

Supplementary Material

Genome-wide identification and bioinformatics analyses of host defense peptides Snakin/GASA in mangrove plants

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1. Supplementary Figures and Tables

1.1. Supplementary Figures

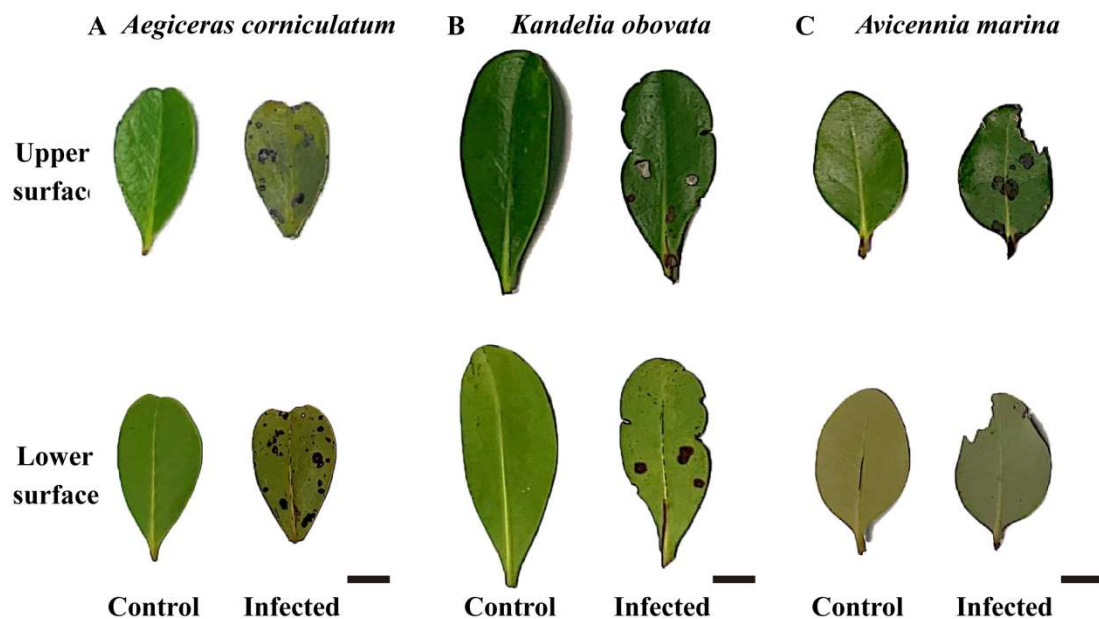


Figure S1: Normal leaves and leaves infected with pathogenic microorganisms of *A. corniculatum*, *K. obovata* and *A. marina*. The scales are 1 cm.

1.2. Supplementary Tables

Table S1: Primers used for qRT-PCR.

Gene	Primer -F (5'-3')	Primer -R (5'-3')
<i>KoGASA1</i>	TGGAACCTGCTATGGCTCAAC	AGAGGGAACACACTTGCCT
<i>KoGASA2</i>	AGATGCACCACAAGATGCTC	GCTTGTTCCTGCTAGGTTCCAG
<i>KoGASA3</i>	CTTTGTGGGGAGAGGTGCAA	CATAAGTCCCTGGTGGCACA
<i>KoGASA4</i>	AGCTCCATCGCTCAGATTGC	GCATTTGGAGCAGCACTTCA
<i>KoGASA5</i>	CAAGGCAGGTTACCAGGACC	ATAGCACGGGCATTCTGACTT
<i>KoGASA6</i>	CCCAATGCCATCACAATGC	GCACACGGCCTTATCCCAT
<i>KoGASA7</i>	TTGTCTTCCAGGCCAAACCTT	AGCAGGGGCAGACATCGTA
<i>KoGASA8</i>	GCGGGGTAGGTGCTCAAAA	AAGGGCACTCGTCCTTGTTA
<i>KoGASA9</i>	AATGGGATTGTGTTTCATCCGGT	CTCATTTGCTTGCTCCACC
<i>AcGASA1</i>	GAGCTCTTGTGTTTGAGCCC	ATTTGAGGCACCGGTCTTGT
<i>AcGASA2</i>	AGATGCTCAAAGGCAGCGAG	TTCGAGGTGCAATTAACGCTG
<i>AcGASA3</i>	AAGAACCAAGCACCACTCA	CCCGAGCTGAGCTAAAACCT
<i>AcGASA4</i>	AAAGGAACATGAAGATTGAGAACG	GTGGTGCTTGGTTCCTGCT
<i>AcGASA5</i>	GCGAGAGATGCTCGGAGG	CAAGGGCACTCGTCCTTGTT
<i>AcGASA6</i>	ATCAACCGAGTCAGTCTTCACAA	CACACTCCTGCCTTTCGTCC
<i>AcGASA7</i>	TGAGCTCTGGTTTGTTGAGC	TATAAATGCCATTGAGGCACCG
<i>AcGASA8</i>	GAGCTCTGGTTTGTTGAGCC	ATAAATGCCATTGAGGCACCG
<i>AcGASA9</i>	AAATGTTTGTTGTTGCCACCT	CCTCCTCTTTTGGTCTTCCAGTT
<i>AcGASA10</i>	ATGGCCTATAAGCCCATGCC	ATCCCGCAATATTCCAAGCATC
<i>AcGASA11</i>	CACCACCAACTCCAGTGACC	CAAAGGGGAACGCAATCGAA
<i>AcGASA12</i>	TTCATCTCTCATCCAGGCGAC	GCAGCATATCCCGCAATACTTC
<i>AcGASA13</i>	GGGTAAAAGCCAGGTGCAAGA	CTTCTTGTTCTCATAGCAAGGGC
<i>AmGASA1</i>	GACACAGGCATTGCGGCTT	GCATGGCTTCTTGATGCTGT
<i>AmGASA2</i>	ATCTTGACAGACGCTATGCCT	CAGCAGTACTTGACGCAACG
<i>AmGASA3</i>	CCTGTCCATGCTCCAAAGGG	TAAATGCACACATTGCCCCAC
<i>AmGASA4</i>	CCTTCTCCACCAGTTAAGGCAT	CTCACGGCGCATAGTGGAG
<i>AmGASA5</i>	CTTCACTGGTTCACACCACAC	ACATTCTCACAGCAGATTCCA
<i>AmGASA6</i>	AGCCTTCAACCTCAGGAGTG	TTGTTCCCATACGTGCCTGG
<i>AmGASA7</i>	GCCACGTCAGAACTGCATAC	CTGCACAGATTGCGCTTCTT
<i>AmGASA10</i>	CAGCAACGATGGTGAAAGGTG	TGCTCTGAGTGTAAGCTGC
<i>AmGASA12</i>	CAGCATCAAGTACCACCACA	ACACATTTGGCCTTGGCAC
<i>AmGASA13</i>	ATACCACAAGCCCTGCATGTT	AGTTGTTGTAGCAAGGGCAAAC
<i>AmGASA15</i>	CGAAGACCGTTTACCTCCTCA	CTTTGAGCATCGGCGCTTG
<i>AmGASA18</i>	TCGAAGGCCACGATCAAGAG	TCTTCTGTCTCGACGCCAAT
<i>AmGASA21</i>	CTCAAAGTGCGCTGTTCCGG	AAGGGCACTCGTCCTTGTTG
<i>AmGASA23</i>	GCTGTCCCTGTCCCAACTC	AAGCAACGATCCCACTTCC
<i>AmGASA25</i>	CATCATGGCAAACCGCCAG	GCGTAGGCCGAGTCTCT

Table S2: Reference genes were used in qRT-PCR.

Internal reference	Primer -F (5'-3')	Primer -R (5'-3')
β -Actin of <i>A. corniculatum</i>	AGCTCATCGGTGGAGAAGAA	GTTGGAACAGGACCTCAGGA
18SrRNA of <i>A. corniculatum</i>	ACCATAAACGATGCCGACCAG	TTCAGCCTTGCGACCATACTC
β -Actin of <i>A. marina</i>	AGATGGCAGAAGCTGAGGA	CCATGCCAACCATCACACC
18SrRNA of <i>A. marina</i>	ACCATAAACGATGCCGACCAG	CCTTTAAGTTTCAGCCTTGCG
GAPDH of <i>K. obovata</i>	TCGTCCAGGTCTCCAAG	AGCCAGATCCACCACTC
18SrRNA of <i>K. obovata</i>	CCTGAGAAACGGCTACCACATC	ACCCATCCCAAGGTCCAACTAC

Table S3: Subcellular localization prediction of Snakin/GASA family members in *A. marina*, *K. obovata* and *A. corniculatum*.

Proteins	WoLF PSORT	Plant-PLoc
AcGASA1	Chloroplast	Extracellular
AcGASA2	Extracellular	Extracellular
AcGASA3	Chloroplast	Chloroplast
AcGASA4	Chloroplast	Chloroplast
AcGASA5	Extracellular	Extracellular
AcGASA6	Nucleus	Nucleus
AcGASA7	Cytoskeleton	Chloroplast
AcGASA8	Chloroplast	Chloroplast
AcGASA9	Chloroplast	None
AcGASA10	Extracellular	Extracellular
AcGASA11	Extracellular	Chloroplast
AcGASA12	Extracellular	Extracellular
AcGASA13	Chloroplast	Extracellular
KoGASA1	Extracellular	Golgi apparatus
KoGASA2	Extracellular	Extracellular
KoGASA3	Extracellular	Chloroplast
KoGASA4	Extracellular	Extracellular
KoGASA5	Extracellular	Extracellular
KoGASA6	Extracellular	Extracellular
KoGASA7	Extracellular	Extracellular
KoGASA8	Extracellular	Extracellular
KoGASA9	Mitochondrion	Chloroplast
AmGASA1	Extracellular	Extracellular
AmGASA2	Chloroplast	Extracellular
AmGASA3	Chloroplast	Cytoplasm
AmGASA4	Extracellular	Chloroplast

AmGASA5	Extracellular	Extracellular
AmGASA6	Extracellular	Extracellular
AmGASA7	Mitochondrion	Extracellular
AmGASA8	Extracellular	Extracellular
AmGASA9	Extracellular	Extracellular
AmGASA10	Extracellular	Extracellular
AmGASA11	Extracellular	Extracellular
AmGASA12	Chloroplast	Chloroplast
AmGASA13	Chloroplast	Extracellular
AmGASA14	Extracellular	Extracellular
AmGASA15	Extracellular	Extracellular
AmGASA16	Extracellular	Extracellular
AmGASA17	Extracellular	Extracellular
AmGASA18	Extracellular	Extracellular
AmGASA19	Extracellular	Chloroplast
AmGASA20	Extracellular	Extracellular
AmGASA21	Extracellular	Extracellular
AmGASA22	Chloroplast	Extracellular
AmGASA23	Extracellular	Extracellular
AmGASA24	Extracellular	Chloroplast
AmGASA25	Extracellular	Chloroplast
AmGASA 26	Chloroplast	Extracellular
AmGASA 27	Extracellular	Extracellular

Table S4: Microbial detection of infected leaves.

Sample species	Infected fungal species	Infection symptoms
<i>A. corniculatum</i>	<i>Tropicoporus texanus</i>	marginal and/or interveinal scorching [1]
<i>K. obovata</i>	<i>Jattaea</i> spp.	yellow and/or ulcerated [2]
<i>A. marina</i>	<i>Berkeleyomyces basicola</i>	Wilt and/or black root rot [3]

Table S5: Identification of pathogenic microorganism

Species	Sequencing results of microbial PCR assays on infected leaves	NCBI search result Scientific Name	E value	Per. ident
<i>A. corniculatum</i>	CGCTCGATTGAGTTGGCTCTTGACTTTACACACCTGTGCACCTTCGGTCTGAATTTCTTGCTTGAATTTTATTCAAGTC CGCTCCCTGGAGTGGGATTAGAGTGTGCGTTGGATTTATTTCCATGGCTCACTCTGCAAGAAAATCGTCCGTTTTTTAC ACCTATTTTGTATGTCTTTGAATTTAATCGATTGCTCCGTGATGGGGTGATTGTAAAAATAAATACAACCTTCAGCAACGG ATCTCTTGGCTCTCCCATCGATGAAGAACGCAGCGAACTGCGATACGTAATGTGAATTGCAGAAATCAGTGAATCATCG AATCTTTGAACGCATCTTGCGCCGCTCGGTTTTCCGAGGGGCACGTCTGTTGAGTGTACGTTAATCTATCACCCACCTT TTGGTGAAGTGGACTTGGACTGTGCTGTCATTTATTTGACGGCTCGTCTCGAAATGCATTGTTGCCTGCAGAGTCTTGCGC GGAGCGAGACTGATGAAACGGTGTGATATTTATATCTGCGCTGAAGTAGTCGGTTTTGAGCTGCTGCACGAGTTGCACTC TGGGCTTATAAAATCGAGGATTTTAATTAATCCCAATTTCTTTGCGTTTGACCTCAAATCAGATGGGACT	<i>Dichostereum eburneum</i>	3.00E-65	94.90%
<i>K. obovata</i>	CCGGGGGCCGCGCGTGGGCGAGTCTCTCGCCGTGCGCCCCATCCCGTCCGACGCGTCCCGTGCCTGCTGGCGG CCAACGAACCCCGCGCGGAACGCGCCAAGGAAAACCGAAACGAAGCGTCAGCTCCCGCCGCCCCGTTTCGCGGTG CGCTCGGGTGGGGGACGAGGCGTCTCTGAATGTCAAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATG AAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCC CGAAGCCATCAGGCCAGGGCACGTCTGCCTGGGCGTCACGCATAGCGTCGCCCCCTCTCCCTCTCCACGGAGCGGAAC CGGAGGGGGCGGACATTGGCCTCCCGTGTCCCTCGGGCGCGGCCGCCAAATGCGATCCCTCGGCGACGCACGTCTG CGACCAGTGGTGGTTGAAAACCTCAACTCGCGTGTGGTGTCTGTTCAACGACGTCGTCCGATCGGGCATCGAGAGCG ACCCAACGGCGCGATGCGCCTTCGACCGCGACCCAGGTGAGGCGGGATCAC	<i>Jattaea discreta</i> <i>Jattaea leucospermi</i> <i>Jattaea tumidula</i> <i>Jattaea taediosa</i> <i>Jattaea ribicola</i> <i>Jattaea mookgoponga</i> <i>Jattaea aphanospora</i>	3.00E-29 3.00E-29 3.00E-29 3.00E-29 3.00E-29 3.00E-29 3.00E-29	87.27% 87.27% 87.27% 87.27% 87.27% 87.27% 87.27%
<i>A. marina</i>	CCACCCGGGGCCGCGCGTGGGCGAGTCTCTCGCCGTGCGCCCCATCCCGTCCGACGCGTCCCGTGCCTGCTGCTG GCGGCCAACGAACCCCGCGCGGAACGCGCCAAGGAAAACCGAAACGAAGCGTCAGCTCCCGCCGCCCCGTTTCGC GGTGCCTCGGGTGGGGGACGAGGCGTCTCTGAATGTCAAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATC GATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTG CGCCCGAAGCCATCAGGCCAGGACGCTCTGCCTGGGCGTCACGCATAGCGTCGCCCCCTCTCCCTCTCCACGGAGCG	<i>Berkeleyomyces basicola</i>	2.00E-36	88.14%

GAACCGAGGGGGCGGACATTGGCCTCCCGTGCTCCCTCGGGCGCGGCCGGCCCAATGCGATCCCTCGGCGACGCAC
GTCGCGACCAGTGGTGGTTGAAACTCAACTCGCGTGCTGGCTGTCGTGTTCAACGACGTCGTCGATCGGGCATCGAG
AGCGACCCAACGGCGCGATGCGCCTTCGACCGCGACCCAGGTCAGGCGGGAT

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