

Review Paper:

CRISPR edited Microbes and their Industrial Potential Review

Jain A., Kachhwaha N.* and Srivastava A.

Department of Zoology, University of Rajasthan, Jaipur (Rajasthan)- 302001, INDIA

*drneetu2011@gmail.com

Abstract

The CRISPR is Clustered Regularly Interspaced Short Palindromic Repeats, these repeated DNA sequences are found in the prokaryotes genome which is used as a tool to detect viral infections. CRISPR associated protein 9 i.e. Cas9 and the CRISPR together are forming the novel platform in the field of biotechnology. Nowadays, industries such as biotech, pharmaceuticals, agriculture, chemical, etc. are using highly engineered industrial strain.

They are used in targeting chromosomes, genetic manipulation, sequencing, gene replacement, embryonic stem cell manipulation and many more. The organisms modified by this CRISPR/Cas9 involved a huge diversity of targeting vectors including bacteria, yeast, fungi, algae (cyanobacteria, microalgae). CRISPR/Cas9 is a new generation genome engineering technology widely used in molecular genetics due to its ease, simplicity, efficiency and versatility.

Keywords: CRISPR, Cas9, Biotechnology, Microorganisms.

Introduction

A CRISPR immunity phenotype is genetically encoded by a so-called CRISPR locus (Clustered Regularly Interspaced Short Palindromic Repeats)—an array of repetitive and unique sequences (repeats and spacers respectively), both of which are typically around 30 nt in length⁵¹. These repeats and spacers are introduced in the bacterial cell by the phage infection which is used as a memory to combat future infections. As new spacers are added at the so-called leader-end of the locus, which is the sequence that contains the CRISPR promoter; CRISPR loci form an inverse chronological record of previous infections from the leader to the trailer end of the locus⁵⁰.

Apart from the genetic CRISPR memory, a functional CRISPR-Cas immune system also requires a set of CRISPR associated genes (cas genes), which encode the protein machinery required for carrying out the immune response¹⁹. Some researchers thoroughly discussed CRISPR/Cas technology and its biology^{52,53}. Industrial microbiology plays a key role in the transition towards a more sustainable industry to produce food and feed ingredients, bio-based materials, biofuels and direct synthesis of cosmetic and pharmaceutical compounds²³.

Based on the notable publications on the internet, it has been researched that about 200- 300 papers have been published in first 6 months of 2019 that depict intense studies which are being performed on microbes of industrial significance using CRISPR/Cas technology. There has been an increasing interest in improving microbial cell factories through metabolic engineering approaches using CRISPR/Cas9 technology¹⁸. The efficiency and versatility offered by CRISPR tools have shown great potential in rewiring the metabolic network of host cells to enhance their production of metabolites used in various areas of industrial biotech ranging from applications as biofuels to chemical building blocks and pharmaceutical¹³.

Earlier methods for genetic modification were not cost-effective, time-consuming and tedious to screen the desired transformants, until the discovery of CRISPR technology. Nowadays, industries such as biotech, pharmaceuticals, agriculture, chemical etc. are using highly engineered industrial strain. The implementation of CRISPR-Cas tools has revolutionized genome editing and mitigated the investment in the metabolic engineering programs required to generate highly engineered microbial cell factories¹⁰.

Continuing the quest for editing microbes of industrial importance, the review provides information about "CRISPR edited microbes and their industrial potential" researched in last six months (2019) from the reputed papers around the globe.

Microorganisms

Bacteria: Bioproducts from the microbes are less reactive, show structural diversity and are easily degradable causing less pollution. Bacteria are perhaps the most prolific microbial producers of bioactive natural products, which are represented by their secondary metabolites⁴⁵. These secondary metabolites are utilized by humans through commercial production according to the need. With the ease of CRISPR Cas mechanism, industrial strain development becomes handy for such industrial productions.

E.coli: Studies suggest that fermentation of glucose and xylose from the agricultural residues can be utilised by *E.coli* in the production of biobutanol. In a study, a dual-operon-based synthetic pathway in the genome of *E. coli* MG1655 engineered to produce n-butanol using CRISPR/Cas9 technology¹. The technology can also be used to suppress the expression of many DNA loci in the genome. Scientists constructed a CRISPRi-mediated multiplex repression system to silence transcription of several endogenous genes

to increase precursor availability in a heterologous isopentenol biosynthesis pathway⁴⁷.

The development of a CRISPR–Cas9 based method for iterative genome editing and metabolic engineering of *Escherichia coli* enables the authors to integrate the β -carotene synthetic pathway into the genome and to optimize the methylerythritol-phosphate (MEP) pathway and central metabolic pathways for β -carotene overproduction²⁷. Studies prominently done on the weak and previously ignored end-joining mechanism in *E.coli* can be now used for efficient large-scale genetic engineering assisted by CRISPR/Cas9¹⁵ which shows its significance in industrial microbiology.

Clostridium: The genus *Clostridium* is composed of bioproducers which are important for the industrial production of chemicals as well as pathogens which are a significant burden to the patients and on the health care industry²⁸. Li et al²⁶ developed a genomic editing tool (pCBEclos) for the use in *C. beijerinckii* based on the fusion of cytidine deaminase (ApoBec1), Cas9^{D10A} nickase and uracil DNA glycosylase inhibitor (UGI), the method through which *C. beijerinckii* can be easily altered to reach its maximum efficiency.

Various clostridia such as *Clostridium acetobutylicum*, *C. tyrobutyricum*, *C. carboxidivorans*, *C. ljungdahlii* and *C. cellulovorans* are researched and modified to enhance butanol production by earlier metabolic engineering methods and hence CRISPR technology seems to be very promising^{2,7,8}.

Bacillus and Lactobacillus: A PCR screening for 81 selected *Lactobacillus sakei* isolates was performed and it identified 25 (31%) isolates as CRISPR–Cas positive with hypervariable spacer content⁴². To achieve higher yields, many researchers have performed genetic modifications and metabolic regulations on industrially important *Bacillus* species. It was demonstrated that the mutant *Bacillus licheniformis* with deletions of the genes amyL and chiA (encoding amylase and chitinase, respectively) by CRISPR/Cas9 system effectively improved the alkaline protease yield by 24.8%⁵⁵.

CRISPR approach is used to observe an editing efficiency of 76% which allowed multiple, rapid rounds of in situ editing of the subtilisin E gene to incorporate a salt bridge triad

present in the *Bacillus clausii* thermotolerant homolog, M-protease³⁷.

CRISPR interference serves as the basis for functional characterization of *B. methanolicus* physiology in which scientists predicted the functions of Spo0A in sporulation and biofilm formation, MtlD for mannitol catabolism and catalase in hydrogen peroxide dismutation⁴⁰. Swiss and Italian hard cheeses are manufactured by the use of *Lactobacillus helveticus*, a lactic acid bacterium which is thermophilic in nature and studies conducted on 25 *Lactobacillus helveticus* genome showed the presence and genetic heterogeneity of CRISPR loci³⁹.

Streptomyces: Controlling the metabolic production in a microbe, there should be a controlled regulatory system which can be easily induced to enhance the industrial yields. To achieve this, researchers and microbiologist employed the modular design approach to build a high performance synthetic inducible regulatory system that displayed a large dynamic range and thus, well-suited for the modulation of secondary metabolite production in *Streptomyces*²⁰.

Presently certain reviews depict attempts to provide a comprehensive summary for stable genomic engineering and to outline recent advances in these strategies such as CRISPR/Cas9, which have successfully manipulated *Streptomyces* strains to improve their biotechnological properties and increase production of natural or new gene-manipulated biologically active compounds²¹.

Moreover, a genome-reduced industrial *Streptomyces chassisi* L321 was rationally constructed and showed to exhibit several emergent and excellent performances for heterologous expression of secondary metabolite like enhanced intracellular energy (ATP) and reducing power (NADPH/NADP⁺), improved productivity of protein and secondary metabolite, more dispersed mycelia, increased transformation efficiency, simplified metabolite profiles, increased genetic stability⁴. Other modified bacteria with the help of CRISPR Cas mechanism are given in table 1.

Yeast: Taking about the various industrial productions in non-conventional yeast, we already know that they have potential role in the formation of biofuels, food additives and high valued proteins but due to deficiency of proper genetic tools in them, it becomes quite cumbersome to modify its genome.

Table 1
Other Bacteria modified by CRISPR Cas mechanism.

Bacteria	Type	Uses
<i>Streptococcus thermophilus</i>	Type I and Type II CRISPR-Cas	Chromosomal targeting ⁶
<i>Corynebacterium glutamicum</i>	CRISPRi	L-lysine production ³⁵
<i>Pseudomonas aeruginosa</i>	CRISPR/Cas9	Genetic manipulation ⁹
<i>Ralstonia eutropha</i>	Type I and Type II CRISPR-Cas	31% RSSC genome have CRISPR ¹¹
<i>Brevibacterium</i>	CRISPR/Cas9	Cheese production ²⁴

However, new studies state that precise and maker free genome editing with CRISPR-Cas9 have shown great potential in synthetic biology and industrial biotechnology⁵.

Saccharomyces: In the study conducted, a novel genome shuffling method was developed for *S. cerevisiae* using CRISPRCas, which results in the creation of the thermotolerant mutant strain T8-292, which can grow well at 39 °C, showing cell viability in low pH and high ethanol concentration³⁰.

The study and research done by Jiangping et al stated that CRISPRi system was constructed in β -amyryn producing strain *S. cerevisiae*SGib to repress the competitive pathway for β -amyryn production.

A CRISPR-based gene editing strategy that allows the systematic and meticulous introduction of a natural occurring mutation in the *FDC1* gene of genetically complex industrial *S. cerevisiae* strains, *S. eubayanus* yeasts and interspecific hybrids was conducted resulting in the cisgenic POF⁻ variants which show great potential for industrial application and diversifying the current lager beer portfolio²⁹.

Yarrowialipolytica: *Yarrowialipolytica* seems to be very promising future microbial cell factory for various bioindustries. In one of the research papers published, author's main goal was the creation of a simple auxotrophic marker to test the efficiency of GoldenMOCS-based CRISPR/Cas9 genome editing in wild-type isolates of *Y. lipolytica*¹².

By using CRISPR as a screening method for biotechnologically important mutants, scientists developed a methodology to quantify the cutting efficiency of each sgRNA in a genome-scale library and in doing so to improve screens in the biotechnologically important yeast *Yarrowia lipolytica*⁴⁴.

Rhodospiridiumtoruloides: A CRISPR/Cas9 system for genome editing in *R. toruloides* based on a fusion 5S rRNA-tRNA promoter for guide RNA (gRNA) expression, capable of greater than 95% gene knockout for various genetic targets⁴¹ was done so that it can be used as a future metabolic engineering strategy.

Transforming a Cas9 expression cassette harboring nourseothricin resistance and selecting transformants on antibiotic resulted in strains of *R. toruloides* exhibiting

successful targeted disruption of the native *URA3* gene³³ increasing editing efficiency upto 50%. Other modified yeast with the help of CRISPR Cas mechanism is given in table 2.

Fungi

Filamentous Fungi: The filamentous fungus *Fusarium fujikuroi* is well-known for its production of natural plant growth hormones: a series of gibberellic acids (GAs) in which some GAs including GA1, GA3, GA4 and GA7, are biologically active and have been widely applied in agriculture⁴⁶.

The little efficiency of old genetic tools resists researchers to modify the fungus but the use of CRISPR technology has removed this limitation. Author described various approaches taken to assure expression of the components necessary for editing and described strategies used to achieve gene disruptions, gene replacements and precise editing⁴³ using CRISPR.

Aspergillus niger: Tong et al⁴⁹ in their review summarized the impact of systems biology on the citric acid molecular regulatory mechanisms, the advances in metabolic engineering strategies for enhancing citric acid production and discussed the development and application of CRISPR/Cas9 systems for genome editing in *A. niger*. Using the CRISPR/Cas9-dependent base editor and inducing nonsense mutations via single base editing, scientist inactivated the uridine auxotroph gene *pyrG* and the pigment gene *fwnA* with an efficiency of 47.36%–100% in *A. niger*¹⁶.

A study conducted showed a modified CRISPR/Cas9 system for *A. niger* highlighted in two aspects: (1) construction of a single and easy-to-use CRISPR/Cas9 tool plasmid derived from pAN7-1 which was widely used in filamentous fungi (2) redesign of the easy-to-switch “ribozyme-gRNA-ribozyme (RGR)” element in the tool plasmid⁵⁴.

Researchers demonstrated the method by targeting the phenotypic marker *alba* and validated it by targeting the *glaA* and *mstC* loci after which 100% gene editing efficiency was observed²⁵.

Trichoderma: Engineering of *T. reesei* by multiplexed CRISPR/Cas9 in combination with the use of our recently established synthetic expression system (SES) enabled accelerated construction of strains which produced high amounts of highly pure lipase B of *Candida antarctica*(calB)³⁸.

Table 2
Other Yeast modified by CRISPR Cas mechanism.

Yeast	Type	Uses
<i>PseudozymaAntarctica</i>	CRISPR/Cas9	Efficient gene-targeting method ²²
<i>Kluyveromyces lactis</i>	CRISPR/Cas9	Sequencing to identify two mutations in KISEC59 gene ⁵⁶

Algae

Microalgae: Researchers have been curiously focusing on the efforts made so far to targeted genome engineering of microalgae, identified scopes about the hurdles related to construction and delivery of CRISPR–Cas components, algae transformation toolbox and outlined the future prospect toward developing the CRISPR platform for high-throughput genome-editing of microalgae³⁶.

In the study conducted, authors developed a highly efficient transgene-free targeted mutagenesis and single-stranded oligodeoxynucleotide (ssODN)-mediated knock-in in *E. gracilis* using Cas9 RNPs, which provides the first evidence that *E. gracilis* is a genome-editable organism³².

Issam et al¹⁷ reviewed the strategies and status of the use of CRISPR technology to improve the efficiency of Eukaryotic microalgae to produce biologically active compounds.

Cyanobacteria: In *Geitlerinemasp*.FC II, a filamentous cyanobacteria is characterized by the presence of multiple CRISPRCas (Clustered Regularly Interspaced Short Palindrome Repeats – CRISPR associated proteins) clusters, multiple variants of genes encoding photosystem reaction centres, biosynthetic gene clusters of alkane, polyketides and

non-ribosomal peptides due to which it has an ecological advantage over other strains for biomass production in large scale cultivation system and hence, FC II may be deliberately used for production of biofuel and other industrially important metabolites³.

Cyanobacterium, *Anabaena* sp. PCC 7120, a heterocyst-specific conditional gene repression system was successfully created by combining a cell type-specific gene induction system with CRISPRi technology¹⁴ which increases its ethanol productivity and hence became suitable for biofuel productions. Other modified actinomycetes with the help of CRISPR Cas mechanism is given in table 3.

Conclusion

Looking forward to the future of industrial biotechnology, CRISPR edited microbes are going to take the first position in the queue of genetic modification techniques. The part of bacterial adaptive immunity which is used to harness the full potential of microbes is gaining more and more recognition worldwide. However, new emerging technologies will outnumber old ones, yet this technology has a potential to revolutionize the way we work with the microbe, not only in industrial but in every field of biological application considering all the ethical aspects.

Table 3
Other Microorganisms modified by CRISPR Cas mechanism

Actinomycetes	Type	Uses
<i>Streptomyces coelicolor</i>	CRISPR/Cas9	Precise gene replacements and reversibly control gene expression ⁴⁸
<i>Streptomyces</i>	Cluster assembly, cloning and expression, CRISPR/Cas9 technologies and chassis strain development	Reprogramming biosynthetic pathways ³⁴

References

- Abdelaal A.S., Jawed K. and Yazdani S.S., CRISPR/Cas9-mediated engineering of *Escherichia coli* for n-butanol production from xylose in defined medium, *J. Ind. Microbiol. Biotechnol.*, **46**, 965-975 (2019)
- Bao T., Zhao J., Li J., Liu X. and Yang S.T., n-Butanol and ethanol production from cellulose by *Clostridium cellulovorans* overexpressing heterologous aldehyde/alcohol dehydrogenases, *Bioresour. Technol.*, doi: 10.1016/j.biortech.2019.121316, **285**, 121316 (2019)
- Batchu N.K., Khater S., Patil S., Nagle V., Das G., Bhadra B., Sapre A. and Dasgupta S., Whole genome sequence analysis of *Geitlerinemasp*. FC II unveils competitive edge of the strain in marine cultivation system for biofuel production, *Genomics*, <https://doi.org/10.1016/j.ygeno.2018.03.004>, **111(3)**, 465-472 (2019)
- Bu Q.T., Yu P., Wang J., Li, Z.Y., Chen, X.A., Mao X.M. and Li Y.Q., Rational construction of genome-reduced and high-efficient industrial *Streptomyces* chassis based on multiple comparative genomic approaches, *Microb. Cell Fact.*, <https://doi.org/10.1186/s12934-019-1055-7>, **18** (2019)
- Cai P., Gao J. and Zhou Y., CRISPR-mediated genome editing in non-conventional yeasts for biotechnological applications, *Microb. Cell Fact.*, <https://doi.org/10.1186/s12934-019-1112-2> **18** (2019)
- Cañez C., Selle K., Goh Y.J. and Barrangou R., Outcomes and characterization of chromosomal self-targeting by native CRISPR-Cas systems in *Streptococcus thermophilus*, *FEMS Microbiol. Lett.*, <https://doi.org/10.1093/femsle/fnz105>, **366(9)** (2019)
- Cheng C., Bao T. and Yang S.T., Engineering *Clostridium* for improved solvent production: recent progress and perspective, *Appl. Microbiol. Biotechnol.*, <https://doi.org/10.1007/s00253-019-09916-7>, 103(14), 5549-5566 (2019)
- Cheng C., Li W., Lin M. and Yang S.T., Metabolic engineering of *Clostridium carboxidivorans* for enhanced ethanol and butanol production from syngas and glucose, *Bioresour. Technol.*, <https://doi.org/10.1016/j.biortech.2019.03.145>, **284**, 415-423 (2019)
- Chen W., Zhang Y., Zhang Y., Pi Y., Gu T., Song L., Wang Y. and Ji Q., CRISPR/Cas9-based Genome Editing in *Pseudomonas aeruginosa* and Cytidine Deaminase-Mediated Base Editing in *Pseudomonas* Species, *iScience*, **6**, 222-231 (2018)

10. Choi K.R., Jang W.D., Yang D., Cho J.S., Park D. and Lee S.Y., Systems metabolic engineering strategies: integrating systems and synthetic biology with metabolic engineering, *Trends Biotechnol.*, doi: <https://doi.org/10.1016/j.tibtech.2019.01.003>, **37(8)**, 817-837 (2019)
11. Da Silva Xavier A., De Almeida J.C., De Melo A.G., Rousseau G.M., Tremblay D.M., De Rezende R.R., Moineau S. and Alfnas-Zerbini P., Characterization of CRISPR-Cas systems in the *Ralstonia solanacearum* species complex, *Mol. Plant Pathol.*, doi:10.1111/mpp.12750, **20(2)**, 223-239 (2019)
12. Egermeier M., Sauer M. and Marx H., Golden Gate-based metabolic engineering strategy for wild-type strains of *Yarrowialipolytica*, *FEMS Microbiol. Lett.*, <https://doi.org/10.1093/femsle/fnz022>, **366(4)** (2019)
13. Ferreira R., David F. and Nielsen J., Advancing biotechnology with CRISPR/Cas9: recent applications and patent landscape, *J. Ind. Microbiol. Biotechnol.*, <https://doi.org/10.1007/s10295-017-2000-6>, **45**, 467-480 (2018)
14. Higo A. and Ehira S., Spatiotemporal Gene Repression System in the Heterocyst-Forming Multicellular Cyanobacterium *Anabaena* sp. PCC 7120, *ACS Synth. Biol.*, <https://doi.org/10.1021/acssynbio.8b00496>, **8(4)**, 641-646 (2019)
15. Huang C., Ding T., Wang J., Wang X., Wang J., Zhu L., Bi C., Zhang X., Ma X. and Huo Y.X., CRISPR-Cas9-assisted native end-joining editing offers a simple strategy for efficient genetic engineering in *Escherichia coli*, *Appl. Microbiol. Biotechnol.*, <https://doi.org/10.1007/s00253-019-10104-w>, **103**, 8497-8509 (2019)
16. Huang L., Dong H., Zheng J., Wang B. and Pan L., Highly efficient single base editing in *Aspergillus niger* with CRISPR/Cas9 cytidine deaminase fusion, *Microbiol. Res.*, <https://doi.org/10.1016/j.micres.2019.03.007>, **223-225**, 44-50 (2019)
17. Issam G.B., Butnariu M. and Bilal E., Insight into crispr system in eukaryotic microalgae, a review, *J. Eurasian Res.*, **2(59)**, 37-48 (2019)
18. Jakočiūnas T., Jensen M.K. and Keasling J.D., CRISPR/Cas9 advances engineering of microbial cell factories, *Metab. Eng.*, doi:10.1016/j.ymben.2015.12.003, **34**, 44-59 (2016)
19. Jansen R., Embden J.D., Gaastra W. and Schouls L.M., Identification of genes that are associated with DNA repeats in prokaryotes, *Mol. Microbiol.*, <https://doi.org/10.1046/j.1365-2958.2002.02839.x>, **43(6)**, 1565-1575 (2002)
20. Ji C.H., Kim H. and Kang H.S., Synthetic Inducible Regulatory Systems Optimized for the Modulation of Secondary Metabolite Production in *Streptomyces*, *ACS Synth. Biol.*, <https://doi.org/10.1021/acssynbio.9b00001>, **8(3)**, 577-586 (2019)
21. Kormanec J., Rezuchova B., Homerova D., Csolleiova D., Sevcikova B., Novakova R. and Feckova L., Recent achievements in the generation of stable genome alterations/mutations in species of the genus *Streptomyces*, *Appl. Microbiol. Biotechnol.*, <https://doi.org/10.1007/s00253-019-09901-0>, **103**, 5463-5482 (2019)
22. Kunitake E., Tanaka T., Ueda H., Endo A., Yarimizu T., Katoh E. and Kitamoto H., CRISPR/Cas9-mediated gene replacement in the basidiomycetous yeast *Pseudozymaantarctica*, *Fungal Genet. Biol.*, <https://doi.org/10.1016/j.fgb.2019.04.012>, **130**, 82-90 (2019)
23. Lee S.Y., Kim H.U., Chae T.U., Cho J.S., Kim J.W., Shin J.H., Kim D.I., Ko Y.S., Jang W.D. and Jang Y.S., A comprehensive metabolic map for production of bio-based chemicals, *Nat. Catal.*, <https://doi.org/10.1038/s41929-018-0212-4>, **2**, 18-33 (2019)
24. Levesque S., de Melo A.G. and Labrie S.J., Moineau Sylvain Mobilome of *Brevibacterium aurantiacum* Sheds Light on Its Genetic Diversity and Its Adaptation to Smear-Ripened Cheeses, *Front. Microbiol.*, <https://doi.org/10.3389/fmicb.2019.01270>, **10**, 1270 (2019)
25. Leynaud-Kieffer L.M.C., Curran S.C., Kim I., Magnuson J.K., Gladden J.M., Baker S.A. and Simmons B.A., A new approach to Cas9-based genome editing in *Aspergillus niger* that is precise, efficient and selectable, *PLoS One*, <https://doi.org/10.1371/journal.pone.0210243>, **14(1)**, e0210243 (2019)
26. Li Q., Seys F.M., Minton N.P., Yang J., Jiang W. and Yang S., CRISPR-Cas9^{D10A} nickase-assisted base editing in the solvent producer *Clostridium beijerinckii*, *Biotechnol. Bioeng.*, <https://doi.org/10.1002/bit.26949>, **116(6)**, 1475-1483 (2019)
27. Li Y., Lin Z., Huang C., Zhang Y., Wang Z., Tang Y.J., Chen T. and Zhao X., Metabolic engineering of *Escherichia coli* using CRISPR-Cas9 mediated genome editing, *Metab. Engin.*, <https://doi.org/10.1016/j.ymben.2015.06.006>, **31**, 13-21 (2015)
28. McAllister K.N. and Sorg J.A., CRISPR genome editing systems in the genus *Clostridium*: a timely advancement, *J. Bacteriol.*, <https://doi.org/10.1128/JB.00219-19>, **201(16)**, e00219-19 (2019)
29. Mertens S., Gallone B., Steensels J., Herrera-Malaver B., Cortebeek J., Nolmans R., Saels V., Vyas V.K. and Verstrepen K.J., Reducing phenolic off-flavors through CRISPR-based gene editing of the *FDCI* gene in *Saccharomyces cerevisiae* x *Saccharomyces eubayanus* hybrid lager beer yeasts, *PLoS One*, <https://doi.org/10.1371/journal.pone.0224525>, **14(10)**, e0224525 (2019)
30. Mitsui R., Yamada R. and Ogino H., CRISPR system in the yeast *Saccharomyces cerevisiae* and its application in the bioproduction of useful chemicals, *World J. Microbiol. Biotechnol.*, <https://doi.org/10.1007/s11274-019-2688-8>, **35** (2019)
31. Ni J., Zhang G., Qin L., Li J. and Li C., Simultaneously down-regulation of multiplex branch pathways using CRISPRi and fermentation optimization for enhancing β -amyrin production in *Saccharomyces cerevisiae*, *Synth. Syst. Biotechnol.*, <https://doi.org/10.1016/j.synbio.2019.02.002>, **4(2)**, 79-85 (2019)
32. Nomura T., Inoue K., Uehara-Yamaguchi Y., Yamada K., Iwata O., Suzuki K. and Mochida K., Highly efficient transgene-free targeted mutagenesis and single-stranded oligodeoxynucleotide-mediated precise knock-in in the industrial microalga *Euglena gracilis* using Cas9 ribonucleoproteins, *Plant Biotechnol. J.*, doi:10.1111/pbi.13174, **17(11)**, 2032-2034 (2019)

33. Otoupal P.B., Ito M., Arkin A.P., Magnuson J.K., Gladden J.M. and Skerker J.M., Multiplexed CRISPR-Cas9-Based Genome Editing of *Rhodospiridium toruloides*, *MSphere*, DOI: 10.1128/mSphere.00099-19, **4(2)**, e00099-19 (2019)
34. Palazzotto E., Tong Y., Lee S.Y. and Weber T., Synthetic biology and metabolic engineering of actinomycetes for natural product discovery, *Biotechnol. Adv.*, <https://doi.org/10.1016/j.biotechadv.2019.03.005>, **37(6)** (2019)
35. Park J., Shin H., Lee S.M., Um Y. and Woo H.M., RNA-guided single/double gene repressions in *Corynebacterium glutamicum* using an efficient CRISPR interference and its application to industrial strain, *Microb. Cell Fact.*, doi: 10.1186/s12934-017-0843-1, **17(1)** (2018)
36. Patel V.K., Soni N., Prasad V., Sapre A., Dasgupta S. and Bhadra B., CRISPR-Cas9 system for genome engineering of photosynthetic microalgae, *Mol. Biotechnol.*, doi: 10.1007/s12033-019-00185-3, **61**, 541-561 (2019)
37. Price M.A., Cruz R., Baxter S., Escalettes F. and Rosser S.J., CRISPR-Cas9 *In Situ* engineering of subtilisin E in *Bacillus subtilis*, *PLoS One*, <https://doi.org/10.1371/journal.pone.0210121>, **14(1)**, e0210121 (2019)
38. Rantasalo A., Vitikainen M., Paasikallio T., Jäntti J., Landowski C.P. and Mojzita D., Novel genetic tools that enable highly pure protein production in *Trichoderma reesei*, *Sci. Rep.*, **9(1)** (2019)
39. Scaltriti E., Carminati D., Cortimiglia C., Ramoni R., Sørensen K., Giraffa G. and Zago M., Survey on the CRISPR arrays in *Lactobacillus helveticus* genomes, *Lett. Appl. Microbiol.*, doi:10.1111/lam.13128, **68(5)**, 394-402 (2019)
40. Schultenkämper K., Brito L.F., López M.G., Brautaset T. and Wendisch V.F., Establishment and application of CRISPR interference to affect sporulation, hydrogen peroxide detoxification and mannitol catabolism in the methylotrophic thermophile *Bacillus methanolicus*, *Appl. Microbiol. Biotechnol.*, <https://doi.org/10.1002/bit.27001>, **103**, 5879-5889 (2019)
41. Schultz J.C., Cao M. and Zhao H., Development of a CRISPR/Cas9 system for high efficiency multiplexed gene deletion in *Rhodospiridium toruloides*, *Biotechnol. Bioeng.*, **116(8)**, 2103–2109 (2019)
42. Schuster J.A., Vogel R.F. and Ehrmann M.A., Characterization and distribution of CRISPR-Cas systems in *Lactobacillus sakei*, *Arch. Microbiol.*, <https://doi.org/10.1007/s00203-019-01619-x>, **201**, 337-347 (2019)
43. Schuster M. and Kahmann R., CRISPR-Cas9 genome editing approaches in filamentous fungi and oomycetes, *Fungal Genet. Biol.*, <https://doi.org/10.1016/j.fgb.2019.04.016>, **130**, 43-53 (2019)
44. Schwartz C., Cheng J.F., Evans R., Schwartz C.A., Wagner J.M., Anglin S., Beitz A., Pan W., Lonardi S., Blenner M., Alper H.S., Yoshikuni Y. and Wheeldon I., Validating genome-wide CRISPR-Cas9 function improves screening in the oleaginous yeast *Yarrowialipolytica*, *Metab. Eng.*, <https://doi.org/10.1016/j.ymben.2019.06.007>, **55**, 102-110 (2019)
45. Sekurova O.N., Schneider O. and Zotchev S.B., Novel bioactive natural products from bacteria via bioprospecting, genome mining and metabolic engineering, *Microb. Biotechnol.*, <https://doi.org/10.1111/1751-7915.13398>, **12(5)**, 828-844 (2019)
46. Shi T.Q., Gao J., Wang W.J., Wang K.F., Xu G.Q., Huang H. and Ji X.J., CRISPR/Cas9-Based Genome Editing in the Filamentous Fungus *Fusarium fujikuroi* and Its Application in Strain Engineering for Gibberellic Acid Production, *ACS Synth. Biol.*, <https://doi.org/10.1021/acssynbio.8b00478>, **8(2)**, 445-454 (2019)
47. Tian T., Kang J.W., Kang A. and Lee T.S., Redirecting Metabolic Flux via Combinatorial Multiplex CRISPRi-Mediated Repression for Isopentenol Production in *Escherichia coli*, *ACS Synth. Biol.*, <https://doi.org/10.1021/acssynbio.8b00429>, **8(2)**, 391-402 (2019)
48. Tong Y., Charusanti P., Zhang L., Weber T. and Lee S.Y., CRISPR-Cas9 Based Engineering of Actinomycetal Genomes, *ACS Synth. Biol.*, <https://doi.org/10.1021/acssynbio.5b00038>, **4(9)**, 1020-1029 (2019)
49. Tong Z., Zheng X., Tong Y., Shi Y.C. and Sun J., Systems metabolic engineering for citric acid production by *Aspergillus niger* in the post-genomic era, *Microb. Cell Fact.*, DOI <https://doi.org/10.1186/s12934-019-1064-6>, **18** (2019)
50. Vale P.F. and Little T.J., CRISPR-mediated phage resistance and the ghost of coevolution past, *Proc. R. Soc.*, doi:10.1098/rspb.2010.0055, **277(1961)**, 2097-2103 (2010)
51. Westra E.R., Houté S., Gandon S. and Whitaker R., The ecology and evolution of microbial CRISPR-Cas adaptive immune systems, *Phil. Trans. R. Soc. Lond. B. Biol. Sci.*, doi: 10.1098/rstb.2019.0101, **374(1772)** (2019)
52. Wright A., Nuñez J.K. and Doudna J.A., Biology and Applications of CRISPR Systems, Harnessing Nature's Toolbox for Genome Engineering, *Cell*, <https://doi.org/10.1016/j.cell.2015.12.035>, **164(1-2)**, 29-44 (2016)
53. Zhang F., Wen Y. and Xiong G., CRISPR/Cas9 for genome editing: Progress, implications and challenges, *Hum. Mol. Gen.*, <https://doi.org/10.1093/hmg/ddu125>, **23(R1)**, R40-R46 (2014)
54. Zhang Y., Ouyang L., Nan Y. and Chu J., Efficient gene deletion and replacement in *Aspergillus niger* by modified *in vivo* CRISPR/Cas9 systems, *Bioresour. Bioprocess*, <https://doi.org/10.1186/s40643-019-0239-7>, **6** (2019)
55. Zhou C., Liu H., Yuan F., Chai H., Wang H., Liu F., Li Y., Zhang H. and Lu F., Development and application of a CRISPR/Cas9 system for *Bacillus licheniformis* genome editing, *Int. J. Biol. Macromol.*, <https://doi.org/10.1016/j.ijbiomac.2018.10.170>, **122**, 329-337 (2019)
56. Ziogiene D., Valaviciute M., Norkiene M., Timinskas A. and Gedvilaite A., Mutations of *Kluyveromyces lactis* dolichol kinase enhances secretion of recombinant proteins, *FEMS Yeast Res.*, <https://doi.org/10.1093/femsyr/foz024>, **19(3)** (2019).

(Received 26th March 2020, accepted 31st May 2020)