



Mini Review

An Innovative Method in Microbial Intellectual Property Protection through Integrating Cryptography with Gene Editing

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Abstract

Microbes play an essential role in the rapid advancement of modern biotechnology. It serves as a key foundation of the biological industry. Enhancing development and innovation across various fields. However, intellectual property protection (IPP) for microbes faces significant challenges. Traditional IPP methods grant right-holders a period of exclusivity while requiring them to publish technical details that may result in underlying damage. On the other hand, although trade secret protection can help avoid the public disclosure of technologies, it faces its own challenges. Rapid information dissemination may lead to an underlying breach that would cause an immediate loss of legal protection on intellectual property (IP). To address the challenge, this study proposes an innovative strategy that combines cryptography with gene editing technology to resolve the dilemma. This strategy illustrated a competitive advantage with its high level of confidentiality, ability to establish unique identities, and potential to drive industrial development. Adopting this strategy holds the promise of resolving the challenges traditional IPP methods face.

Current landscape and key challenges

Microbes play an essential role in the rapid advancement of modern biotechnology. It serves as a key foundation of the biological industry. Enhancing development and innovation across various fields. However, intellectual property protection (IPP) for microbes faces significant challenges. Traditional IPP methods grant right-holders a period of exclusivity while requiring them to publish technical details that may result in underlying damage. When patents offer legal protection, they also provide a pathway for imitation, facilitating potential plagiarism and theft. On the other hand, although trade secret protection can help avoid the public disclosure of technologies, it faces its own challenges. Rapid information dissemination may lead to an underlying breach that would cause an

immediate loss of legal protection on intellectual property (IP). Once the secret is exposed, it becomes difficult to trace the source of the breach, and the cooperation or the research institute may suffer substantial losses.

Innovative solution framework

To address the above challenge, this study proposes an innovative strategy that combines cryptography with gene editing technology to resolve the dilemma. The approach begins by encrypting the protective information utilizing the Vigenère Cipher. Subsequently, the encrypted data is transformed into base sequences through a specially designed correspondence rule (Table 1) between alphabets and codons. Afterward, these sequences are inserted into neutral sites within the microbial genome. Additionally, the accuracy and stability of inserted

sequences are ensured through various methods, including polymerase chain reaction (PCR) amplification and DNA sequencing. Thus, this process provides a reliable and unique form of evidence for determining IP ownership. For example, the study demonstrated the method by applying it to a microbe from the Modern Biotechnology and Environmental Protection Research Group, Department of Bioengineering, School of Pharmaceutical and Food Engineering, Liaocheng University, Dongcheng District, Liaocheng City, Shandong Province, China. A DNA sequence, as illustrated in Figure 1, was inserted into the genome of the microbe. To verify IP ownership, the encrypted information was carried within the inserted sequence, which can be transformed back into alphabets according to the correspondence rule. These alphabets can be decrypted using Vigenère Cipher to reveal the hidden protective information, thus providing clear evidence for the ownership of microbes.

Table 1: A novel designed correspondence rules for codons.

Rules	Codons	Rules	Codons	Rules	Codons	Rules	Codons
A/a	GCA	Q/q	ACA	0	ACG	"	CGT
B/b	TGC	R/r	GTA	1	ACT	(ATC
C/c	GAC	S/s	TGG	2	CTC)	ATT
D/d	GAA	T/t	TAC	3	CTG	--	GGG
E/e	TTC	U/u	GCC	4	CTT	...	GGT
F/f	GGA	V/v	TGT	5	CCC	+	GCG
G/g	CAC	W/w	GAT	6	CCG	-	GCT
H/h	ATA	X/x	GAG	7	CCT	×	GTC
I/i	AAA	Y/y	TTT	8	TAA	÷	GTG
J/j	CTA	Z/z	GGC	9	TAG	%	TAT
K/k	ATG	space	TCT	.	GTT	#	TTA
L/l	AAC	《	AAG	,	CAG	=	TTC
M/m	CCA	》	AAT	?	CAT	~	TCA
N/n	CAA	<	AGG	!	CGA	\	TCC
O/o	AGA	>	AGT	:	CGC	@	TCG
P/p	AGC	/	ACC	;	CGG	,	TGA



Figure 1: An example to illustrate the encryption process.

Key advantages over conventional methods

This strategy enables accurate, unique editing of specific gene sequences within microbes. These sequences serve as ciphertexts, which can be decrypted through cryptography with specially designed cryptographic rules and keys. By integrating cryptography knowledge with gene editing technology, this strategy presents several advantages in IPP in the following aspects:

First, it ensures a high level of confidentiality. Traditional IPP methods often require the publication of technological details, which facilitates imitation and plagiarism. In contrast, this novel strategy offers an encryption method that allows right-owners to avoid disclosing key information about microbes. The usage of the Vigenère Cipher for encryption provides high confidentiality, preventing sensitive IP details of microbes from unauthorized access. Furthermore, it enhances trade secret protection. While legal trade secret protections are vulnerable to breaches, this technology provides a more robust cryptographic solution. Since the information is encrypted and inserted into microbes, it remains difficult to understand or utilize even if leakage occurs due to the rapid dissemination of information. Assuming the base sequence is acquired and correspondent rule between alphabets and codons, along with the Vigenère Cipher key, is concealed, the contained protective information remains intact.

Additionally, this strategy provides a unique identity for the microbes. A targeted modification of a certain gene sequence creates a distinct genetic “brand” for each microbe. The encrypted information is transformed into base sequences, which are then inserted into neutral sites in the genomes. This ensures that each processed microbe possesses a particular gene sequence that allows for its clear identification. Moreover, the strategy offers reliable verification methods for IP ownership. Various techniques can be applied to check the inserted base sequence, including PCR amplification and DNA sequencing. The resulting sequence can then be converted back into protective information using the correspondence rules and decryption algorithm, thus confirming ownership.

Furthermore, this strategy can potentially drive the development of related industries. By offering a novel method of IPP, researchers and enterprises can focus on microbial research and production without the concern of plagiarism associated with traditional IPPs. This robust IPP strategy can stimulate innovation, fostering development in a legally protected and organized manner. Additionally, it will bring benefits across multiple sectors. The healthy growth of the biological industry can enhance well-being in fields including health, agriculture, and environmental protection. For example, improved IPP for microbes can motivate the development of new medical microbes, providing more efficient medicines. It can also boost agriculture yields and quality by offering innovative agricultural microbes, thus contributing to progress in other fields like environmental protection.

Conclusion and future implications

This strategy integrated cryptography with gene editing, providing enlightening insights into microbial IPP. It illustrated a competitive advantage with its high level of confidentiality, ability to establish unique identities, and potential to drive industrial development. Adopting this strategy holds the promise of resolving the challenges traditional IPP methods face. Therefore, it provides a solid foundation for the innovation and growth of biological industries and paves the way for the future development of innovative IPP.

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Author contributions

Xiongyan Du and Chaobo Zhang devised and formulated the project, Long Tan, Haibo Zhang, and Zhenxia Zhu engaged in productive talks and analyzed the importance of this work. Xiongyan Du drafted the paper, and Jie Cheng and Chaobo Zhang conducted a thorough review of the text and made the final revisions. The final version of the work was reviewed and approved by all authors.

Competing interest statement

The authors affirm the absence of any conflict of interest. This study is exempt from conflicts, informed consent, and human or animal rights considerations.

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