

RESEARCH PAPERS | Published: 16 July 2020

Predicting Characteristics of the Potentially Binding Sites for miRNA in the mRNA of the TCP Transcription Factor Genes of Plants

[A. K. Rakhmetullina](#), [A. Yu. Pyrkova](#), [A. V. Goncharova](#) & [A. T. Ivashchenko](#) [Russian Journal of Plant Physiology](#) **67**, 606–617(2020) | [Cite this article](#)**63** Accesses | [Metrics](#)

Abstract

The expression of the TCP transcription factor family genes depends on miRNA, whose effect on the translation of their mRNA is poorly studied. Interactions between miRNA and mRNA were studied with the MirTarget program, which allows estimating of quantitative characteristics of binding of the whole nucleotide sequence of miRNA to mRNA. The analysis of binding of 125 miRNAs to mRNAs of 28 genes of the TCP family of *Triticum aestivum* L. revealed eight target genes for miR319-3p, miR444a-3p, miR5086-5p, miR9666a-3p, and miR9780-3p. miRNA binding sites in mRNA of the TCP family genes of *T. aestivum* were located in the CDS only. Only 12 of 22 mRNAs of the TCP family genes of *Oryza sativa* L. bounded to the miR1487b-5p, miR1846a-5p, miR1848-5p, miR1858a-5p,

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)[Accept All Cookies](#)

AC213524.3_FGP003, AC233950.1_FGP002, and GRMZM2G034638_P01. Only one miRNA was bound to mRNAs of the genes GRMZM2G035944_P01, AC190734.2_FGP003, and AC205574.3_FGP006. miRNA binding sites were located in the 5'UTR and CDS regions of mRNAs of the TCP family genes of *Z. mays*. Ten of 27 TCP family genes of *Arabidopsis thaliana* (L.) Heynh. were shown to be targets for the miR319-3p, miR4228-5p, miR4228-3p, miR5021-5p, miR5658-5p, and miR8181-5p out of 429 miRNAs of *A. thaliana*. mRNAs of the AT1G53230 and AT2G31070 genes had binding sites for the miR319c-3p, miR5021-5p, and miR5658-5p, while mRNA of the AT3G15030 gene had binding site for the miR319a-3p and miR4228-3p. Two miRNAs bounded to mRNAs of the genes AT1G69690, AT3G02150, and AT3G47620. One miRNA bounded to mRNAs of the genes AT1G30210, AT4G18390, and AT5G08330. miRNA binding sites were located in the 5'UTR, CDS and 3'UTR regions of mRNA of the TCP gene family of *A. thaliana*. mRNAs of six groups of the TCP family genes had binding sites for the miR319-3p, miR444a-3p, miR5021-5p, miR5658-5p, and miR2102-5p, which encode the oligopeptides QRGPLQS, STSETS, SSSSSS, HHHHHH, GGGGGG, and AAAAAA conservative in the TCP family proteins of different plant species. Quantitative characteristics of miRNA binding to mRNAs of plant transcription factors of the TCP family, which participate in regulation of growth and development of plants, have been predicted.

This is a preview of subscription content, access via your institution

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

Manage Settings

Accept All Cookies

[Learn more about Institutional subscriptions](#)

REFERENCES

- 1 Li, S., The *Arabidopsis thaliana* TCP transcription factors: a broadening horizon beyond development, *Plant Signal. Behav.*, 2015, vol. 10: e1044192.

<https://doi.org/10.1080/15592324.2015.1044192>

[CAS](#) [Article](#) [PubMed](#) [PubMed Central](#) [Google Scholar](#)

- 2 Manassero, N., Viola, I., Welchen, E., and Gonzalez, D., TCP transcription factors: architectures of plant form, *Biomol. Concepts*, 2013, vol. 4, p. 111.

<https://doi.org/10.1515/bmc-2012-0051>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

- 3 Sengupta, A. and Hileman, L., Novel traits, flower symmetry, and transcriptional autoregulation: new hypotheses from bioinformatic and experimental data, *Front. Plant Sci.*, 2018, vol. 9: 1561. <https://doi.org/10.3389/fpls.2018.01561>

[Article](#) [PubMed](#) [PubMed Central](#) [Google Scholar](#)

- 4 Mart, M. and Cubas, P., TCP genes: a family snapshot ten years later, *Trends*

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

<https://doi.org/10.1105/tpc.113.113159>

[CAS](#) [Article](#) [PubMed](#) [PubMed Central](#) [Google Scholar](#)

7 Navarro, L., Dunoyer, P., Jay, F., Arnold, B., and Dharmasiri, N., A plant miRNA contributes to antibacterial resistance by repressing auxin signaling, *Science*, 2006, vol. 312, p. 436. <https://doi.org/10.1126/science.aae0382>

[CAS](#) [Article](#) [Google Scholar](#)

8 Zhang, L., Zheng, Y., Jagadeeswaran, G., Li, Y., Gowdu, K., and Sunkar, R., Identification and temporal expression analysis of conserved and novel microRNAs in *Sorghum*, *Genomics*, 2011, vol. 98, p. 460.

<https://doi.org/10.1016/j.ygeno.2011.08.005>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

9 Phillips, J.R., Dalmay, T., and Bartels, D., The role of small RNAs in abiotic stress, *FEBS Lett.*, 2007, vol. 581, p. 3592.

<https://doi.org/10.1016/j.febslet.2007.04.007>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

10 Yan, Y., Wang, H., Hamera, S., Chen, X., and Fang, R., miR444a has multiple functions in the rice nitrate-signaling pathway, *Plant J.*, 2014, vol. 78, no. 1, p.

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

12 Tomotsugu, K., Fumihiko, S., and Masaru, O., Roles of miR319 and TCP transcription factors in leaf development, *Plant Physiol.*, 2017, vol. 175, p. 874.
<https://doi.org/10.1104/pp.17.00732>

[CAS](#) [Article](#) [Google Scholar](#)

13 Li, Z., An, X., Zhu, T., Yan, T., Wu, S., Tian, Y., Li, J., and Wan, X., Discovering and constructing ceRNA-miRNA-target gene regulatory networks during anther development in maize, *Int. J. Mol. Sci.*, 2019, vol. 20, no. 14: e3480.
<https://doi.org/10.3390/ijms20143480>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

14 Yusuf, N.H., Ong, W.D., Redwan, R.M., Latip, M.A., and Kumar, S.V., Discovery of precursor and mature microRNAs and their putative gene targets using high-throughput sequencing in pineapple (*Ananas comosus* var. *comosus*), *Gene*, 2016, vol. 571, p. 71. <https://doi.org/10.1016/j.gene.2015.06.050>

[CAS](#) [Article](#) [Google Scholar](#)

15 Wu, F.Y., Tang, C.Y., Guo, Y.M., Yang, M.K., Yang, R.W., Lu, G.H., and Yang, Y.H., Comparison of miRNAs and their targets in seed development between two maize inbred lines by high-throughput sequencing and degradome analysis, *PLoS One*, 2016, vol. 11, no. 7: e0159810.
<https://doi.org/10.1371/journal.pone.0159810>

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

T.D., Development-related miRNA expression and target regulation during staggered in vitro plant regeneration of Tuxpeño VS-53--5 maize cultivar, *Int. J. Mol. Sci.*, 2019, vol. 20, no. 9: e2079. <https://doi.org/10.3390/ijms20092079>

- 18 Wang, Y., Peng, M., Wang, W., Chen, Y., He, Z., Cao, J., Lin, Z., Yang, Z., Gong, M., and Yin, Y., Verification of miRNAs in ginseng decoction by high-throughput sequencing and quantitative real-time PCR, *Heliyon*, 2019, vol. 5, no. 4: e01418. <https://doi.org/10.1016/j.heliyon.2019.e01418>

[Article](#) [PubMed](#) [PubMed Central](#) [Google Scholar](#)

- 19 Aydinoglu, F. and Lucas, S.J., Identification and expression profiles of putative leaf growth related microRNAs in maize (*Zea mays* L.) hybrid ADA313, *Gene*, 2019, vol. 690, p. 57. <https://doi.org/10.1016/j.gene.2018.12.042>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

- 20 Zhang, Q., Zhang, Y., Wang, S., Hao, L., Wang, S., Xu, C., Jiang, F., and Li, T., Characterization of genome-wide microRNAs and their roles in development and biotic stress in pear, *Planta*, 2019, vol. 249, no. 3, p. 693. <https://doi.org/10.1007/s00425-018-3027-2>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

- 23 Garg, A. and Heinemann, U., A novel form of RNA double helix based on G·U and C·A⁺ wobble base pairing, *RNA*, 2018, vol. 24, p. 209.

<https://doi.org/10.1261/rna.064048.117>

[CAS](#) [Article](#) [PubMed](#) [PubMed Central](#) [Google Scholar](#)

- 24 Dai, X., Zhuang, Z., and Zhao, P., Computational analysis of miRNA targets in plants: current status and challenges, *Brief. Bioinform.*, 2011, vol. 12, p. 115.

<https://doi.org/10.1093/bib/bbq065>

[CAS](#) [Article](#) [PubMed](#) [Google Scholar](#)

- 25 Niyazova, R., Berillo, O., Atambayeva, Sh., Pyrkova, A., Alybayeva, A., and Ivashchenko, A., miR-1322 binding sites in paralogous and orthologous genes, *Mol. Phylogenet.*, 2014, vol. 2015, p. 962637.

<https://doi.org/10.1155/2015/962637>

[CAS](#) [Article](#) [Google Scholar](#)

- 26 Kamenova, S.U., The characteristics of miRNA binding sites in mRNA of *ZFHX3* gene and its orthologs, *Vavilov J. Genet. Breed.*, 2018, vol. 22, p. 438.

<https://doi.org/10.18699/VJ18.380>

[Article](#) [Google Scholar](#)

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

plants, *Russ. J. Plant Physiol.*, 2014, vol. 61, p. 807.

<https://doi.org/10.1134/S1021443714050033>

[CAS](#) [Article](#) [Google Scholar](#)

29 Bari, A., Orazova, A., and Ivashchenko, A., miR156- and miR171-binding sites in the protein-coding sequences of several plant genes, *Biomed. Res. Int.*, 2013, vol. 2013: 307145. <https://doi.org/10.1155/2013/307145>

[CAS](#) [Article](#) [PubMed](#) [PubMed Central](#) [Google Scholar](#)

[Download references](#) ↓

Author information

Affiliations

Al-Farabi Kazakh National University, Almaty, Kazakhstan

A. K. Rakhmetullina, A. Yu. Pyrkova, A. V. Goncharova & A. T. Ivashchenko

Corresponding author

Correspondence to [A. T. Ivashchenko](#).

Ethics declarations

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

Abbreviations: CDS—coding sequence; miRNA—small RNA that inhibits mRNA translation; mRNA—messenger ribonucleic acid; ΔG —free energy of miRNA binding; ΔG_m —free energy of miRNA binding to a fully complementary nucleotide sequence; n.—nucleotide; TCP—the transcription factor family of plants (Teosinte branched1/Cinnamata/proliferating cell factor (TCP) family); 3'UTR—3'-untranslated region; 5'UTR—5'-untranslated region.

Rights and permissions

[Reprints and Permissions](#)

About this article



Check for
updates

Cite this article

Rakhmetullina, A.K., Pyrkova, A.Y., Goncharova, A.V. *et al.* Predicting Characteristics of the Potentially Binding Sites for miRNA in the mRNA of the TCP Transcription Factor Genes of Plants. *Russ J Plant Physiol* **67**, 606–617 (2020).

<https://doi.org/10.1134/S1021443720040147>

[Download citation](#) 

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)

Issue Date

July 2020

DOI

<https://doi.org/10.1134/S1021443720040147>

Keywords:

plant

miRNA

mRNA

binding site

genes

transcription factor

TCP

Over 10 million scientific documents at your fingertips

[Academic Edition](#)

[Corporate Edition](#)

[Home](#)

[Impressum](#)

[Legal information](#)

[Privacy statement](#)

[California Privacy Statement](#)

[How we use cookies](#)

[Manage cookies/Do not sell my data](#)

[Accessibility](#)

[Contact us](#)

Not logged in - 49.12.85.158

Not affiliated

SPRINGER NATURE

© 2021 Springer Nature Switzerland AG. Part of [Springer Nature](#).

Your privacy

We use cookies to ensure the functionality of our website, to personalize content and advertising, to provide social media features, and to analyze our traffic. If you allow us to do so, we also inform our social media, advertising and analysis partners about your use of our website. You can decide for yourself which categories you want to deny or allow. Please note that based on your settings not all functionalities of the site are available. [View our privacy policy.](#)

[Manage Settings](#)

[Accept All Cookies](#)