

**Table S1.** Factorial ANOVA results of the tested parameters (maize genotype, aphid species, number of aphids, infestation time) and the interactions on relative expression of the examined thioredoxins-encoding genes (*Trx-f*, *Trx-h*, *Trx-m*, *Trx-x*, *Trx-lp4B*) in the maize seedlings.

| Tested Effects and Interactions | <i>Trx-f</i>              | <i>Trx-h</i>              | <i>Trx-m</i>              | <i>Trx-x</i>              | <i>Trx-lp4B</i>         |
|---------------------------------|---------------------------|---------------------------|---------------------------|---------------------------|-------------------------|
| Maize genotype (G)              | $F_{1, 96} = 1,615$ (***) | $F_{1, 96} = 1,240$ (***) | $F_{1, 96} = 2,065$ (***) | $F_{1, 96} = 2,532$ (***) | $F_{1, 96} = 14.5$ (ns) |
| Aphid species (S)               | $F_{1, 96} = 408$ (***)   | $F_{1, 96} = 625$ (***)   | $F_{1, 96} = 692$ (***)   | $F_{1, 96} = 818$ (***)   | $F_{1, 96} = 8.2$ (ns)  |
| Number of aphids (A)            | $F_{2, 96} = 545$ (***)   | $F_{2, 96} = 432$ (***)   | $F_{2, 96} = 998$ (***)   | $F_{2, 96} = 1,056$ (***) | $F_{2, 96} = 6.4$ (ns)  |
| Infestation time (T)            | $F_{5, 96} = 1,247$ (***) | $F_{5, 96} = 780$ (***)   | $F_{5, 96} = 1,520$ (***) | $F_{5, 96} = 1,745$ (***) | $F_{5, 96} = 11.0$ (ns) |
| G × S                           | $F_{1, 96} = 438$ (***)   | $F_{1, 96} = 523$ (***)   | $F_{1, 96} = 615$ (***)   | $F_{1, 96} = 729$ (***)   | $F_{1, 96} = 8.4$ (ns)  |
| S × A                           | $F_{2, 96} = 245$ (**)    | $F_{2, 96} = 296$ (**)    | $F_{2, 96} = 355$ (***)   | $F_{2, 96} = 318$ (***)   | $F_{2, 96} = 9.5$ (ns)  |
| G × A                           | $F_{2, 96} = 206$ (**)    | $F_{2, 96} = 362$ (***)   | $F_{2, 96} = 604$ (***)   | $F_{2, 96} = 643$ (***)   | $F_{2, 96} = 3.5$ (ns)  |
| S × T                           | $F_{5, 96} = 110$ (**)    | $F_{5, 96} = 154$ (**)    | $F_{5, 96} = 490$ (***)   | $F_{5, 96} = 378$ (***)   | $F_{5, 96} = 6.2$ (ns)  |
| G × T                           | $F_{5, 96} = 215$ (**)    | $F_{5, 96} = 376$ (***)   | $F_{5, 96} = 512$ (***)   | $F_{5, 96} = 740$ (***)   | $F_{5, 96} = 4.7$ (ns)  |
| A × T                           | $F_{10, 96} = 408$ (***)  | $F_{10, 96} = 257$ (**)   | $F_{10, 96} = 705$ (***)  | $F_{10, 96} = 764$ (***)  | $F_{10, 96} = 2.0$ (ns) |
| G × S × A                       | $F_{2, 96} = 95$ (*)      | $F_{2, 96} = 145$ (**)    | $F_{2, 96} = 186$ (**)    | $F_{2, 96} = 316$ (***)   | $F_{2, 96} = 2.5$ (ns)  |
| G × S × T                       | $F_{5, 96} = 80$ (*)      | $F_{5, 96} = 105$ (*)     | $F_{5, 96} = 248$ (**)    | $F_{5, 96} = 291$ (***)   | $F_{5, 96} = 1.8$ (ns)  |
| S × A × T                       | $F_{10, 96} = 52$ (*)     | $F_{10, 96} = 74$ (*)     | $F_{10, 96} = 121$ (**)   | $F_{10, 96} = 205$ (**)   | $F_{10, 96} = 1.6$ (ns) |
| G × A × T                       | $F_{10, 96} = 35$ (*)     | $F_{10, 96} = 92$ (*)     | $F_{10, 96} = 165$ (**)   | $F_{10, 96} = 180$ (**)   | $F_{10, 96} = 0.9$ (ns) |
| G × S × A × T                   | $F_{10, 96} = 4$ (ns)     | $F_{10, 96} = 1$ (ns)     | $F_{10, 96} = 43$ (*)     | $F_{10, 96} = 62$ (*)     | $F_{10, 96} = 0.3$ (ns) |

(\*)  $p < 0.05$ ; (\*\*)  $p < 0.01$ ; (\*\*\*)  $p < 0.001$ ; (ns) – non-significant. Variables: i) maize genotype – Waza and Złota Karłowa; ii) aphid species – *R. padi* and *M. dirhodum*; iii) number of aphids – 0, 30 and 60 females of *R. padi* or *M. dirhodum* per plant; iv) infestation time – 0, 3, 6, 24, 48 and 96 h.

**Table S2.** Factorial ANOVA results of the tested parameters (maize genotype, aphid species, number of aphids, infestation time) and the interactions on the relative expression of the thioredoxin reductase genes (*Ftr1*, *Trxr2*), and the total activity of thioredoxin reductase (TrxR) in the maize seedlings.

| Tested Effects and Interactions | <i>Ftr1</i>               | <i>Trxr2</i>              | TrxR                      |
|---------------------------------|---------------------------|---------------------------|---------------------------|
| Maize genotype (G)              | $F_{1, 96} = 1,875$ (***) | $F_{1, 96} = 2,150$ (***) | $F_{1, 96} = 3,025$ (***) |
| Aphid species (S)               | $F_{1, 96} = 1,470$ (***) | $F_{1, 96} = 1,641$ (***) | $F_{1, 96} = 1,220$ (***) |
| Number of aphids (A)            | $F_{2, 96} = 663$ (***)   | $F_{2, 96} = 858$ (***)   | $F_{2, 96} = 984$ (***)   |
| Infestation time (T)            | $F_{5, 96} = 1,584$ (***) | $F_{5, 96} = 1,105$ (***) | $F_{5, 96} = 2,513$ (***) |
| G × S                           | $F_{1, 96} = 1,255$ (***) | $F_{1, 96} = 986$ (***)   | $F_{1, 96} = 1,108$ (***) |
| S × A                           | $F_{2, 96} = 652$ (***)   | $F_{2, 96} = 905$ (***)   | $F_{2, 96} = 615$ (***)   |
| G × A                           | $F_{2, 96} = 470$ (***)   | $F_{2, 96} = 743$ (***)   | $F_{2, 96} = 1024$ (***)  |
| S × T                           | $F_{5, 96} = 215$ (**)    | $F_{5, 96} = 560$ (***)   | $F_{5, 96} = 522$ (***)   |
| G × T                           | $F_{5, 96} = 284$ (**)    | $F_{5, 96} = 637$ (***)   | $F_{5, 96} = 712$ (***)   |
| A × T                           | $F_{10, 96} = 142$ (**)   | $F_{10, 96} = 415$ (***)  | $F_{10, 96} = 435$ (***)  |
| G × S × A                       | $F_{2, 96} = 115$ (*)     | $F_{2, 96} = 187$ (**)    | $F_{2, 96} = 218$ (**)    |
| G × S × T                       | $F_{5, 96} = 90$ (*)      | $F_{5, 96} = 151$ (**)    | $F_{5, 96} = 180$ (**)    |
| S × A × T                       | $F_{10, 96} = 63$ (*)     | $F_{10, 96} = 127$ (**)   | $F_{10, 96} = 92$ (*)     |
| G × A × T                       | $F_{10, 96} = 74$ (*)     | $F_{10, 96} = 65$ (*)     | $F_{10, 96} = 140$ (**)   |
| G × S × A × T                   | $F_{10, 96} = 1.6$ (ns)   | $F_{10, 96} = 0.8$ (ns)   | $F_{10, 96} = 45$ (*)     |

(\*)  $p < 0.05$ ; (\*\*)  $p < 0.01$ ; (\*\*\*)  $p < 0.001$ ; (ns) – non-significant. Variables: i) maize genotype – Waza and Złota Karłowa; ii) aphid species – *R. padi* and *M. dirhodum*; iii) number of aphids – 0, 30 and 60 females of *R. padi* or *M. dirhodum* per plant; iv) infestation time – 0, 3, 6, 24, 48 and 96 h.

**Table S3.** List of primers and *TaqMan* fluorescent probe for real-time qRT-PCR quantification of *Ftr1* maize gene.

| Target Gene                                                            | Genbank<br>Accession no.<br>(Reference<br>Sequence) | GenBank<br>Gene ID | Sequences of Primers<br>and <i>TaqMan</i> Fluorescent Probe                                        |
|------------------------------------------------------------------------|-----------------------------------------------------|--------------------|----------------------------------------------------------------------------------------------------|
| <i>Ftr1</i><br>(encoding<br>ferredoxin-<br>thioredoxin<br>reductase 1) | X73549.1<br>(NM_001305869.1)                        | LOC542532          | F: CCGCTCCAACACTTTCTTC<br>R: TGGCATTCTTCCTCTCAC<br>P: 5'-FAM-CGACAAGACAGTCACTGCCGTCGTCATCAA-BBQ-3' |

Sequences of primers and *TaqMan* fluorescent probe were designed using *GenScript Real-time PCR (TaqMan) Primer Design* software (<https://www.genscript.com/ssl-bin/app/primer>; accessed September 02, 2019). *Custom TaqMan Gene Expression Assay* for maize *Ftr1* gene was purchased from Thermo Fisher Scientific Inc., Waltham, Massachusetts, USA ([www.thermofisher.com](http://www.thermofisher.com)). F – forward primer; R – reverse primer; P – *TaqMan* fluorescent probe.