Chinese Chemical Letters 37 (2026) 112450

Contents lists available at ScienceDirect

Chinese Chemical Letters

journal homepage: www.elsevier.com/locate/cclet

Artificial mismatch-assisted Cas12a crRNA splicing mechanism enabling interference-free discrimination of homologous microRNAs with single-nucleotide resolution

Xinrui Fei, Chao Lei, Zhaowei Tian, Xinyu Zhang, Wei Ren*, Chenghui Liu*

Key Laboratory of Applied Surface and Colloid Chemistry, Ministry of Education, Key Laboratory of Analytical Chemistry for Life Science of Shaanxi Province, School of Chemistry & Chemical Engineering, Shaanxi Normal University, Xi'an 710119, China

ARTICLE INFO

Article history:
Received 21 November 2025
Revised 21 January 2026
Accepted 22 January 2026
Available online 24 January 2026

Keywords:
Homologous microRNA
CRISPR/Cas12a
CrRNA splicing
Single-base discrimination
Interference-free

ABSTRACT

How to precisely discriminate homologous microRNA sequences from each other has always been a big challenge. Herein, we proposed an artificial mismatch-assisted Cas12a crRNA splicing mechanism that enables completely interference-free discrimination of homologous microRNAs with single-nucleotide resolution. Specifically, a truncated crRNA (tcrRNA) can recover its ability to activate Cas12a trans-cleavage activity when spliced with a miRNA. Since the miRNA splicing region itself is relatively short, rationally tuning the tcrRNA splicing length can render the proposed system with high sensitivity for base-variation discrimination. More importantly, we innovatively introduced an extra artificial mismatch in the miRNA splicing region, which enables the system to distinguish single-nucleotide variants in an interference-free manner. In this way, only the perfectly matched target miRNA can trigger the complete assembly of the spliced crRNA to active Cas12a, while non-target RNAs even with a single-base mismatch cannot. This mechanism ensures that the target miRNA can be accurately hooked even in the presence of a large excess of non-target homologous RNAs (100-fold). The discrimination capability of the proposed method has been proven by achieving the interference-free discrimination of the members within the let-7 family, which can hardly be achieved by conventional hybridization-based amplification methods. This work fully taps into the potential of the Cas12a system in interference-free homologous miRNA discrimination, offering a new tool for precise RNA analysis in molecular diagnostics.

© 2026 Published by Elsevier B.V. on behalf of Chinese Chemical Society and Institute of Materia Medica, Chinese Academy of Medical Sciences.

MicroRNAs (miRNAs) are a class of small noncoding RNA molecules (about 18~25 nucleotides in length) that play crucial roles in gene expression regulation [1,2]. The aberrant expression of microRNAs is closely associated with various diseases and physiological dysfunctions [3,4]. Notably, different miRNAs, even homologous miRNAs with only one or two-nucleotide differences, exhibit different biological functions and associate with different types of diseases [5–8]. Thus, the precise detection and discrimination of homologous miRNAs with highly similar sequences are important in molecular diagnostics, disease monitoring, and fundamental biological studies. Conventionally, microRNA quantification methods typically start with either miRNA-primed DNA synthesis or transcribing target miRNA into complementary DNA, followed by various nucleic acid amplification techniques [9–13]. However, these methods mainly rely on nucleic acid hybridization to distinguish target and non-target RNAs, which cannot effectively discriminate highly similar sequences, let alone sequences with single nucleotide differences [14,15]. Therefore, the interference-free discrimination and detection of homologous miRNAs with quite similar sequences remains a significant challenge.

Due to the unique target-activated trans-cleavage activity, clustered regularly interspaced short palindromic repeats/CRISPR-associated (CRISPR/Cas) systems, represented by Cas12a, have shown immense potential in precise nucleic acid analysis [16–22]. Traditionally, Cas12a can only recognize and detect DNA [23–26]. In recent years, several pioneering Cas12a systems have achieved direct detection of RNA [27–35]. For example, our group has found that with the assistance of a flexible DNA activator, any RNA can splice a sequence-conserved truncated crRNA (tcrRNA), forming a "splice-at-will" crRNA with ~100% Cas12a activation ability for the detection of ultrashort RNAs [32]. Herein, we wish to report that by finely tuning the splicing length of tcrRNA and introducing an extra artificial mismatch in the auxiliary DNA activator, the crRNA splicing system can precisely discriminate homologous microRNAs, even those with only single-base differences, in an interference-

* Corresponding authors.
E-mail addresses: wei.ren@snnu.edu.cn (W. Ren), liuch@snnu.edu.cn (C. Liu).

https://doi.org/10.1016/j.cclet.2026.112450
1001-8417/© 2026 Published by Elsevier B.V. on behalf of Chinese Chemical Society and Institute of Materia Medica, Chinese Academy of Medical Sciences.

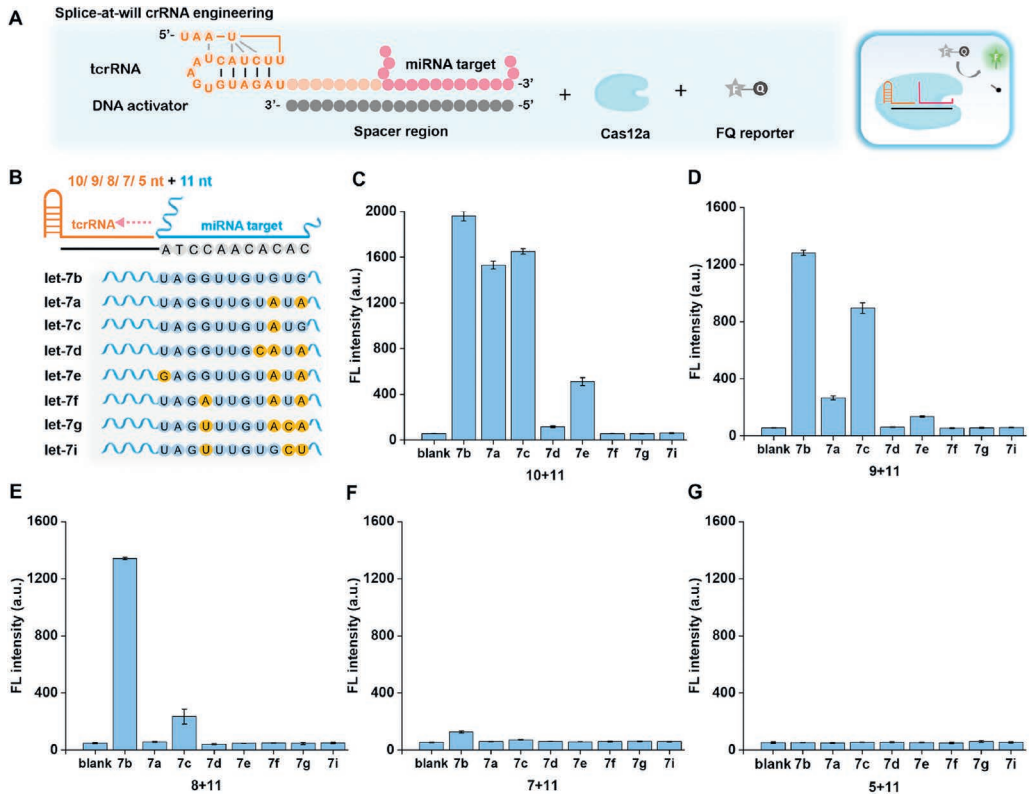


Fig. 1. Investigating the effect of tcrRNA's splicing length on homologous let-7 miRNA family discrimination. (A) Schematic representation of the spliced crRNA/activator complex induced Cas12a trans-cleavage mechanism for miRNA detection. (B) Schematic representation of splicing let-7 family members with tcrRNAs of different splicing lengths. The splicing length of let-7 family members (blue) was fixed at 11 nt (positions 9∼19 from the 5′-end), while the splicing length of the tcrRNAs (orange) was shortened from 10 nt to 5 nt. Discrimination performance of 10+11 (C), 9 + 11 (D), 8 + 11 (E), 7 + 11 (F), and 5 + 11 (G) combination modes to let-7 family members. Corresponding $X+11$ auxiliary DNA activators are composed of X nt complementary to the short spacer region of tcrRNA and 11 nt complementary to the splicing sequences of let-7 family members. The concentration of each let-7 family member was fixed at 5 nmol/L. Error bars were calculated from triplicate experiments.

free manner. Exemplified by the let-7 family member let-7b as the proof-of-concept analyte, only let-7b produced a distinct signal, while the other family members did not at all, demonstrating completely interference-free homologous microRNA discrimination capability. What is more, even in the presence of an excess of single-base variants, the target miRNA can still be effectively and accurately detected without any interference. This work not only exhibits excellent capability in single-nucleotide variant discrimination but also promotes the CRISPR/Cas12a-based precise short RNA quantification.

A conventional Cas12a crRNA comprises a sequence-conserved repeat region and a variable spacer region that base-pairs with the DNA activator [36,37]. Our recent study has discovered that a truncated crRNA motif (tcrRNA) could cooperate with arbitrary short RNAs to rebuild the spacer region and form a "splice-at-will" crRNA to activate Cas12a trans-cleavage activity [32], which can efficiently cut the surrounding fluorophore/quencher-labeled reporter (FQ reporters, 5′-FAM-CCCCCCCCCC-BHQ1–3′) and generate strong fluorescence (Fig. 1A), allowing the Cas12a system to directly detect short RNA molecules. Besides its capability for detecting short RNAs of varied lengths, the system's compatibility with flexible splicing designs offers a possibility for addressing the challenge of precisely discriminating homologous miRNAs.

Since the spliced crRNA is composed of two very short sequences, it is inherently sensitive to base variants. Thus, we speculate it is a promising tool for achieving accurate RNA analysis with single-base resolution. To investigate this potential of the crRNA splicing mechanism, we selected let-7b, an important biomarker for major depression and breast cancer, but faces severe interference from multiple homologous miRNAs with similar sequences [38–41], as a proof-of-concept target (Table S1, Figs. S1 and S2 in Supporting information). The corresponding splicing region for let-7 homologous family members was fixed at 11 nt, which covers almost all mutations and various cases, including one to four base mismatches (Fig. 1B). In this case, we discover that the homologous let-7 miRNA discrimination capability can be rationally tuned by adjusting the tcrRNA length. As shown in Figs. 1C–E, upon gradually reducing the tcrRNA splicing length from 10 to 8 nt, the signal induced by let-7b slightly diminishes, yet the distinction between the let-7 family is gradually enhanced. When the tcrRNA splicing length is further shortened from 7 nt to 5 nt (Figs. 1F and G), the signal generated by the target let-7b becomes too weak to be discriminated. This is because shorter tcrRNAs can only form weak base-pairing with the DNA activator, hindering the efficient assembly of the spliced crRNA to activate Cas12a. Moreover, the total spacer length of the 5 + 11 mode may be also too short to efficiently activate Cas12a trans-cleavage, resulting in insufficient signal output to distinguish target let-7b from non-targets. Specifically, the 8 + 11 combination mode stands out as the optimal condition, effectively distinguishing between other let-7 family members while still giving high target fluorescence. However, by using the 8 + 11 combination, compared with the signals arising from other members of the let-7 family that can be effectively suppressed, let-7c with one-base difference generates a weak yet obvious interference signal.

To further eliminate the interference of let-7c, which only has a single-base mismatch with let-7b, we introduce artificial mismatches on the activator to enhance the specificity of the proposed system. Given that mismatches at the terminal region have the least impact on binding stability, we introduced an extra

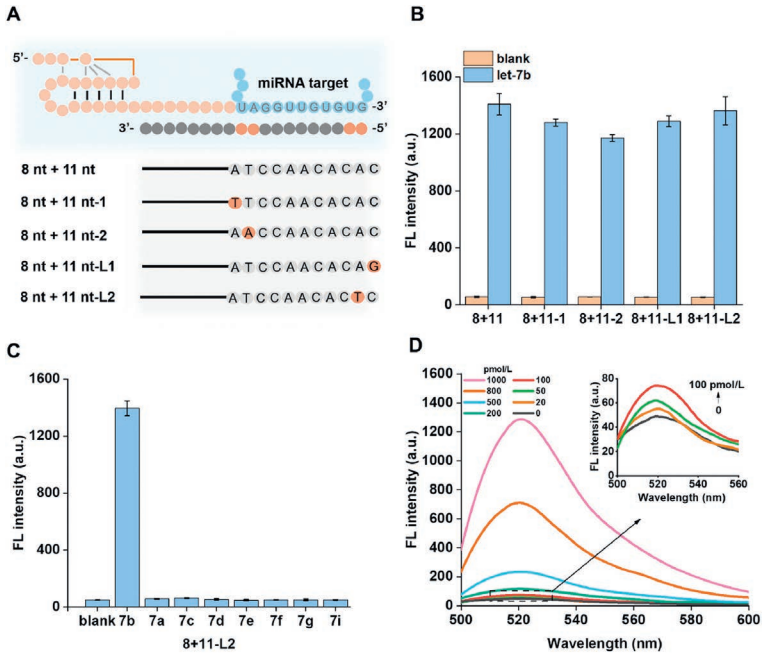


Fig. 2. Investigating the effect of artificial mismatch in the activator on let-7 miRNA family discrimination. (A) Schematic representation of introducing an additional mismatch to the splicing region of the activator complementary to the miRNA target. (B) Fluorescence intensity of the system in response to different artificial mismatch sites introduced in the auxiliary DNA activator. (C) Discrimination performance of the 8 + 11-L2 combination mode towards let-7 family members. The concentration of each let-7 family member was fixed at 5 nmol/L. (D) Fluorescence spectra of the system in response to different concentrations of let-7b using the 8 + 11-L2 combination mode. The fluorescence spectra from bottom to top correspond to let-7b miRNA concentrations of 0 (blank), 20, 50, 100, 200, 500, 800, and 1000 pmol/L, respectively.

mismatch at the splicing terminus and the nearby sites of the activator that are complementary to let-7b. Specifically, a series of activators with extra artificial mismatches at the first (from 3′-end), second, last, and second-to-last splicing sites complementary to let-7b were designed and denoted as 8 + 11–1, 8 + 11–2, 8 + 11-L1, and 8 + 11-L2, respectively (Fig. 2A). As shown in Fig. 2B, the four single-base mismatched activators show an insignificant effect on the fluorescence signal of let-7b. Among them, the 8 + 11-L2 activator performs best, generating almost the same fluorescence signal as that of the fully matched activator (8 + 11). This may be attributed to the fact that it only disrupts a weak A-T base pairing (Fig. S3 in Supporting information). By using the 8 + 11-L2 activator, the finely-tuned system can specifically recognize let-7b, producing a significant fluorescence signal, while other family members, even let-7c with only a single-base mismatch, no longer generate any interference signal (Fig. 2C). The sensitivity of the finely-tuned system for let-7b detection was also tested. As shown in Fig. 2D, the fluorescence response of the system increased gradually as the let-7b concentration increased from 20 pmol/L to 1 nmol/L. A good linear relationship (with $R^2 = 0.9950$) was obtained between the fluorescence intensity (at 518 nm) and let-7b concentration within the range of 20 pmol/L to 500 pmol/L (Fig. S4 in Supporting information), showing a good sensing performance. Overall, the finely-tuned crRNA splicing system, with shortened splicing region and carefully-selected mismatch, sharpens the selectivity without compromising sensitivity, achieving the ability of interference-free discrimination and detection of homologous miRNAs.

To investigate the interference-free discrimination mechanism of the finely-tuned crRNA splicing system, homologous target miRNA (let-7b), non-target with single-base mismatch (let-7c), tcrRNA, DNA activator, and Cas12a were pre-mixed in different orders and tested by non-denaturing polyacrylamide gel electrophoresis (PAGE) to check their interactions. As displayed in Fig. 3A, for tcrRNA-8 with a short binding region, it cannot form a heteroduplex with the DNA activator (lane 3). On this basis, the addition of let-7b and let-7c can be clearly identified by the upward bands in lane 4 and lane 5. When tcrRNA and DNA activator are premixed with Cas12a, the bands corresponding to those of tcrRNA and DNA activator slightly faded (lane 6), indicating that the tcrRNA and DNA activator can still partly bind with Cas12a in the absence of let-7b but yield a Cas12a-unactivated conformation. Compared with lane 6, further adding let-7b resulted in the disappearance of the tcrRNA and DNA activator bands (lane 7), revealing that the target miRNA promotes the complete assembly of spliced crRNA and Cas12a. However, when let-7b is replaced by let-7c, the bands of tcrRNA and let-7c remain visible (lane 8), suggesting that non-targets with even a single-base mismatch are not allowed to access and interact with Cas12a.

To further verify this discrimination mechanism, the crRNA splicing system with 10 + 11 splicing mode was tested (Fig. 3B). Unlike tcrRNA-8, tcrRNA-10 has a relatively longer binding region and can form a tcrRNA/DNA activator heteroduplex (lane 4). After mixing let-7b or let-7c with the tcrRNA/DNA activator, the bands (lane 5 and lane 6) show almost no change with those in lane 4. When mixing tcrRNAs/DNA activator heteroduplex with Cas12a, the band of the heteroduplex is still visible (lane 7). However, regardless of further adding target (let-7b) or non-target with a single-base mismatch (let-7c), all the bands disappear (lane 8 and lane 9), indicating the 10 + 11 splicing mode provides a relatively loose discrimination mechanism, giving target and non-target the same chance to bind with Cas12a. Importantly, the above electrophoresis results for the 10 + 11 and 8 + 11-L2 splicing modes align perfectly with the fluorescence detection results depicted in Figs. 1C and 2C. Specifically, for the 8 + 11-L2 combination mode, only the perfectly matched target miRNA can drive the complete assembly of the spliced crRNA and activate Cas12a, whereas non-target RNAs with even a single-base mismatch cannot. This endows the finely-tuned crRNA splicing system with single-base discrimination capability.

To confirm the robustness of the discrimination capability of this system towards similar miRNA species, further tests were con-

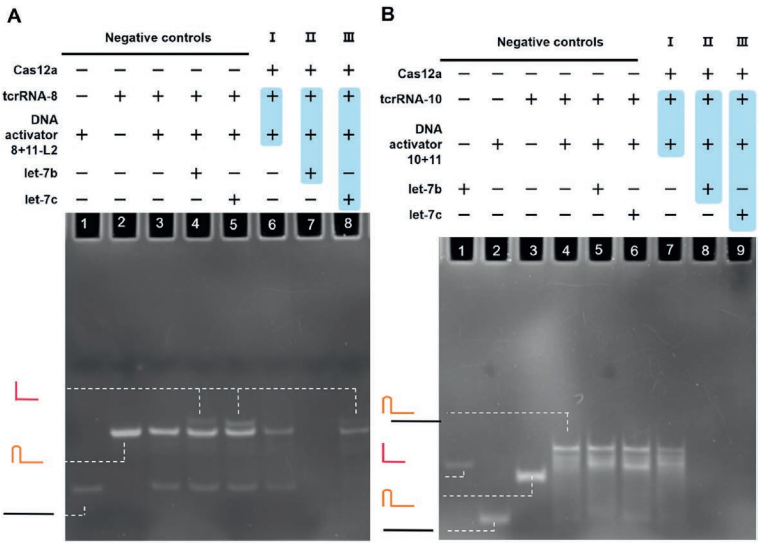


Fig. 3. Investigating the interference-free discrimination mechanism of the finely-tuned crRNA splicing system. (A) Non-denaturing PAGE results using 8 + 11-L2 combination modes with short splicing length and an extra mismatch. (B) Non-denaturing PAGE results using 10+11 combination modes. The pre-assembled portions are highlighted with a blue frame.

ducted in mixture samples (schematically illustrated in Fig. 4A). First, let-7b was mixed with miRNA-21, a non-let-7 family member, at the ratios of 1:0, 1:1, 1:10, and 1:100 for detection. As shown in Fig. 4B, the fluorescence intensity was almost unchanged even when the proportion of miRNA-21 increased to 1:100. The results suggested that the RNAs with unrelated sequences have a negligible impact on the system. Then, a more complicated sample containing let-7b and let-7c (with a single-base mismatch) was tested. As a result, the fluorescence intensity did not change much when let-7c was present at a 100-fold higher concentration than let-7b (Fig. 4C). This demonstrates that the system maintains its high specificity even in the co-existence of numerous single-base variants. The system's performance was also assessed with samples containing other let-7 family members. According to Fig. 4D, even when challenged with samples containing 10-fold concentrations of each let-7 family member, the fluorescence signal was almost identical to that of the pure let-7b sample. Thus, despite the increased complexity, our system can still selectively distinguish let-7b from other let-7 family members without cross-interference. These results demonstrate that the system can accurately identify the target miRNA even when it is present with a large amount of highly similar homologous sequences, which is suitable for precise miRNA detection and discrimination in complex biological environments.

To emphasize the advantage of the finely-tuned crRNA splicing system in discriminating the homologous let-7 miRNA family, we compared it with a classical real-time stem-loop PCR method (RT-qPCR) [11]. Here, the target was detected in a mixed sample that contains not only the target but also non-targets with only one or two base mismatches. In the conventional RT-qPCR assay, the miRNA target binds to the RT stem-loop primers for reverse transcription. And then, the resulting DNA product is quantified using real-time PCR (Fig. S5 in Supporting information). During this process, targets and non-targets are simply distinguished via minor free energy changes of strand hybridization. Thus, the non-target RNAs can easily interfere with the detection. This is also illustrated by the RT-qPCR results (Fig. 4E), where the CT value of let-7b in the mix sample is much lower than that obtained in the pure sample. This underestimation of CT value suggests that the detection of let-7b may be affected by the presence of let-7a and let-7c, leading to a much higher quantification value (230.6 pmol/L) compared to the actual concentration (100 pmol/L) (Fig. 4F). In contrast, in our finely-tuned crRNA splicing system, due to the strict Cas12a binding recognition, the target miRNA can be accurately hooked among the potential interference of the highly similar sequences, yielding more accurate quantification.

To further evaluate the detection performance of the finely-tuned crRNA splicing strategy in real biological samples, total small RNA samples extracted from HeLa cells were tested. As shown in Fig. S6 (Supporting information), the content of let-7b in 10 ng of small RNA sample was determined to be 43.6 pmol/L (in 10 μL) using the RT-qPCR method, which was higher than that determined by the proposed method (23.0 pmol/L in 10 μL). We further spiked 100 pmol/L let-7b into 10 ng total small RNA samples, and the determination results from the RT-qPCR method and the proposed method were 149.5 pmol/L and 124.3 pmol/L, respectively. Notably, the two methods achieved similar recovery rates (104.1 % for RT-qPCR and 101.1 % for the proposed method). Therefore, we suppose the lower let-7b content detected in the cell extraction by the proposed method is due to its superb nucleotide discrimination capability to preclude the interference of homologous microRNAs. To further prove this, 100 pmol/L let-7a was added to the total small RNA samples instead of let-7b. As to the RT-qPCR method, the quantification of let-7b was interfered with and presented an overestimated quantification value (102.0 pmol/L). In contrast, utilizing the finely-tuned crRNA splicing sensing system, the content of let-7b can still be accurately detected (21.2 pmol/L), further demonstrating the reliability of the proposed method in analyzing real complex samples. To sum up, the finely-tuned crRNA splicing system shows a unique advantage in quantifying miRNAs with high specificity and anti-interference capability, which cannot be achieved by traditional hybridization-initiated amplification methods. It effectively solves the challenges of interference-free discrimination of single-nucleotide variants in a simple way, expanding the CRISPR/Cas-based toolbox.

In this work, an artificial mismatch-assisted Cas12a crRNA splicing mechanism is presented, which enables the precise discrimination of homologous miRNAs with single-base resolution. Specifically, a truncated crRNA (tcrRNA) can splice with the target miRNA to activate Cas12a, and shortening the tcrRNA splicing length decreases the Cas12a tolerance for mismatches in homologous miRNAs. By further innovatively introducing extra artificial mismatches, the crRNA splicing system's ability in interference-free discrimination of single-base mutations is significantly

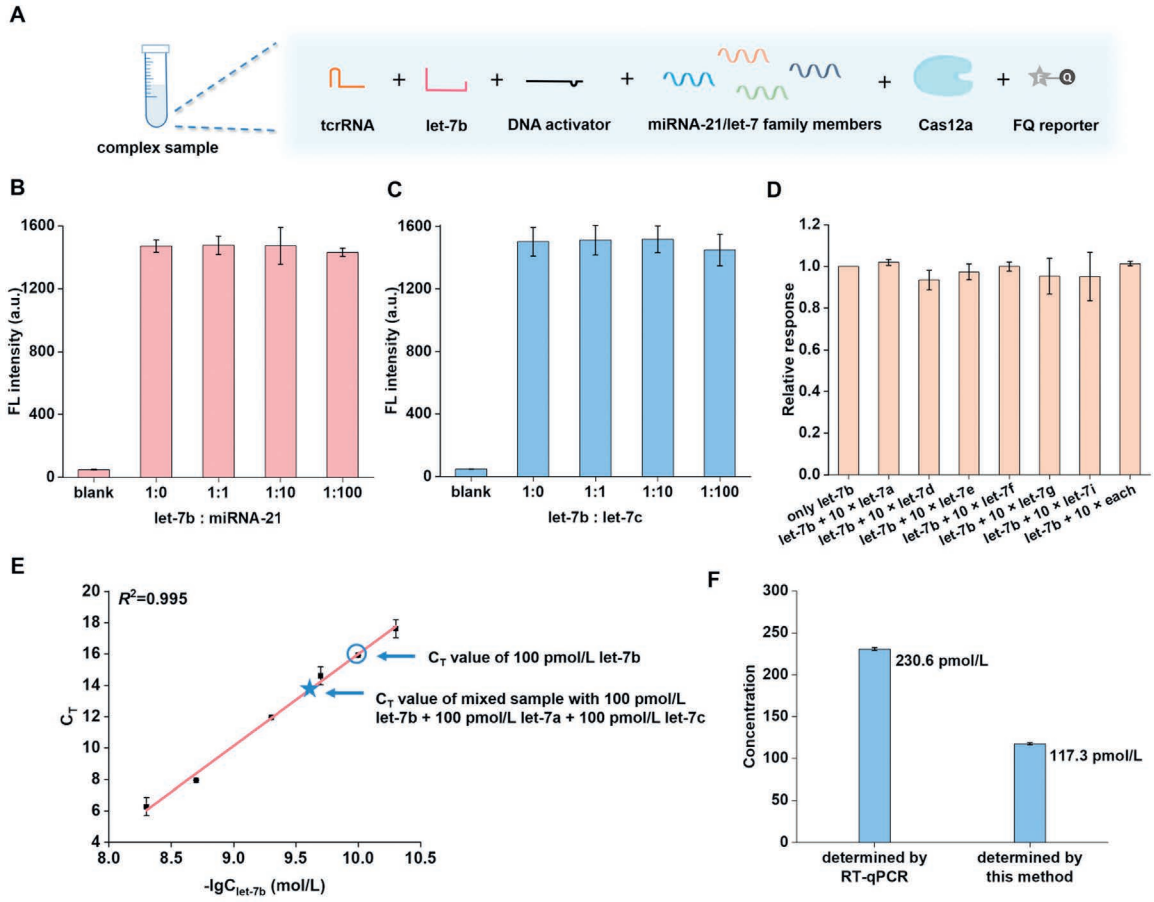


Fig. 4. Anti-interference detection performance of the finely-tuned crRNA splicing system in complex samples. (A) Schematic diagram of detecting let-7b in complex samples. Fluorescence detection results for the complex samples containing different ratios of let-7b and miRNA-21 (B) or let-7b and let-7c (C). The concentration of let-7b was maintained at 5 nmol/L, while the concentrations of the other let-7 family members (or miRNA-21) were spiked at 0-, 1-, 10-, and 100-fold molar equivalents relative to let-7b. (D) Relative responses induced by let-7b and the complex samples containing let-7b and other let-7 family members, with a ratio of 1:10. Error bars were calculated from triplicate experiments. (E) Standard calibration curve of the stem-loop RT-PCR system for the quantification of let-7b. (F) Quantitative performance comparison between conventional RT-PCR and the finely-tuned crRNA splicing system for detecting 100 pmol/L let-7b in the mixed sample containing 100 pmol/L let-7b, 100 pmol/L let-7a, and 100 pmol/L let-7c. Error bars were calculated from triplicate experiments.

improved. After a comprehensive investigation, it is suggested that only perfectly matched target miRNA can facilitate the complete assembly of spliced crRNA and activation of Cas12a, while the non-target RNA with even a single-base mismatch cannot. In this way, target miRNA can be effectively distinguished and detected with no interference even when non-target RNAs were present in substantial excess (100-fold). Therefore, the finely-tuned crRNA splicing design with introduced artificial mismatch endows the Cas12a system with robust interference-free single-nucleotide discrimination capabilities, which cannot be achieved by conventional hybridization-initiated amplification methods, making it a powerful and promising tool for the accurate discrimination of similar miRNA markers. This work primarily focuses on establishing a high specific and interference-free method for distinguishing homologous miRNA species. In the future, we envision that by integrating this high-specificity Cas12a activation mechanism with diverse signal amplification methods, the detection sensitivity could be further boosted without affecting the discrimination performance, thereby expanding the real-world application scenarios of the Cas12a-based miRNA detection strategy.

CRediT authorship contribution statement

Xinrui Fei: Writing – original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Chao Lei:** Methodology, Investigation, Formal analysis. **Zhaowei Tian:** Methodology, Investigation, Formal analysis. **Xinyu Zhang:** Methodology, Investigation. **Wei Ren:** Writing – review & editing, Resources, Project administration, Formal analysis, Data curation, Conceptualization. **Chenghui Liu:** Writing – review & editing, Supervision, Resources, Project administration, Funding acquisition, Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This work was supported by the National Natural Science Foundation of China (No. 22074088); the Program for Changjiang Scholars and Innovative Research Team in University (No. IRT_15R43); the Innovation Capability Support Program of Shaanxi Province (No. 2025RS-CXTD-058); the Xi'an Science and Technology Project (No. 25ZQRC00009); the Natural Science Basic Research Program of Shaanxi (No. 2025JC-YBMS-117); and the Fundamental Research Funds for the Central Universities (No. GK202501013).

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.cclet.2026.112450.

References

[1] L. He, G.J. Hannon, Nat. Rev. Genet. 5 (2004) 522–531.
[2] D.P. Bartel, Cell 136 (2009) 215–233.
[3] R.M. O'Connell, D.S. Rao, A.A. Chaudhuri, D. Baltimore, Nat. Rev. Immunol. 10 (2010) 111–122.
[4] S. Quah, G. Subramanian, J.S.L. Tan, K.H. Utami, P. Sampath, Trends Mol. Med. 31 (2025) 21–35.
[5] G.A. Calin, C.M. Croce, Nat. Rev. Cancer 6 (2006) 857–866.
[6] E. Mogilyansky, I. Rigoutsos, Cell Death. Differ. 20 (2013) 1603–1614.
[7] J.K. Wang, Z. Wang, G. Li, Cancer Lett. 454 (2019) 134–145.
[8] E. Chirshev, K.C. Oberg, Y.J. Ioffe, J.J. Unternaehrer, Clin. Transl. Med. 8 (2019) 24.
[9] Y. Zhou, Q. Huang, J. Gao, et al., Nucleic. Acids. Res. 38 (2010) e156.
[10] D.M. Zhou, W.F. Du, Q. Xi, J. Ge, J.H. Jiang, Anal. Chem. 86 (2014) 6763–6767.
[11] C. Chen, D.A. Ridzon, A.J. Broomer, et al., Nucleic. Acids. Res. 33 (2005) e179.
[12] T. Nolan, R.E. Hands, S.A. Bustin, Nat. Protoc. 1 (2006) 1559–1582.
[13] P. Androvic, L. Valihrach, J. Elling, R. Sjoback, M. Kubista, Nucleic. Acids. Res. 45 (2017) e144.
[14] K.A. Cissell, S. Shrestha, S.K. Deo, Anal. Chem. 79 (2007) 4754–4761.
[15] T. Ouyang, Z. Liu, Z. Han, Q. Ge, Anal. Chem. 91 (2019) 3179–3186.
[16] Y. Dai, Y. Wu, G. Liu, J.J. Gooding, Angew. Chem. Int. Ed. 59 (2020) 20754–20766.
[17] Y. Tang, L. Gao, W. Feng, et al., Chem. Soc. Rev. 50 (2021) 11844–11869.
[18] Z. Weng, Z. You, J. Yang, et al., Angew. Chem. Int. Ed. 62 (2023) e202214987.
[19] H. Hu, Z. Ye, L. Zhang, et al., Chin. Chem. Lett. 37 (2026) 111184.
[20] N. Song, S. Li, Z. Lv, et al., Chin. Chem. Lett. 34 (2023) 108134.
[21] Q.N. Li, A.X. Ma, D.X. Wang, et al., Anal. Chem. 96 (2024) 6426–6435.
[22] Z. Feng, R. Liu, E. Yang, R. Lian, J. Zhang, J. Anal. Test. 9 (2025) 1–11.
[23] J.S. Chen, E. Ma, L.B. Harrington, et al., Science 360 (2018) 436–439.
[24] S.Y. Li, Q.X. Cheng, J.M. Wang, et al., Cell Discov. 4 (2018) 20.
[25] D.C. Swarts, M. Jinek, Mol. Cell 73 (2019) 589–600.
[26] K. Shi, S. Xie, R. Tian, et al., Sci. Adv. 7 (2021) eabc7802.
[27] S.R. Rananaware, E.K. Vesco, G.M. Shoemaker, et al., Nat. Commun. 14 (2023) 5409.
[28] M. Hu, X. Cheng, T. Wu, Nucleic Acids Res. 52 (2024) 7384–7396.
[29] S. Zhao, Q. Zhang, R. Luo, et al., Chem. Sci. 15 (2024) 18347–18354.
[30] J. Moon, C. Liu, Nat. Commun. 14 (2023) 7504.
[31] Y. Chen, X. Wang, J. Zhang, et al., Nat. Commun. 15 (2024) 8342.
[32] X. Fei, C. Lei, W. Ren, C. Liu, Nucleic Acids Res. 53 (2025) gkaf002.
[33] Z. Hu, S. Ling, J. Duan, et al., Nucleic Acids Res. 53 (2025) gkaf017.
[34] S. Zhao, Q. Zhang, J. Sun, et al., Nano Lett. 25 (2025) 8431–8441.
[35] X. Xia, Z. Liang, G. Xu, et al., Anal. Chem. 97 (2025) 2873–2882.
[36] D. Dong, K. Ren, X. Qiu, et al., Nature 532 (2016) 522–526.
[37] D.C. Swarts, J. Van Der Oost, M. Jinek, Mol. Cell 66 (2017) 221–233.
[38] S. Roush, F.J. Slack, Trends. Cell Biol. 18 (2008) 505–516.
[39] J. Schultz, P. Lorenz, G. Gross, S. Ibrahim, M. Kunz, Cell Res. 18 (2008) 549–557.
[40] S.A. Joosse, V. Müller, B. Steinbach, K. Pantel, H. Schwarzenbach, Br. J. Cancer 111 (2014) 909–917.
[41] A. Gururajan, M.E. Naughton, K.A. Scott, et al., Transl. Psychiatry 6 (2016) e862.