



Fig.S1 Set up of petiole absorption of a diluted blue food colouring solution in broad bean (left) and grapevine (right) whole plants (a). Blue staining of apical leaves of broad bean (b) and grapevine (c), after 2 hours from the beginning of treatment. Black arrows indicate blue stained tissues

Table S1. List of primers used in this work

Application	Primer name	5'-3' sequences	Organism/ target gene	Prod. Size	qPCR efficiency	R ²	Melt peak
dsRNA synthesis	Eva_T7ATPsynBeta ^{f1}	TAATACGACTCACTATAGTACGGCCAGATGAACGAGCC	<i>E. variegatus</i> / ATP synthase	469 nt	/	/	/
	Eva_T7ATPsynBeta ^{r1}	TAATACGACTCACTATAGGGACACCACGAGCAATGTTG	β				
	EvaLegum_F_T7 [#]	TAATACGACTCACTATAGACGCTTACCAGATTTCCGC	<i>E. variegatus</i> / legumain	329 nt	/	/	/
	EvaLegum_R_T7 [#]	TAATACGACTCACTATAGGTAGTCGTTAGGGAAGGCCGA					
	EvaNatt_F_T7 [#]	TAATACGACTCACTATAGGGAAGCTTCATTGCCCCGAA	<i>E. variegatus</i> / natterin	326 nt	/	/	/
	EvaNatt_R_T7 [#]	TAATACGACTCACTATAGTGTCTCGTCTGCATGAACT					
	St_T7ATPsynBeta ^{f2}	TAATACGACTCACTATAGTGGCGCTGGTATACGGACAG	<i>S. titanus</i> / ATP synthase	480 nt	/	/	/
	St_T7ATPsynBeta ^{r2}	TAATACGACTCACTATAGGGACGCCCTCGAGCAATGTTG	β				
	T7GFPr ¹	TAATACGACTCACTATAGCTTTTCACTGGAGTTGTCCC	GFP	403 nt	/	/	/
T7GFPr ¹	TAATACGACTCACTATAGGTTTGTGTCCGAGAATGTTTC						
qPCR target genes	ATP β Fw622 ³	CGCTTTACTCAGGCTGGTTC	<i>E. variegatus</i> / ATP synthase	171 nt	100%	0.995	84.5°C
	ATP β Rv792 ³	GTCATCAGCTGGCACGTAGA	β				
	EvaLegum_F [#]	CTACAGCACACCCACCTTGT	<i>E. variegatus</i> / legumain	119 nt	96.2%	0.927	80.0°C
	EvaLegum_R [#]	GCTCGGTGGACATCTGACTC					
	EvaNatt_F [#]	GGACAAACAGCAGATGGGGA	<i>E. variegatus</i> / natterin	123 nt	90.9%	0.934	81.5°C
	EvaNatt_R [#]	GATCTCGTGCCTCCGTATG					
	St_ATP β Fw622 ²	CGTTTCACTCAGGCTGGTTC	<i>S. titanus</i> / ATP synthase	171 nt	85.4%	0.999	82.5°C
	St_ATP β Rv792 ²	ATCATCAGCCGGCACATAGA	β				
qPCR reference genes	EF1- α _F215 ⁴	CCATCGACATTGCCCTGTGG	<i>E. variegatus</i> / elong. factor- 1 α	111 nt	87.9%	0.997	78.5°C
	EF1- α _R325 ⁴	CCTGTGAGGTTCCAGTGATCATG					
	GST1_F257 ⁴	CCAAGGACCCCAAGAAGCGA	<i>E. variegatus</i> / glut. S- transfer.	113 nt	87.3%	0.997	79.0°C
	GST1_R369 ⁴	TGGCGCTCTCCAAACATCA					
	St_EF1- α _F215 ²	CCATTGACATTGCCCTGTGG	<i>S. titanus</i> / elong. factor- 1 α	110 nt	98.0%	0.999	77.5°C
	St_EF1- α _R325 ²	CCTGAGAAGTCCAGTAATCATG					
	St_GST1_F257 ²	CTAAGGATGCCAGAAACGA	<i>S. titanus</i> / glut. S- transfer.	113 nt	94.5%	0.998	79.0°C
	GST1_R369 ⁴	TGGCGCTCTCCAAACATCA					

T7 promoter sequence is boldfaced.

#Primers designed in this work.

¹ Abbà et al., 2019

² Ripamonti et al., 2022

³ Galetto et al., 2013

⁴ Galetto et al., 2018

Table S2 Tissue-specific expression of legumain and natterin transcripts in *Euscelidius variegatus*. Mean \pm standard error of the mean (SEM), total number of pooled samples (N, each made of ten dissected organs), maximum/minimum and median of normalized relative expression of target transcripts measured in *Euscelidius variegatus* organs

Target gene	Dissected organ	Expression level of target genes		
		Mean \pm SEM (N)	Max/Min	Median
legumain	Salivary glands	1.55E-03 \pm 5.56E-03 (4)	2.07E-03/8.80E-04	1.63E-03
	Guts	3.64E+00 \pm 3.35E-01 (4)	5.18E+00/1.04E+00	4.17E+00
	Ovaries	3.75E-05 \pm 1.18E-03 (4)	7.00E-05/2.00E-05	3.00E-05
	Testes	5.15E-04 \pm 2.30E-03 (2)	5.30E-04/5.00E-04	5.15E-04
natterin	Salivary glands	2.04E-02 \pm 2.53E-02 (4)	3.56E-02/1.42E-02	1.58E-02
	Guts	3.63E+00 \pm 3.35E-01 (4)	5.08E+00/1.06E+00	4.20E+00
	Ovaries	2.79E-03 \pm 5.41E-03 (4)	3.28E-03/2.28E-03	2.80E-03
	Testes	2.30E-01 \pm 1.50E-01 (2)	2.94E-01/1.66E-01	2.30E-01

Table S3 Expression of gut-specific transcripts measured in *Euscelidius variegatus* injected with specific dsRNAs. Mean \pm standard error of the mean (SEM), total number of samples (N), maximum/minimum and median of normalized relative expression of target transcripts measured in *Euscelidius variegatus* sampled at 7 days post injection with dsRNAs targeting green fluorescent protein (dsGFP), legumain (dsLeg) or natterin (dsNat)

Target gene	Treatment	Expression level of target genes		
		Mean \pm SEM (N)	Max/Min	Median
legumain	dsGFP	1.539 \pm 0.259 (12)	3.845/0.695	1.226
	dsLeg	0.111 \pm 0.019 (12)	0.252/0.028	0.107
natterin	dsGFP	1.522 \pm 0.301 (12)	3.665/0.513	1.179
	dsNat	0.048 \pm 0.007 (12)	0.091/0.016	0.048

Table S4 Expression of gut-specific transcripts measured in *Euscelidius variegatus* fed on dsRNA-treated plants.

Mean \pm standard error of the mean (SEM), total number of samples included in the analyses (N), maximum/minimum and median of normalized relative expression of target transcripts measured in *Euscelidius variegatus* sampled at 11, 15 and 22 days post feeding (dpf) on plants treated with dsRNAs targeting green fluorescent protein (dsGFP), legumain (dsLeg) or natterin (dsNat)

Target gene	Sampling date	Treatment	Total number of quantified insects	Expression level of target genes		
				Mean \pm SEM (N)	Max/Min	Median
legumain	13 dpf	dsGFP	6	1.444 \pm 0.553 (6)	4.116/0.539	0.939
		dsLeg	5	0.621 \pm 0.143 (4)	0.861/0.230	0.697
	17 dpf	dsGFP	5	1.021 \pm 0.103 (5)	1.373/0.759	1.026
		dsLeg	5	0.722 \pm 0.111 (4)	0.878/0.403	0.804
	24 dpf	dsGFP	8	1.548 \pm 0.173 (8)	2.071/0.855	1.579
		dsLeg	8	1.070 \pm 0.144 (7)	1.452/0.435	1.071
natterin	13 dpf	dsGFP	6	1.215 \pm 0.232 (6)	2.099/0.597	1.204
		dsNat	5	0.533 \pm 0.192 (3)	0.908/0.271	0.419
	17 dpf	dsGFP	5	1.033 \pm 0.128 (5)	1.459/0.666	1.049
		dsNat	5	0.643 \pm 0.128 (3)	0.896/0.491	0.541
	24 dpf	dsGFP	8	1.556 \pm 0.190 (8)	2.718/0.874	1.461
		dsNat	11	0.883 \pm 0.138 (8)	1.335/0.063	0.936

Table S5. Expression of ATP synthase β transcript in *Euscelidius variegatus* and *Scaphoideus titanus* fed on dsRNA-treated plants.

Mean \pm standard error of the mean (SEM), total number of samples included in the analyses (N), maximum/minimum and median of normalized relative expression of target transcripts measured in *Euscelidius variegatus* and *Scaphoideus titanus* sampled at 14 days post feeding on plants treated with dsRNAs targeting green fluorescent protein (dsGFP) or ATP synthase β (dsATP)

Species	Treatment	Total number of quantified insects	ATP synthase β expression		
			Mean \pm SEM (N)	Max/Min	Median
<i>E. variegatus</i>	dsGFP	10	1.665 \pm 0.122 (10)	2.154/1.201	1.568
	dsATP	8	0.399 \pm 0.083 (6)	0.667/0.124	0.365
<i>S. titanus</i>	dsGFP	32	1.811 \pm 0.131 (32)	4.133/0.809	1.591
	dsATP	32	1.183 \pm 0.094 (25)	1.771/0.031	1.198