

Supplementary Materials

Comparative profiling of microRNAs in the winged and wingless English grain aphid, *Sitobion avenae* (F.) (Homoptera: Aphididae)

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Table Legends

Table S1. Summary of conserved miRNA.

Table S2. Summary of predicted miRNA.

Table S3. The predicted targets for *S. avenae* miRNAs based on sequences from a model species *D. melanogaster* and four aphid species, *A. pisum*, *M. persicae*, *T. citricida*, and *A. gossypii*.

Table S4. GO annotation for identified *S. avenae* miRNAs.

Table S5. KEGG analysis for targets of differentially expressed *S. avenae* miRNAs.

Table S6. Criteria used for miRNA prediction.

Figure Legends

Figure S1. Homology analysis of *S. avenae*Let-7 with other insects. api: *Acyrtosiphon pisum*; bmo: *Bombyx mori*; tca: *Tribolium castaneum*; der: *Drosophila erecta*; dpe: *Drosophila persimilis*; dan: *Drosophila ananassae*; dwi: *Drosophila will*; isc: *Ixodes scapularis*; ame: *Apis mellifera*;cqu: *Culex quinquefasciatus*; dmo: *Drosophila mojavenensis*; mse: *Manduca sexta*; dgr: *Drosophila grimshawi*; aga: *Anopheles gambiae*; dme: *Drosophila melanogaster*; dvi: *Drosophila virilis*; aae: *Aedes aegypti*; hme: *Heliconius Melpomene*; tur: *Tetranychus urticae*; dya: *Drosophila yakuba*; dse: *Drosophila sechellia*; ngi: *Nasonia giraulti*; dsi: *Drosophila simulans*; nlo: *Nasonia longicornis*; nvi: *Nasonia vitripennis*. (The red box indicates the miRNA seedpositions 2-8)

Figure S2. Homology analysis of *S. avenaemiRNA-7* with other insects. api: *Acyrtosiphon pisum*; bmo: *Bombyx mori*; tca: *Tribolium castaneum*; der: *Drosophila erecta*; dpe: *Drosophila persimilis*; dan: *Drosophila ananassae*; dwi: *Drosophila will*; isc: *Ixodes scapularis*; ame: *Apis mellifera*;cqu: *Culex quinquefasciatus*; dmo: *Drosophila mojavenensis*; mse: *Manduca sexta*; dgr: *Drosophila grimshawi*; aga: *Anopheles gambiae*; dme: *Drosophila melanogaster*; dvi: *Drosophila virilis*; aae: *Aedes aegypti*; hme: *Heliconius Melpomene*; tur: *Tetranychus urticae*; dya: *Drosophila yakuba*; dse: *Drosophila sechellia*; ngi: *Nasonia giraulti*; dsi: *Drosophila simulans*; nlo: *Nasonia longicornis*; nvi: *Nasonia vitripennis*. (The red box indicates the miRNA seedpositions 2-8)

Figure S3. Predicted stem-loop structures for three novel miRNA precursors.

Figure S4. PCR Products of nine selected miRNAs potentially involved in *S. avenae* wing development. cDNAs from the winged *S. avenae* were used for template. **Lane 1:** 100bp ladder marker; **Lane 2:** *miR-315*; **Lane 4:** *miR-1*; **Lane 6:** *miR-9a*; **Lane 8:** *PC-5p-113190_15*; **Lane 10:** *PC-3p-2743_844*; **Lane 12:** *miR-7*; **Lane 14:** *miR-8*; **Lane 16:** *miR-277*; **Lane 18:** *Let-7*. The other uneven lanes were negative controls for each target miRNA.

Figures

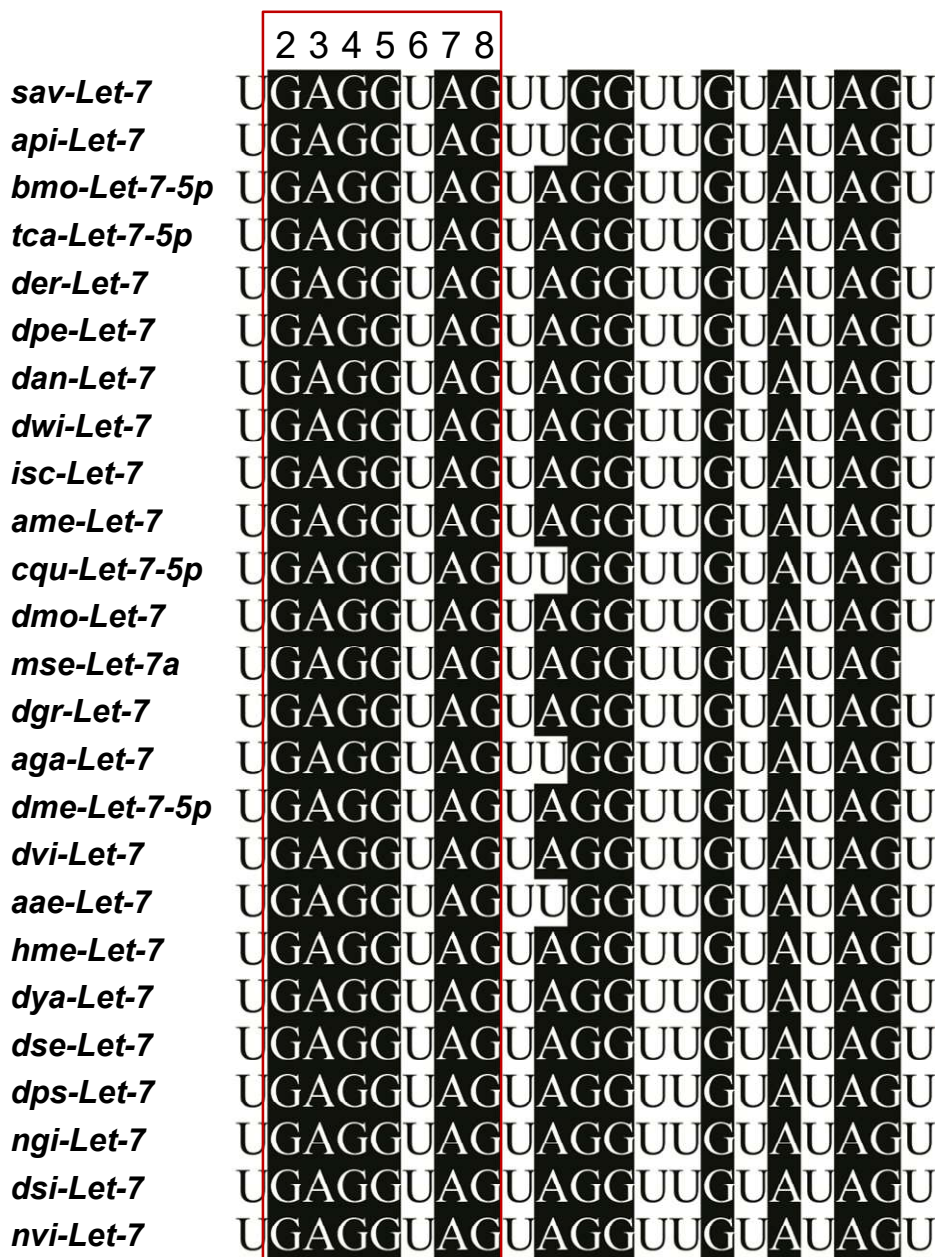
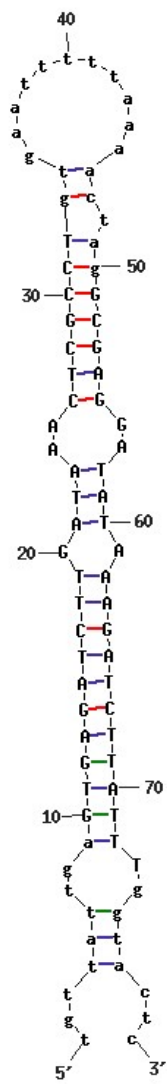


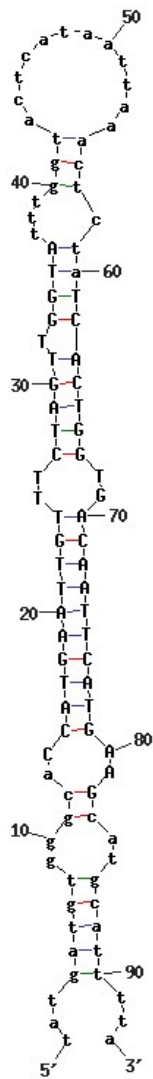
Figure S1

	2	3	4	5	6	7	8
<i>sav-miR-7</i>	U	G	G	A	A	G	A
<i>api-miR-7</i>	U	G	G	A	A	G	A
<i>bmo-miR-7-5p</i>	U	G	G	A	A	G	A
<i>tca-miR-7-5P</i>	U	G	G	A	A	G	A
<i>dpe-miR-7</i>	U	G	G	A	A	G	A
<i>dpu-miR-7</i>	U	G	G	A	A	G	A
<i>dan-miR7</i>	U	G	G	A	A	G	A
<i>dwi-miR-7</i>	U	G	G	A	A	G	A
<i>isc-miR-7</i>	U	G	G	A	A	G	A
<i>ame-miR-7</i>	U	G	G	A	A	G	A
<i>cqu-miR-7</i>	U	G	G	A	A	G	A
<i>dmo-miR-7</i>	U	G	G	A	A	G	A
<i>mse-miR-7</i>	U	G	G	A	A	G	A
<i>dgr-miR-7</i>	U	G	G	A	A	G	A
<i>aga-miR-7</i>	U	G	G	A	A	G	A
<i>dme-miR-7-5p</i>	U	G	G	A	A	G	A
<i>dvi-miR-7-5p</i>	U	G	G	A	A	G	A
<i>aae-miR-7</i>	U	G	G	A	A	G	A
<i>hme-miR-7</i>	U	G	G	A	A	G	A
<i>tur-miR-7-5p</i>	U	G	G	A	A	G	A
<i>dya-miR-7</i>	U	G	G	A	A	G	A
<i>dse-miR7</i>	U	G	G	A	A	G	A
<i>dps-miR-7</i>	U	G	G	A	A	G	A
<i>dsi-miR-7</i>	U	G	G	A	A	G	A
<i>nlo-miR-7</i>	U	G	G	A	A	G	A
<i>nvi-miR-7</i>	U	G	G	A	A	G	A

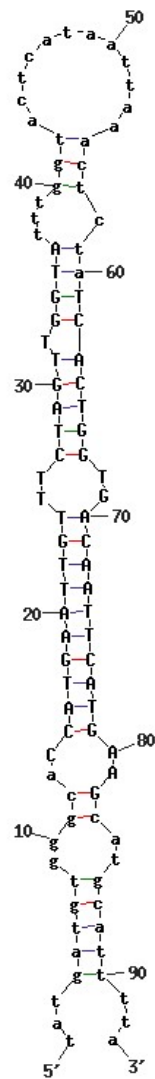
Figure S2



PC-3p-99145_16



PC-3p-55615_34



PC-5p-373819_3

Figure S3

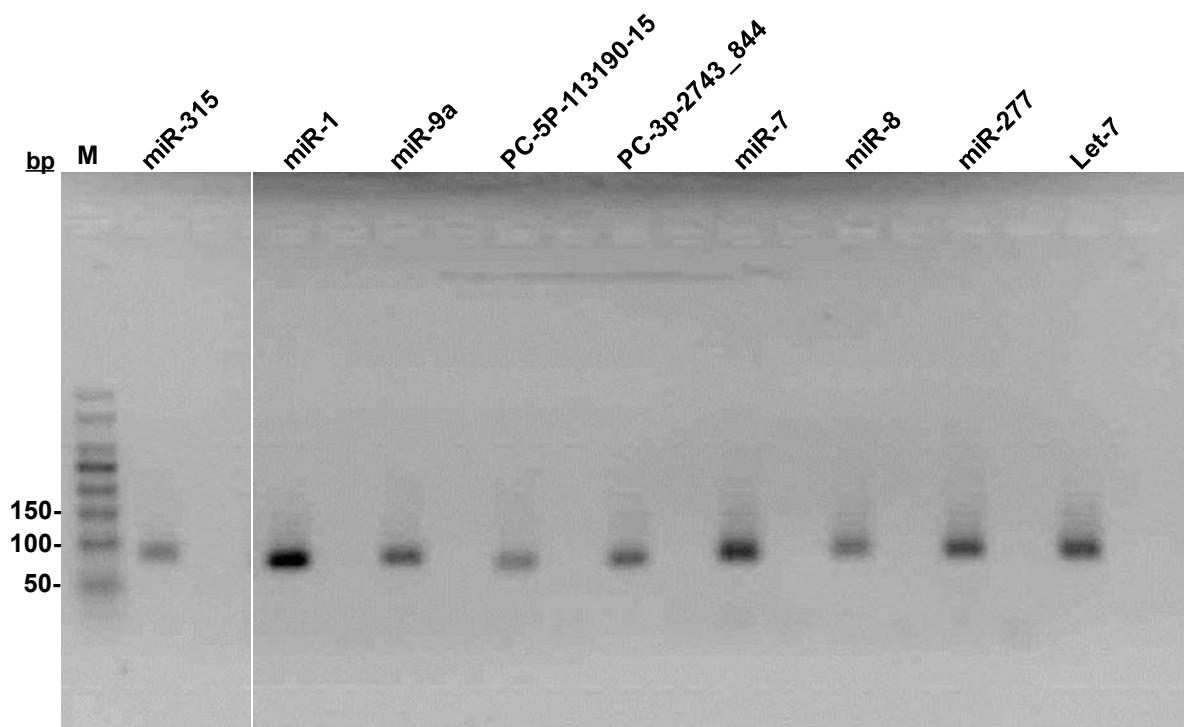


Figure S4