

## Supplementary Materials:

**Table S1.** Overview of the resistance tests carried out in the complete and partial screening. x represents complete runs (control, Foxy II and Foxy III with 10 seedlings each). Deviations are defined more precisely.

Genotype		Resistance test	
		complete screening	partial screening
<i>A. aethiopicus</i>	wild relative	x	x
<i>A. amarus</i>	wild relative	x	x
<i>A. densiflorus</i>	wild relative	control + Foxy III	-
<i>A. stipularis</i>	wild relative	control + Foxy III	-
CGN25609	landraces	x	-
CGN25611	landraces	(Foxy III only 9 plants)	-
Argenteuil	cultivar	x	x
Grolim	cultivar	x	-
Ivancicky	cultivar	x	x
Leistungsauselese	cultivar	x	control + Foxy III
Ramada	cultivar	x	x
Ramires	cultivar	x	x
Ravel	cultivar	x	x
Ruhm von Braunschweig	cultivar	(control only 6 plants)	-
Schwetzingen Meisterschuss	cultivar	x	x
Start	cultivar	x	x
Thielim	cultivar	x	x

**Table S2.** Resistance test against *Fusarium oxysporum* isolates Foxy II and Foxy III, 14 dpi. Comparison of the percentage of diseased tissue measured in complete and partial resistance screening for *A. amarus*, *A. aethiopicus*, *A. officinalis* cv. Ravel, and *A. officinalis* cv. Start. Asterisks behind the average and SE show significant differences between the complete and partial resistance screening ( $p < 0.05$ ). <sup>Δ</sup> indicates significance between control and Foxy II or Foxy III for each genotype ( $p < 0.05$ ).

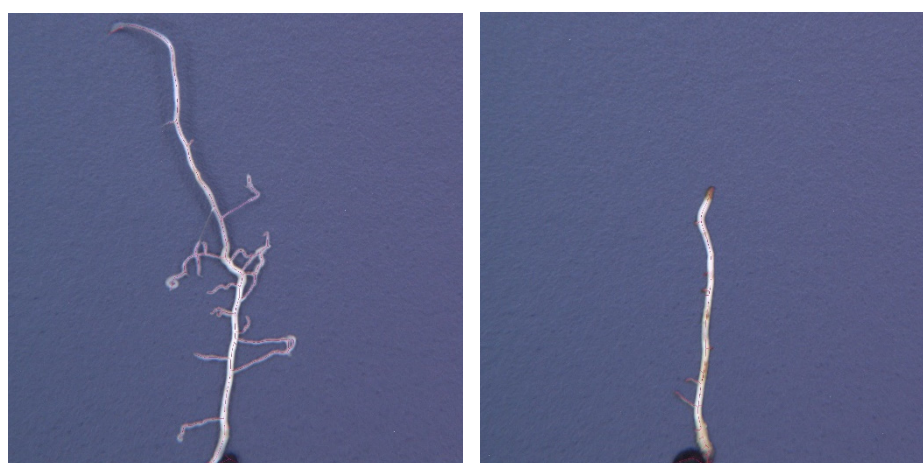
Genotype	control		Foxy II		Foxy III	
	complete screening	partial screening	complete screening	partial screening	complete screening	partial screening
1	9.37 ± 0.69	10.08 ± 0.98	25.76 ± 1.00* <sup>Δ</sup>	17.78 ± 1.41* <sup>Δ</sup>	25.98 ± 2.34 <sup>Δ</sup>	31.69 ± 2.62 <sup>Δ</sup>
2	26.34 ± 1.34	29.05 ± 1.44	24.56 ± 1.30*	30.22 ± 1.69* <sup>Δ</sup>	26.87 ± 0.96	31.86 ± 2.18 <sup>Δ</sup>
13	15.12 ± 0.94*	13.19 ± 1.09*	28.99 ± 1.95* <sup>Δ</sup>	23.03 ± 1.83* <sup>Δ</sup>	21.92 ± 1.96 <sup>Δ</sup>	22.79 ± 1.80 <sup>Δ</sup>
16	14.1 ± 1.13	15.93 ± 1.05	20.04 ± 1.57 <sup>Δ</sup>	21.97 ± 1.35 <sup>Δ</sup>	39.56 ± 3.65 <sup>Δ</sup>	30.15 ± 2.72 <sup>Δ</sup>

**Table S3.** SSR primer used for the distance analysis.

SSR marker	Forward primer <sup>1</sup>	Reverse primer	Fragment size range (bp) <sup>2</sup>
asp c45	GGAGGAATGCCGACAAGG	TTTCTTCAATCGATCTCTGG	105-116
asp c957	TGATGAACCACTCAATACATTCG	TGTGTCTTGTGTTGTGGTGC	117-134
asp c1319	TGCTCAAGGCGTATGTGAAG	ACTGATTCTCGCTTTGCAGG	154-182
asp c1401	AATGGTTGCCAATGGAGAAG	GCCTGCAGTGTCAATCAGTGT	161-175
asp c1505	ATCCCACGCACTGGTAAATC	AGGATATGGTTATGGCGGTG	99-156
asp c1779	CTGTGACATTAGCACAACTTAGCA	CAACCTTTCCTCGGAACGTA	163-180
asp c2370	AGCCTGCCATAATCCTTTCC	TCCCTCTCCACATCTCTTCG	167-184
asp c3803	TAAACTGATGGTGAGGCTCG	TTGTAGGCGGCAGGCTATT	130-158
asp c4593	TCCTCCTTCGACACCTTCAG	GACTCCGGAATCGAGAAGC	149-167
asp c5587	TTTGTGGAGGGAGAGGGAG	CCACAAACAACCTTTCATCC	121-137
asp c6290	CGGCGATAAATTGAAAGACC	ACTCAAGAAGCCGGAGGAAT	108-140
asp c6470	AGAAAGTCACGGGCCTCC	TATCCTCCTCCTGATTCGCA	207-234
asp c8280	CAATCTCTCCACAAGCTCA	GATTGCTGGATTTGGTGAGG	121-169
asp c9020	GCAGCCAACCCTAGAAACAA	TATTATGAGCCTGTGGCTGG	94-140
asp c9810	AGGCAGAAGCTGAAGAGGC	TTCTTGCTCTCTGTTCCAGC	114-150
asp c11979	CAGAAGGTGTATTGTTTGCCC	CCTCTTCATCTTGGCTTTCA	174-204
asp c12796	TGAATCGGGATCAAATTAGAGG	CGTTATCCTCACGACCCAAT	110-133
asp c12877	GAACGCATAGTACATGGCAAA	TTGATATCGATCTTGCTCGC	98-133
asp c14231	CCACAGGATGCAAGTCCTTC	AGAGAGACTCGGGCTCATTG	129-157
asp c15627	CTCTCATTGTTGAAACGAGC	TGCTGCGATGCTAGAGAAGA	105-125
asp c17381	AGGGCTCCCAGTATCCAGTC	TTCATTGAACATGGCATTCTG	151-171
asp c17476	AAGCCAGCCACAAGAACCTA	AAGAGCCTTGGCTAGCGTTT	159-198
asp c21312	CCTCCAGTTCCCATCAGAAG	GGCTATAACCGTGGAGGAGG	122-135
asp c22306	GATCATCATCTTGCGCATTG	AGAGGAAGCACGAGGAAGAA	164-171
asp c22357	CAATCGACGGAGGAGAAAGA	AAGGCTTGTCTTCCATAGCG	113-140

<sup>1</sup> All forward primer were 5' elongated by the 19 bp M13 sequence CACGACGTTGTAAAACGAC.

<sup>2</sup> Fragment size range in the tested material.



(a)

(b)

**Figure S1.** Analysis of root length evaluated with LemnaTec Scanalyzer PL. *A. officinalis* cv. Grolim 14 dpi. (a) Control; (b) Foxy III.