclease that affords most per chance benefits over Cas9, together with requiring simply a single CRISPR guide RNA for expresses and making staggered (rather than dulling) twofold deserted DNA cuts. The changed nuclease houses gave conceivably extra easy command over the consolidation of substitution DNA moves than was once practicable with Cas9, essentially in specific conditions. Specialists bet that minuscule animals house different genome-altering proteins also, the developmental grouping of which have to show indispensable in extra refining the accuracy and flexibility of considerable honestly well worth evolving progresses[29].

APPLICATIONS OF CRISPR AND ITS CONTROVERSIES

CRISPR-Cas9 has been utilized in an assortment of ways. For instance, it has been utilized to early insufficient with regards to natural elements to make hereditarily changed everyday substances, and it has been blended into the circulatory form in research workplace creatures to accomplish nice large altering in subsets of tissues[30]. Approaches based upon CRISPR-Cas9 have been utilized to exchange the genomes of harvest plants, creatures, and lab model dwelling animals, including mice, rodents, and nonhuman primates. By altering the genomes of bacteriophages (microorganisms killing illnesses) with CRISPR-Cas9 progression, professionals have had the choice to urge techniques to spoil inoculating professional poison blanketed life forms. CRISPR-Cas9 constructions, in addition, empowered the improvement of creature models for human affliction and the discharge of HIV from defiled cells[31,32]. In a mouse mannequin of human torment, CRISPR-Cas9 used to suitably tackle an inborn slip-up, assignment the clinical salvage of susceptible mice. In 2015 a get-together of specialists that recollected Doudna pushed limit for the use of CRISPR-Cas9 headway to people, in a well-known ride till flourishing and ethical repercussions of outstanding human changing ought to be sufficiently idea of[33]. Different scientists incited a "max stifle ahead" approach, doing combating that the

new development held the first-rate way to deal with backing off a big load of human torment and that maintaining it would be conniving. Concerning an equal time, reports from China confirmed that pleasant altering tests had been carried out on human early dwelling things[34]. In late 2018 a Chinese expert broadcasted the introduction of the world's first high-quality modified youthful human people; the newborn children, twin young ladies, have been stated to leave out on a modified exquisite that lowered the chance of becoming tainted with HIV. The high quality and disastrous effects of these workouts had been considered as per chance, renaming the future of human hereditary qualities[35-42].

CONCLUSION

We appear to the gene bettering process, for the betterment of humanity through the ability of designing embryos ,with a notable deal of hope . But the latest state of affairs is not very promising so as to take such a daring step is an entire no. To that impact we all can't justify this mission barring looking at the very positive collateral injury that it brings along. The gaining expertise of curve concerning fashion designer babies is a very lengthy technique in time and will for high- quality have a pinnacle notch deal fatality if no longer treaded on with the required precaution. Thus at the give up ,I strongly advise getting to know and speculating patiently.

REFERENCES

1. Tan WS, Carlson DF, Walton MW, Fahrenkrug SC, Hackett PB (2012). "Precision editing of large animal genomes". *Advances in Genetics* Volume 80. *Advances in Genetics*. 80. Pp. 37–97. Doi:10.1016/B978-0-12-404742-6.00002-8. ISBN 9780124047426. PMC 3683964. PMID 23084873.
2. Altae-Tran, Han; Kannan, Soumya; Demircioglu, F. Esra; Oshiro, Rachel; Nety, Suchita P.; McKay, Luke J.; Dlakić, Mensur; Inskeep, William P.; Makarova, Kira S.; Macrae, Rhianon K.; Koonin, Eugene V. (2021-10-01). "The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases". *Science*. 374 (6563): 57–65. Doi:10.1126/science.abj6856.
3. Redondo P, Prieto J, Muñoz IG, Alibés A, Stricher F, Serrano L, et al. (November 2008). "Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered

- meganucleases". *Nature*. 456 (7218): 107–11. Bibcode:2008Natur.456..107R. doi:10.1038/nature07343. PMID 18987743. S2CID 4300643
4. Yaskowiak, ES; Shears, MA; Agarwal-Mawal, A; Fletcher, GL (August 2006). "Characterization and multi-generational stability of the growth hormone transgene (EO-1alpha) responsible for enhanced growth rates in Atlantic Salmon". *Transgenic Research*. Springer. 15 (4): 465–480. Doi:10.1007/s11248-006-0020-5. PMID 16906447. S2CID 22247493
 5. Zhang F, Maeder ML, Unger-Wallace E, Hoshaw JP, Reyon D, Christian M, et al. (June 2010). "High frequency targeted mutagenesis in *Arabidopsis thaliana* using zinc finger nucleases". *Proceedings of the National Academy of Sciences of the United States of America*. 107 (26): 12028–33. Bibcode:2010PNAS..10712028Z. doi:10.1073/pnas.0914991107. PMC 2900673. PMID 20508152.
 6. Osakabe K, Osakabe Y, Toki S (June 2010). "Site-directed mutagenesis in *Arabidopsis* using custom-designed zinc finger nucleases". *Proceedings of the National Academy of Sciences of the United States of America*. 107 (26): 12034–9. Bibcode:2010PNAS..10712034O. doi:10.1073/pnas.1000234107. PMC 2900650. PMID 20508151.
 7. Rocha-Martins M, Cavaleiro GR, Matos-Rodrigues GE, Martins RA (August 2015). "From Gene Targeting to Genome Editing: Transgenic animals applications and beyond". *Anais da Academia Brasileira de Ciencias*. 87 (2 Suppl): 1323–48. Doi:10.1590/0001-3765201520140710. PMID 26397828.
 8. Kim YG, Cha J, Chandrasegaran S (February 1996). "Hybrid restriction enzymes: zinc finger fusions to Fok I cleavage domain". *Proceedings of the National Academy of Sciences of the United States of America*. 93 (3): 1156–60. Bibcode:1996PNAS.93.1156K. doi:10.1073/pnas.93.3.1156. PMC 40048. PMID 8577732.
 9. Ma H, Marti-Gutierrez N, Park SW, Wu J, Lee Y, Suzuki K, Koski A, Ji D, Hayama T, Ahmed R, Darby H, Van Dyken C, Li Y, Kang E, Park AR, Kim D, Kim ST, Gong J, Gu

- Y, Xu X, Battaglia D, Krieg SA, Lee DM, Wu DH, Wolf DP, Heitner SB, Belmonte JC, Amato P, Kim JS, Kaul S, Mitalipov S (August 2017). "Correction of a pathogenic gene mutation in human embryos". *Nature*. 548 (7668): 413–419. Bibcode:2017Natur.548..413M. doi:10.1038/nature23305. PMID 28783728.
10. Rodríguez-Rodríguez, Diana Raquel; Ramírez-Solís, Ramiro; Garza-Elizondo, Mario Alberto; Garza-Rodríguez, María De Lourdes; Barrera-Saldaña, Hugo Alberto (April 2019). "Genome editing: A perspective on the application of CRISPR/Cas9 to study human diseases (Review)". *International Journal of Molecular Medicine*. 43 (4): 1559–1574. Doi:10.3892/ijmm.2019.4112. ISSN 1791-244X. PMC 6414166. PMID 30816503.
 11. Baltimore D, Berg P, Botchan M, Carroll D, Charo RA, Church G, Corn JE, Daley GQ, Doudna JA, Fenner M, Greely HT, Jinek M, Martin GS, Penhoet E, Puck J, Sternberg SH, Weissman JS, Yamamoto KR (April 2015). "Biotechnology. A prudent path forward for genomic engineering and germline gene modification". *Science*. 348 (6230): 36–8. Bibcode:2015Sci...348 36B. doi:10.1126/science.aab1028. PMC 4394183. PMID 25791083.
 12. Liang P, Xu Y, Zhang X, Ding C, Huang R, Zhang Z, Lv J, Xie X, Chen Y, Li Y, Sun Y, Bai Y, Songyang Z, Ma W, Zhou C, Huang J (May 2015). "CRISPR/Cas9-mediated gene editing in human triprounuclear zygotes". *Protein & Cell*. 6 (5): 363–372. Doi:10.1007/s13238-015-0153-5. PMC 4417674. PMID 25894090.
 13. Zeng Y, Li J, Li G, Huang S, Yu W, Zhang Y, Chen D, Chen J, Liu J, Huang X (November 2018). "Correction of the Marfan Syndrome Pathogenic FBN1 Mutation by Base Editing in Human Cells and Heterozygous Embryos". *Molecular Therapy*. 26 (11): 2631–2637. Doi:10.1016/j.ymthe.2018.08.007. PMC 6224777. PMID 30166242.
 14. Handyside, A. H.; Kontogianni, E. H.; Hardy, K; Winston, R. M. L (19 April 1990). "Pregnancies from biopsied human preimplantation embryos sexed by Y-specific DNA amplification". *Nature*. 344 (768–770): 768–770. Bibcode:1990Natur.344..768H. doi:10.1038/344768a0. PMID 2330030. S2CID 4326607.
 15. Gianaroli, Luca; Crivello, Anna Maria; Stanghellini, Ilaria; Ferraretti, Anna Pia; Tabanelli, Carla; Magli, Maria Cristina (2014). "Reiterative changes in the Italian regulation on IVF: the effect on PGD patients' reproductive decisions". *Reproductive BioMedicine Online*. 28 (1): 125–132. Doi:10.1016/j.rbmo.2013.08.014. ISSN

1472-6483. PMID 24268726.

16. Tachibana, Masahito; Amato, Paula; Sparman, Michelle; Woodward, Joy; Sanchis, Dario Melguizo; Ma, Hong; Gutierrez, Nuria Marti; Tippner-Hedges, Rebecca; Kang, Eunju; Lee, Hyo-Sang; Ramsey, Cathy; Masterson, Keith; Battaglia, David; Lee, David; Wu, Diana; Jensen, Jeffrey; Patton, Phillip; Gokhale, Sumita; Stouffer, Richard; Mitalipov, Shoukhrat (2012). "Towards germline gene therapy of inherited mitochondrial diseases". *Nature*. 493 (7434): 627–631. Doi:10.1038/nature11647. ISSN 0028-0836. PMC 3561483. PMID 23103867
17. "Convention for the protection of human rights and dignity of the human being with regard to the application of biology and medicine: convention on human rights and biomedicine (adopted by the Committee of Ministers on 19 November 1996). Council of Europe Convention of Biomedicine". *Human Reproduction* (Oxford, England). 12 (9): 2076–2080. September 1997. Doi:10.1093/humrep/12.9.2076. ISSN 0268-1161. PMID 9363733.
18. Li, Jing-ru; Walker, Simon; Nie, Jing-bao; Zhang, Xin-qing (January 2019). "Experiments that led to the first gene-edited babies: the ethical failings and the urgent need for better governance". *Journal of Zhejiang University. Science. B*. 20 (1): 32–38. Doi:10.1631/jzus.B1800624. ISSN 1673-1581. PMC 6331330. PMID 30614228.
19. Cyranoski, David (27 November 2018). "How the genome-edited babies revelation will affect research – Some scientists worry the startling claim will lead to knee-jerk regulations and damage the public's trust in gene editing". *Nature*. Doi:10.1038/d41586-018-07559-8. Archived from the original on 27 November 2018. Retrieved 27 November 2018.
20. Wee, Sui-Lee (30 December 2019). "Chinese Scientist Who Genetically Edited Babies Gets 3 Years in Prison – He Jiankui's work was also carried out on a third infant, according to China's state media, in a new disclosure that is likely to add to the global uproar over such experiments". *The New York Times*. Retrieved 30 December 2019.

21. Cyranoski, David (20 May 2019). "China set to introduce gene-editing regulation following CRISPR-baby furore – The draft rules mean that anyone who manipulates human genes in adults or embryos is responsible for adverse outcomes". *Nature*. Doi:10.1038/d41586-019-01580-1. PMID 32424191. Retrieved 20 May 2019.
22. Regalado, Antonio (3 December 2019). "China's CRISPR babies: Read exclusive excerpts from the unseen original research - He Jiankui's manuscript shows how he ignored ethical and scientific norms in creating the gene-edited twins Lulu and Nana". *MIT Technology Review*. Retrieved 3 December 2019.
23. Cyranoski, David (27 November 2018). "How the genome-edited babies revelation will affect research – Some scientists worry the startling claim will lead to knee-jerk regulations and damage the public's trust in gene editing". *Nature*. Doi:10.1038/ d41586-018-07559-8. Archived from the original on 27 November 2018. Retrieved 27 November 2018.
24. Trecarichi, Enrico M; Tumbarello, Mario; Donati, Katleen; Tamburrini, Enrica; Cauda, Roberto; Brahe, Christina; Tiziano, Francesco D (2006). "Partial protective effect of CCR5-Delta 32 heterozygosity in a cohort of heterosexual Italian HIV-1 exposed uninfected individuals". *AIDS Research and Therapy*. 3 (1): 22.Doi:10.1186/1742-6405-3-22. PMC 1592103. PMID 16999868
25. Yang, Hui; Wang, Haoyi; Shivalila, Chikdu S.; Cheng, Albert W.; Shi, Linyu; Jaenisch, Rudolf (2013). "One-step generation of mice carrying reporter and conditional alleles by CRISPR/Cas-mediated genome engineering". *Cell*. 154 (6): 1370–1379. Doi:10.1016/j.cell.2013.08.022. PMC 3961003. PMID 23992847.
26. Niu, Yuyu; Shen, Bin; Cui, Yiqiang; Chen, Yongchang; Wang, Jianying; Wang, Lei; Kang, Yu; Zhao, Xiaoyang; Si, Wei; Li, Wei; Xiang, Andy Peng (2014). "Generation of gene-modified cynomolgus monkey via Cas9/RNA-mediated gene targeting in one-cell embryos". *Cell*. 156 (4): 836–843. Doi:10.1016/j.cell.2014.01.027. PMID 24486104. S2CID 612983.
27. Wang, Shuang; Ren, Shuaiwei; Bai, Raoxian; Xiao, Puhao; Zhou, Qin; Zhou, Yin; Zhou, Zhigang; Niu, Yuyu; Ji, Weizhi; Chen, Yongchang (2018). "No off-target mutations in functional genome regions of a CRISPR/Cas9-generated monkey model of muscular

- dystrophy". The Journal of Biological Chemistry. 293 (30): 11654–11658. Doi:10.1074/jbc.AC118.004404. PMC 6066302. PMID 29941452.
28. Frangoul, Haydar; Altshuler, David; Cappellini, M. Domenica; Chen, Yi-Shan; Domm, Jennifer; Eustace, Brenda K.; Foell, Juergen; de la Fuente, Josu; Grupp, Stephan; Handgretinger, Rupert; Ho, Tony W. (21 January 2021). "CRISPR-Cas9 Gene Editing for Sickle Cell Disease and β -Thalassemia". The New England Journal of Medicine. 384 (3): 252–260. Doi:10.1056/NEJMoa2031054. ISSN 1533-4406. PMID 33283989. S2CID 227521558.
 29. Esrick, Erica B.; Lehmann, Leslie E.; Biffi, Alessandra; Achebe, Maureen; Brendel, Christian; Ciuculescu, Marioara F.; Daley, Heather; MacKinnon, Brenda; Morris, Emily; Federico, Amy; Abriss, Daniela (21 January 2021). "Post-Transcriptional Genetic Silencing of BCL11A to Treat Sickle Cell Disease". The New England Journal of Medicine. 384 (3): 205–215. Doi:10.1056/NEJMoa2029392. PMC 7962145. PMID 33283990.
 30. Stadtmauer, Edward A.; Fraietta, Joseph A.; Davis, Megan M.; Cohen, Adam D.; Weber, Kristy L.; Lancaster, Eric; Mangan, Patricia A.; Kulikovskaya, Irina; Gupta, Minnal; Chen, Fang; Tian, Lifeng (2020). "CRISPR-engineered T cells in patients with refractory cancer". Science. 367 (6481): eaba7365 (1–12). Doi:10.1126/ science.aba7365. PMID 32029687. S2CID 211048335.
 31. Coenen, Christopher (2007). "Utopian Aspects of the Debate on Converging Technologies" (PDF). In Gerhard Banse; et al. (eds.). Assessing Societal Implications of Converging Technological Development (1st ed.). Berlin: edition sigma. Pp. 141– 172. ISBN 978-3-89404-941-6. OCLC 198816396
 32. Sandberg, Anders; Boström, Nick (2008). Whole Brain Emulation: A Roadmap (PDF). Technical Report #2008- 3. Future of Humanity Institute, Oxford University. Retrieved April 5, 2009. The basic idea is to take a particular brain, scan its structure in detail, and construct a software model of it that is so faithful to the original that, when run on appropriate hardware, it will behave in essentially the same way as the original brain.
 33. Arnall, Alexander Huw (2003). "Future technologies, today's choices: nanotechnology, artificial intelligence and robotics" (PDF). Greenpeace U.K. Archived from the original (PDF) on April 14, 2006. Retrieved April 29, 2006.

34. Newman, Stuart A. (2003). "Averting the clone age: prospects and perils of human developmental manipulation" (PDF). *Journal of Contemporary Health Law & Policy*. 19 (2): 431–63. PMID 14748253. Archived from the original (PDF) on December 16, 2008. Retrieved September 17, 2008.
35. Rees, Martin (2003). *Our Final Hour: A Scientist's Warning: How Terror, Error, and Environmental Disaster Threaten Humankind's Future In This Century—On Earth and Beyond*. Basic Books. Bibcode:2003ofhs.book. R. ISBN 978-0-465-06862-3. OCLC51315429
36. Gupta V, Agarwal P, Deshpande P. Impact of RASSF1A gene methylation on clinico-pathological features of tumor and non-tumor tissue of breast cancer. *ANNALS OF DIAGNOSTIC PATHOLOGY*. 2021 Jun;52.
37. Kinkar JS, Jameel PZ, Kumawat BL, Kalbhor P. Heterozygous deletion in exon 6 of STEX gene causing ataxia with oculomotor apraxia type 2 (AOA-2) with ovarian failure. *BMJ CASE REPORTS*. 2021 Jun;14(6).
38. Abbafati, Cristiana, Kaja M. Abbas, Mohammad Abbasi, Mitra Abbasifard, Mohsen Abbasi-Kangevari, Hedayat Abbastabar, Foad Abd-Allah, et al. "Five Insights from the Global Burden of Disease Study 2019." *LANCET* 396, no. 10258 (October 17, 2020): 1135–59.
39. Abbafati, Cristiana, Kaja M. Abbas, Mohammad Abbasi, Mitra Abbasifard, Mohsen Abbasi-Kangevari, Hedayat Abbastabar, Foad Abd-Allah, et al. "Global Burden of 369 Diseases and Injuries in 204 Countries and Territories, 1990-2019: A Systematic Analysis for the Global Burden of Disease Study 2019." *LANCET* 396, no. 10258 (October 17, 2020): 1204–22.
40. Franklin, Richard Charles, Amy E. Peden, Erin B. Hamilton, Catherine Bisignano, Chris D. Castle, Zachary Dingels V, Simon Hay I, et al. "The Burden of Unintentional Drowning: Global, Regional and National Estimates of Mortality from the Global Burden of Disease 2017 Study." *INJURY PREVENTION* 26, no. SUPP_1, 1 (October 2020): 83–95. <https://doi.org/10.1136/injuryprev-2019-043484>.
41. James, Spencer L., Chris D. Castle, Zachary Dingels V, Jack T. Fox, Erin B. Hamilton, Zichen Liu, Nicholas L. S. Roberts, et al. "Estimating Global Injuries Morbidity and Mortality: Methods and Data Used in the Global Burden of Disease 2017 Study." *INJURY PREVENTION* 26, no. SUPP_1, 1 (October 2020): 125–53. <https://doi.org/10.1136/injuryprev-2019-043531>.

42. James, Spencer L., Chris D. Castle, Zachary Dingels V, Jack T. Fox, Erin B. Hamilton, Zichen Liu, Nicholas L. S. Roberts, et al. "Global Injury Morbidity and Mortality from 1990 to 2017: Results from the Global Burden of Disease Study 2017." *INJURY PREVENTION* 26, no. SUPP_1, 1 (October 2020): 96–114. <https://doi.org/10.1136/injuryprev-2019-043494>.

UNDER PEER REVIEW