

## TABLES

**Table 1** Sequences of the internal transcribed spacers (ITS) region of the selected Acari species used in this study.

Species (Family)	Origin	Target region <sup>1</sup>	Primer sequence (5'→3') <sup>2</sup>	Size <sup>3</sup>	T <sub>a</sub> <sup>4</sup>	References	Accession number
<i>Panonychus citri</i> (Tetranychidae)	Castelló, Spain	ITS2	GGCAAAGATACATCTTCAAGC (for) <sup>5</sup> TTCTTTTCCTCCGCTTAGTGATATGCTTAA (rev) <sup>6</sup>	434	50	Hurtado <i>et al.</i> 2008	AM408039
<i>Tetranychus urticae</i> (Tetranychidae)	Betxí, Spain	ITS2	GGCAAAGATACATCTTCAAGC (for) <sup>5</sup> TTCTTTTCCTCCGCTTAGTGATATGCTTAA (rev) <sup>6</sup>	482	50	Hurtado <i>et al.</i> 2008	AM408043
<i>Neoseiulus barkeri</i> (Phytoseiidae)	Castelló, Spain	ITS	AGAGGAAGTAAAAGTCGTAACAAG (for) <sup>7</sup> TTCTTTTCCTCCGCTTAGTGATATGCTTAA (rev) <sup>6</sup>	720	50	This work	KP642055
<i>Typhlodromus phialatus</i> (Phytoseiidae)	Montcada, Spain	ITS	AGAGGAAGTAAAAGTCGTAACAAG (for) <sup>7</sup> TTCTTTTCCTCCGCTTAGTGATATGCTTAA (rev) <sup>6</sup>	770	50	This work	GU565315
<i>Neoseiulus californicus</i> (Phytoseiidae)	Koppert Biol. Syst.	ITS	AGAGGAAGTAAAAGTCGTAACAAG (for) <sup>7</sup> ATATGCTTAAATTCAGGGGG (rev) <sup>7</sup>	673	50	Navajas <i>et al.</i> 1999	Y18269
<i>Euseius stipulatus</i> (Phytoseiidae)	Montcada, Spain	ITS	AGAGGAAGTAAAAGTCGTAACAAG (for) <sup>7</sup> ATATGCTTAAATTCAGGGGG (rev) <sup>7</sup>	651	50	This work	GU565290
<i>Phytoseiulus persimilis</i> (Phytoseiidae)	Koppert Biol. Syst.	ITS	AGAGGAAGTAAAAGTCGTAACAAG (for) <sup>7</sup> ATATGCTTAAATTCAGGGGG (rev) <sup>7</sup>	606	50	Navajas <i>et al.</i> 1999	Y18268
<i>Amblyseius swirskii</i> (Phytoseiidae)	Koppert Biol. Syst.	ITS	AGAGGAAGTAAAAGTCGTAACAAG (for) <sup>7</sup> ATATGCTTAAATTCAGGGGG (rev) <sup>7</sup>	623	50	This work	GU565289

<sup>1</sup> ITS: DNA ribosomal ITS1, 5.8S and ITS2 region; ITS2: DNA ribosomal ITS2 region; <sup>2</sup> for: forward primer; rev: reverse primer; <sup>3</sup> Size: Size amplified fragment (bp); <sup>4</sup> T<sub>a</sub>: annealing temperature (°C); <sup>5</sup> Hurtado *et al.* (2008); <sup>6</sup> Ji *et al.* (2003); <sup>7</sup> Ben-Ali *et al.* (2000)

**Table 2** Primer sequences and expected product size in the designed multiplex PCR.

Species		Primer sequence (5'→3') <sup>1</sup>	Size (bp)
Prey	<i>Panonychus citri</i>	GTTAGTAGCGCATGTATCCCG (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	243
		GGTTCTGTTGTTGTAATACTT (for) <sup>2</sup> TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	176
	<i>Tetranychus urticae</i>	GATTTACGTTGCTTGCTTGC (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	121
Predator	<i>Neoseiulus barkeri</i>	CACTCCATCACATGGAAGAATG (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	605
	<i>Typhlodromus phialatus</i>	GAGGTCAGTCCTACTGCTCG (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	570
	<i>Neoseiulus californicus</i>	GCCTGCTGGCCGTCGTACGT (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	540
	<i>Euseius stipulatus</i>	TACGTATTGCGGTTCACTTG (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	475
	<i>Phytoseiulus persimilis</i>	CGCGAGTCGGTACCAACCAG (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	409
	<i>Amblyseius swirskii</i>	CTTTGGAAGTAAGTTGTGC (for) TTCTTTTCCTCCGCTTAGTGATATGTTAA (rev)	369

<sup>1</sup> for: forward primer; rev: reverse primer

<sup>2</sup> Second forward primer designed for *P. citri*

**Table 3** Percentage of successful prey detection for *E. stipulatus* and *P. persimilis* depending on the order of the species offered.

Predator	Time elapsed after 2nd prey attacked <sup>1</sup>	# predators	Positive for 1 <sup>st</sup> prey (%) <sup>2</sup>	Positive for 2 <sup>nd</sup> prey (%)
<i>E. stipulatus</i>	0 h	9 <sup>3</sup>	77.8	22.2
<i>P. persimilis</i>	0 h	16	12.5	100
	2 h	10	0	90.0
	4 h	10	0	80.0
	16 h	6	0	50.0

<sup>1</sup> Time elapsed until the predator is frozen for subsequent molecular analysis.

<sup>2</sup> For *E. stipulatus* the first prey was *T. urticae* and for *P. persimilis*, *P. citri*. Second prey was the alternative prey.

<sup>3</sup> One out of 10 failed in the amplification.

**Table 4** Time invested in feeding and rate of successful encounters of *E. stipulatus* and *P. persimilis* when preying on *T. urticae* and *P. citri*.

Predator	Successful encounter on 1 <sup>st</sup> prey (%)	Successful encounter on 2 <sup>nd</sup> prey (%)	Time feeding on 1 <sup>st</sup> prey <sup>2, 3</sup> (min)	Time feeding on 2 <sup>nd</sup> prey <sup>3</sup> (min)	Time elapsed between attacks (min)
<i>E. stipulatus</i>	30.4 n = 191	17.2 n = 58	20.48 ± 3.01	20.36 ± 5.40	120.02 ± 26.02
<i>P. persimilis</i>	39.9 n = 148	71.2 n = 59	22.53 ± 1.53	61.48 ± 3.51	61.24 ± 8.13

<sup>1</sup> An encounter was considered successful when resulting in prey death.

<sup>2</sup> For *E. stipulatus* the first prey was *T. urticae* and for *P. persimilis* is *P. citri*. Second prey was the opposite combination.

<sup>3</sup> Time was considered only in those cases where the predator preyed on both tetranychid species.

**Table 5** Predation values corresponding to the three different predators identified in the nine field samplings for which predation was molecularly quantified. Based on  $DS_{50}$  values,  $DS_{50}^{\text{weighted}}$  were calculated. Maximum, minimum and mean corrected predation values for each predator-prey combination were obtained by combining positive prey detections for each sampling and  $DS_{50}^{\text{weighted}}$ .

Predator	Prey	$DS_{50}$ (h)	Total positive prey detection (#)	$DS_{50}^{\text{weighted}}$ (A)	Positive prey detection (#) (B)	Corrected predation value (A*B)
<i>E. stipulatus</i>	<i>T. urticae</i>	18.33	145	0.010	3 - 28	0.154 (0.030 - 0.280)
	<i>P. citri</i>	2.99	24	0.060	0 - 8	0.160 (0 - 0.480)
<i>N. californicus</i>	<i>T. urticae</i>	14.99	1	0.012	0 - 1	0.001 (0 - 0.012)
	<i>P. citri</i>	3.16	0	0.057	0	0
<i>P. persimilis</i>	<i>T. urticae</i>	10.67	54	0.017	0 - 19	0.102 (0 - 0.323)
	<i>P. citri</i>	0.18	1	1	0 - 1	0.111 (0 - 1.000)