Coevolution Pattern and Functional Conservation or Divergence of miR167 and their targets across Diverse Plant Species

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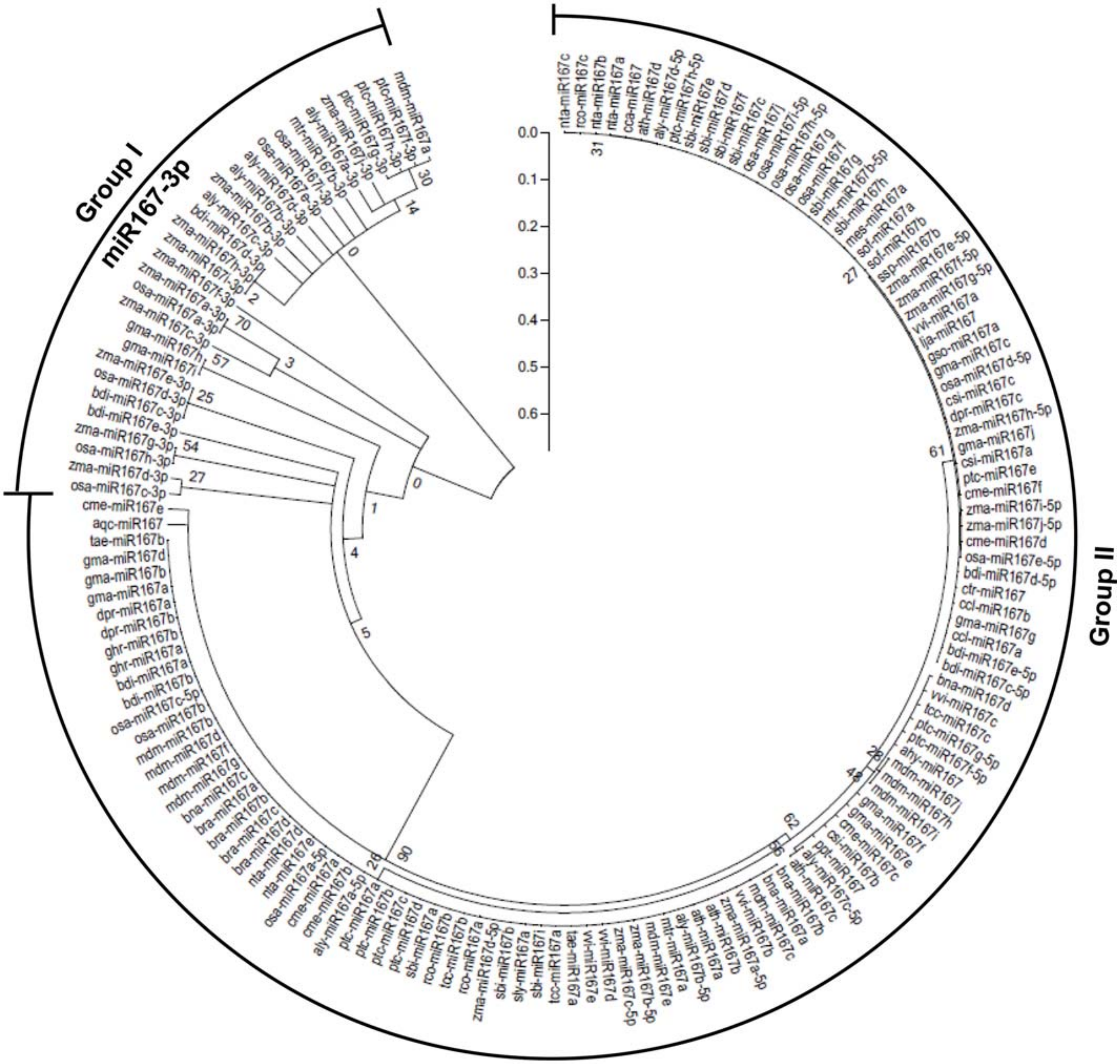
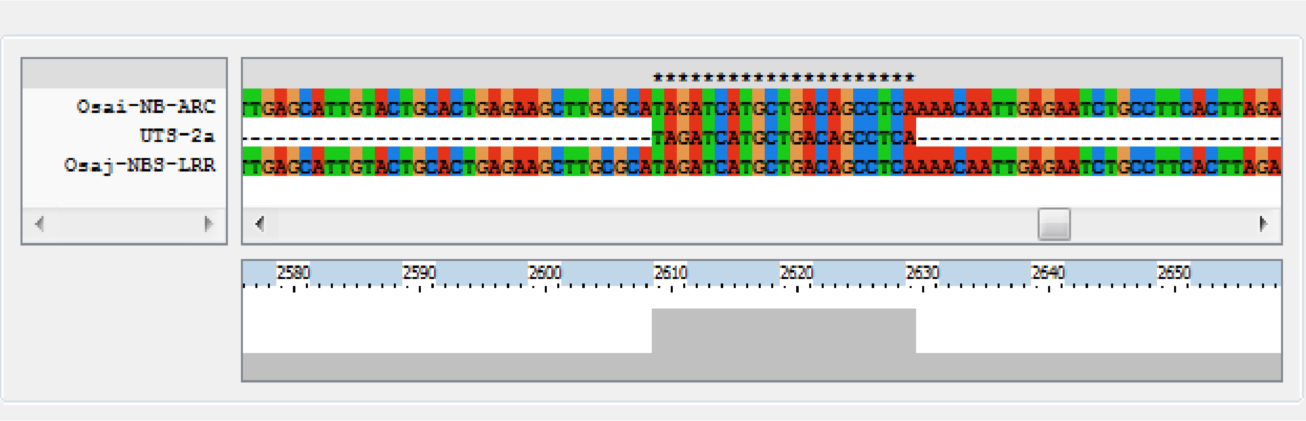
Supplementary Figure S**1.** A NJ phylogeny of miR167s using MEGA5. The tree is divided into group I and group II. The group I contains three miR167-3p sequences, whereas all other miRNA167s (-5p) belong to the group II. The scale bar represents the nucleotide substitution rate.

Supplementary Figure S2. Multiple sequence alignment between UTS-2a (target of UmiR167-2), Osa-NBS-LRR (japonica rice cultivar-group) and Osa-NB-ARC (indica rice cultivar-group).

Supplementary Information S3. Novel target sequences and their cleavage or complementarity with miR167s. (**A**) Target sequence of mdm-miR167a and sequenced 5' RLM RACE PCR products (with ligated RNA adapter). The *Mdm-CNBL10* gene sequence has complementary biding sites (yellow) and cleavage sites (where underline starts within mRNAs) and primer location have been indicated. (**B**) Complementarity between UmiR167-7 and *Gma-MCCC* and red arrow shows cleavage site. The *Gma-MCCC* gene sequence has complementary biding sites (yellow) and cleavage sites (where underline starts within mRNAs) and primer location have been indicated. (**C**) Complementarity between UmiR167-8 and *Gma-LRPK* and red arrow shows cleavage site. The *Gma-LRPK* gene sequence has complementary biding sites (yellow) and cleavage sites (where underline starts within mRNAs) and primer location have been indicated



Supplementary Figure S1



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Osai-NB-ARC   TTGAGCATTGTACTGCACTGAGAAGCTTGCGCATAGATCATGCTGACAGCCTCAAAACAATTGAGAATCTGCCTTCACTTAGA
UTS-2a        ---------------------------------TAGATCATGCTGACAGCCTCA-----------------------------
Osaj-NBS-LRR  TTGAGCATTGTACTGCACTGAGAAGCTTGCGCATAGATCATGCTGACAGCCTCAAAACAATTGAGAATCTGCCTTCACTTAGA
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Supplementary Figure S2

Supplementary Information S3

S3A. Target sequence of mdm-miR167a and sequenced 5’ RLM RACE PCR products

Mdm-CNBL10 sequence

>gi|657971446|ref|XM_008379288.1| PREDICTED: Malus x domesticacalcineurin B-like protein 10 (LOC103440590), mRNA

5’AGCAAATKTATAATCCGCGCCAGCGGCGCGAGAGAGAAGCAGCCCCTCGAAGCCTTCTGGTGCA
CCCGAGGACATTTTTCATYGAAAAGCACAAGGCACAGAAGAAGTAGCCTCKATCTGATGAATTGT
TGCAGACGACAGCAATGGAATTCTCGAGATCGAGTTCGTTATCAATCGGAGAGAAGATCTGCGCG
GCGTTTATACCGTTTGTAGCTATGGTAGAGGCGCTGGTTTTCGCCGTGAGCGGTTGCTGCAGCCAC
CGTTCCYGCCGCCCAATCAACCGCGGTTTCGCTTGCGGCTATATGTCTCACCTCGCCGATGAAACC
AGATTTACTGTTAATGAGCTGGAGGCGTTGTATGAGCTTTTTAAGAAGCTGAGCAGCTCGATTATC
GACGACGGATCGATTCACAAGGAGGAGCTTCAATTAGCACTATTTCAAACTCCCCAAGGCGAAAA
TCTGTTCCTTGACCGGGTTTTTGATCTATTTGATGAAAAGAAAAATGGTGTCATTGAATTTGATGAG
TTTGTTCATGCACTCAATRTCTTCCATCCTTACGCCCCTATTGATGACAAAATCGATTTTGCATTTC
GGCTGTATGATCTGAGACAAACCGGATTCATTGAGMGAGAAGAGGTTAAGCAAATGGTGATTGCC
ATATTGATGGAATCCGACGTGAAATTGCCGGAT^{x}GATATTCTTGAGGAAATCATTGAGAAGACATT
TGCCGACGCTGATGCTGACAAAGATGGGAAAATTAACAAAGAAGAATGGAAGGTTTTCGTGCTTC
GGCATCCATCGCTTCTAAAAAACATGACTCTTCCTTATTTGAAGGACATCACGACAGTATTTCCGA
GTTATATTTTTCACACCGAAGTTGAAGACTGAGCATTTGAAAGCCTTTTCCTACAGAGGATCTTTA
GAAGAAGAGCATAATTCCAAAGCTCCTGCGTATTGCGGAGATACTTCCATCAATTCAAAGGGGGW
MACATCCGAGTTTTAGGCAAGGCCGGGATGGC -3’

(Note: ^{x}: cleavage site by mdm-mR167a).

5’ RLM RACE PCR products (from band at ~316 bp)

Sequence 1

>Mdm-CNBL10-Seq1
GAACACGAAAACCTTCCATTCTTCTTTGTTAATTTTCCCATCTTTGTCACATCA
CGTCGGCAAATGTCTTCTCAATGATTTCCTCAAGAATATCTTTCTACTCCTTCA
GTCCATGTCAGTGTCCAC

Sequence 2

>Mdm-CNBL10-Seq2
CGATGGATGCCGAAGCACGAAAACCTTCCATTCTTCTTTGTTAATTTTCCCATC
TTTGTCAGCATCAGCGTCGGCAAATGTCTTCTCAATGATTTCCTCAAGAATATC
TTTCTACTCCTTCAGTCCATGTCAGTGTCC

S3B. Sequence alignment of gma-miR167h and its target *Gma-MCCC*

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gma-miR167h   21 UCAACUUCGACGGUCGUACUA 1
                  ::::::::::::..:..: ::
Gma-MCCC    1810 AGUUGAAGCUGCUGGUGUAAU 1830
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Gma-MCCC **sequence**

>TC440662 UniRef100_Q42777 Cluster: Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial precursor; n=1; Glycine max|Rep: Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial precursor - Glycine max (Soybean), complete

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GGCACCAACCTCCATGGCTTCTCTGGCGTTGCTCCGCAGAACCACGCTCTCCCAC
TCGCACGTGCGTGCACGAGCCTTCTCTGAGGGGAAGAGCAGCAACAGACACCGC
ATCGAGAAGATTCTAGTAGCCAACCGCGGTGAAATCGCTTGCAGGATCACGAGG
ACCGCGCGGAGGCTCGGCATTCAAACCGTCGCCGTTTACAGCGACGCCGACAAG
GACTCGCTCCACGTTGCGTCCGCCGACAAGGCCATCCGAATCGGACCGCCACCG
GCGCGGCTCAGTTACTTGAACGGAGCCTCCATCGTCGACGCCGCCATTCGCTCCG
GCGCGCAGGCTATTCACCCTGGGTATGGATTCTTGTCGGAGAGTGCTGACTTCGC
CAAGCTCTGTGAGGAGAGTGGTCTCACTTTTATAGGGCCTCCTGCGTCTGCTATT
CGAGATATGGGTGACAAGAGTGCATCGAAGAGAATAATGGGAGCTGCAGGTGTG
CCTCTTGTACCTGGATATCACGGATATGATCAAGATATTGAAAAAATGAAGTTGG
AAGCTGATAGAATTGGATATCCAGTCCTAATTAAGCCAACTCATGGTGGAGGTG
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ACCCTTATCAGGTCATGCTTTTGAAGCTCGAATCTATGCTGAAAATGTTCAAAAA
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AGTCCGAGTGGAGACTGGAGTTAAAGAAGGAGACAAAGTTAGCATGCACTATGA
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AAACTGAAGGATAGTTTGTCAAAGTTTCAGGTTGCAGGTCTGCCAACCAATGTCC
ACTTTCTTCAAAAGCTTGCTAATCACAGGGCATTTGCAATTGGCAATGTGGAGAC
TCATTTTATTGATAACTACAAAGAAGACCTCTTTGTTGATGCTAACAATTCAGTGT
CTGTGAAAGAAGCATATGAAGCTGCTAGACTTAATGCATCCCTGGTGGCCGCAT
GCCTCATTGAAAAAGAGCATTTCATATTGGCTAGAAATCCACCTGGGGGCAGCA
GCTTGCTCCCTATATGGTATTCTTCTCCACCTTTCAGAATCCATCATCAAGCTAAG
CGTAGAATGGAACTTGAGTGGGATAATGAATATGGTAGTGGTAGCTCAAAGATC
ATGAAGCTTACCATCACTTATCAGCCTGATGGGAGATACCTAATTGAGACAGAA
CAAAATGGATCTCCTGTTTTAGAAGTGAAATCAACATATGTAAAAGATAACTATT
TTAGAGTTGAAGCTGCTGGTGTAATCAATGATGTTAATGTAGCTGTTTATTCAAA
GGATCAAATAAGGCATATTCATATTTGGCAAGGGTCCTGTCATCATTATTTCAGA
GAGAAACTAGGCCTGGAGCTGTCTGAGGATGAAGAATCCCAACATAAACCCAAA
GTTGAAACATCAGCCAACCCTCAAGGGACAGTTGTAGCACCCATGGCAGGCTTG
GTAGTTAAGGTTCTAGTGGAGAACAAGACAAGAGTGGAGGAAGGACAACCTGTG
TTAGTATTGGAAGCAATGAAGATGGAGCATGTTGTAAAGCACCTTCTTCTGGCTA
TGTGCATGGGCTTCAACTTATGGTGGGTGAACAGGTTTCAGATGGCAGTGTTCTT
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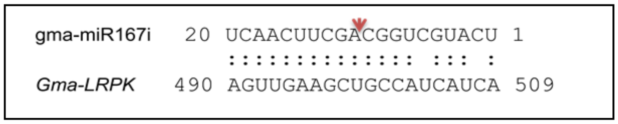
TTCAGTGTAAAGGATCAATAAAATCGCACTTGACAGCTTTACGCCAAGACTTTGG
CAAGGGGGACATTATCTGGAATTCTGGATGGATAGTTATACGCAGGTTAACAAC
CGAACACCCGAACACCTGGGAGTTGATTACTTGCTTAACACTCTTTGTAACTCAA
TTTTTCAAGTTACAAAAGTTGAAATATACTTTACAATAATGCAAGTAGTTCCTCC
AGCCATTAATAACAAAGCTGTAATTTGCTTCATGTTTAGATATTCTTCCATCAACG
GGTCTTCACCTGCCCCTTAAATAAATCTCTAAAGGGGAGATGCCCACACGCCTAA
AATCATGTGATAGTCGGAACACCATATTCCAACTACGAATCCAAGATTCAATTGT
CTTGGGGGAAAC

S3C. Sequence alignment of gma-miR167i and its target *Gma-LRPK*



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gma-miR167i    20 UCAACUUCGACGGUCGUACU 1
                  :::::::::::::: ::: :
Gma-LRPK      490 AGUUGAAGCUGCCAUCAUCA 509
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***Gma-LRPK* sequence**

>gi|571475916|ref|XM_003534705.2| PREDICTED: Glycine max uncharacterized LOC100779669 (LOC100779669), transcript variant X1, mRNA

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CCTCCTCATGCTGACCATCTCCAATTCCAAACCTTGAATGAAATGCAGAGGCAAA
ATCAGAGGTAAAATTGAGGATGAATAAGTGATGCATCCAAATCAATTAAGCCAA
GTACAGACTTGAAGTTGGGCACTAACTACTGGTAAGGATTTCCCATGTGTGCATT
ATCTACATACCATGGGGTGTTTTTCTTCAAAAGTCATAGCCAGATCAATCAGCTT
CCATGAAGAGAGAAAGAAGAGATCACAGAGAAAAACTAACGGCATTCCATTGCT
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CGGTGTCGAATATCCAGCAATTGCTAGTCTTAGAGAATGGCTCCCTGCAAGTGGA
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CATTAGAAATGCAAATGAATCCAGTGAGGATTCTGTATTTAGTCCAGAGTTGGTG
TCTGCCTTTGAACAATGTATGCAAAAACTTGAAGCAGATGAAGAAAACATTCTG
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