

1. Supplementary Tables and Table Legends

Table S1: Crossing parents and number of offspring per cross for individuals included in population T₂.

Female crossing parent	Male crossing parent	Number of individuals in bi-parental family
Cicero	Toluca	4
Cicero	Aracy	9
Carolus	Orla	9
Aracy	Carolus	11
Cicero	Carolus	16
Maestro	Carolus	7
Mandel	Carolus	6
Orla	Carolus	1
Carolus	Valor	1
Maestro	Orla	16
Princess	Orla	9
93-1015	Maestro	7
Maestro	Toluca	4
0902170	Maestro	1
Amour	Orla	5
Mandel	Toluca	1
Bionica	Sarpo Mira	1

C08II69	Sarpo Mira	2
L4	Sarpo Mira	1
Lady Balfour	Arielle	1
G09 2:4 1101	Amandine	2
G09 2:4 1101	Solist	6
G09 2:5 1702	Solist	2
G09 2:6 1101	Solist	1
0902170	Fakse	3
93-1015	Satina	2
C08II69	Amandine	2
C08II69	Solist	2
G09 2:4 1101	Mandel	6

Table S2: Crossing parents and number of offspring per cross for individuals included in population T₃₋₇.

Female crossing parent	Male crossing parent	Number of individuals in bi-parental family
Aracy	Carolus	2
Carolus	Satina	3
Cicero	Carolus	2
D09 1:2 1701	Carolus	4
Kina	Carolus	1
Mandel	Carolus	1
Orla	Carolus	3
Princess	Carolus	1
Toluca	Carolus	2
Carolus	Orla	9
Aracy	Carolus	11
Cicero	Carolus	16
Maestro	Carolus	7
Mandel	Carolus	6
Orla	Carolus	1
Carolus	Valor	8
Maestro	Toluca	1
Cicero	Toluca	4
Cicero	Aracy	9
93-1015	Maestro	7
Maestro	Toluca	4
Maestro	Orla	16

Princess	Orla	9
Mandel	Toluca	1
Orla	Lady Balfour	1
Amour	Orla	5
G09 2:4 1101	Mandel	6
D09 1:2 1701	Fontane	2
Aracy	Sarpo Mira	1
I09 2:2 2501	Sarpo Mira	1
93-1015	Fontane	1
D08I56	Fakse	1
C08I43	Mayan Gold	2
I08I06	Fontane	2
Princess	Toluca	1
Satina	0903059	3
0902170	Bionica	1
0902170	Satina	3
0902188	Satina	1
Bionica	Sarpo Mira	3
C08II69	Sarpo Mira	3
C08II69	Solist	2
L4	Arielle	1
L4	Sarpo Mira	1
Lady Balfour	Arielle	1
Lady Balfour	Sarpo Mira	3
Sarpo Mira	Salad Blue	2
G09 2:4 1101	Amandine	2
G09 2:4 1101	Solist	6

G09 2:5 1702	Solist	2
G09 2:6 1101	Solist	1
0902170	Fakse	3
0902170	Maestro	1
93-1015	Satina	2
C08II69	Amandine	2
C08II69	Solist	2
GRR	Superb	2
2-IV	2-IV	2

Table S3: Analysis of variance of phenotypic traits included in the study.

	Degrees of freedom	Sum of squares	Mean of squares	F-value	P(>F)	Significance
Tuber weight						
Population	2	76.820	38.410	545.900	<2E-16	***
Residuals	667	46.930	0.070			
Tuber number						
Population	2	6.099E+03	3.049E+03	456.500	<2E-16	***
Residuals	645	4.308E+03	6.700			
Average tuber weight						
Population	2	0.152	0.076	51.100	<2e-16	***
Residuals	645	0.962	0.001			
Specific gravity						
Population	1	0.001	0.001	10.580	0.001	**
Residuals	198	0.013	6.530E-05			
Tuber size						
Population	1	8.500	8.495	8.252	0.005	**
Residuals	198	203.800	1.029			
Tuber shape						
Population	1	0.220	0.223	0.157	0.692	-
Residuals	198	218.170	1.420			
Tuber eyes						
Population	1	0	0.003	0.002	0.965	-
Residuals	198	296.000	1.495			

Table S4: Analysis of variance of phenotypic traits included in the study for the T₁ population.

	Degrees of freedom	Sum of squares	Mean of squares	F-value	P(>F)	Significance
	Tuber weight					
Population	4	2.443	0.611	12.290	1.66E-09	***
Residuals	460	22.849	0.050			
	Tuber number					
Population	4	123.800	30.944	6.739	2.82E-05	***
Residuals	460	2112.300	4.592			
	Average tuber weight					
Population	4	0.040	0.010	6.051	9.44E-05	***
Residuals	460	0.754	0.002			
	Late blight resistance					
Population	4	261556.000	65389.000	7.742	4.82E-06	***
Residuals	460	3885219.000	8446.000			

Table S5: Results obtained for Tukey's range test for differences among the five full-sib families from T₁ for the four traits tuber weight per plant, tuber number per plant, average weight per tuber and host plant resistance to foliar late blight. Non-significant differences are denoted by '-'.

Populations	Difference in means	Lower confidence level	Upper confidence level	Adjusted p-value	Significance
Tuber weight					
B-A	0.066	-0.055	0.187	0.568	-
C-A	0.006	-0.093	0.105	1.000	-
D-A	0.168	0.069	0.267	4.18E-05	***
E-A	0.024	-0.0911	0.140	0.979	-
C-B	-0.060	-0.159	0.039	0.462	-
D-B	0.102	0.003	0.201	0.039	*
E-B	-0.042	-0.157	0.074	0.861	-
D-C	0.162	0.091	0.232	<2E-16	***
E-C	0.018	-0.074	0.111	0.983	-
E-D	-0.144	-0.236	-0.052	2.24E-04	***
Tuber number					
B-A	1.044	-0.118	2.206	0.102	-
C-A	0.364	-0.588	1.316	0.834	-
D-A	1.395	0.445	2.344	6.43E-04	***
E-A	0.458	-0.651	1.568	0.790	-
C-B	-0.680	-1.632	0.272	0.289	-
D-B	0.351	-0.599	1.300	0.850	-
E-B	-0.586	-1.695	0.524	0.598	-
D-C	1.031	0.354	1.707	3.45E-04	***
E-C	0.095	-0.792	0.981	0.998	-
E-D	-0.936	-1.821	-0.052	0.032	*

Average tuber weight					
B-A	0.004	-0.018	0.026	0.986	-
C-A	-0.004	-0.022	0.014	0.968	-
D-A	0.018	-1.10E-04	0.036	0.052	-
E-A	0.002	-0.019	0.023	1.000	-
C-B	-0.008	-0.026	0.010	0.708	-
D-B	0.014	-0.004	0.032	0.227	-
E-B	-0.003	-0.023	0.018	0.997	-
D-C	0.022	0.009	0.035	3.05E-05	***
E-C	0.006	-0.011	0.023	0.876	-
E-D	-0.016	-0.033	4.98E-04	0.062	-
Late blight resistance					
B-A	48.676	-1.165	98.518	0.059	-
C-A	-8.464	-49.296	32.368	0.980	-
D-A	-20.775	-61.504	19.954	0.630	-
E-A	-41.851	-89.431	5.729	0.115	-
C-B	-57.141	-97.973	-16.309	0.001	***
D-B	-69.451	-110.180	-28.722	3.89E-05	***
E-B	-90.527	-138.107	-42.948	2.80E-06	***
D-C	-12.311	-41.326	16.705	0.773	-
E-C	-33.387	-71.424	4.651	0.116	-
E-D	-21.076	-59.003	16.851	0.549	-

2. Supplementary Figure Legends

Figure S1: Principal coordinate analysis (PCoA) based on the Euclidian genetic distance between genotyped individuals in population T₁. The five full-sib families of population T₁ are separated by color. Four cultivars or breeding clones from the bi-parental crosses that produced the T₁ families are included as breeding parents. PC1 and PC2 are the percent variance explained by the two first principal components.

Figure S2: Principal coordinate analysis (PCoA) based on the Euclidian genetic distance between genotyped individuals in populations T₂ and T₃₋₇. Populations are separated by color. PC1 and PC2 are the percent variance explained by the two first principal components.

Figure S3A-D: Phenotypic scores for (A) tuber weight per plant, (B) tuber number per plant, (C) average tuber weight and (D) host plant resistance to late blight, across the five families in the T₁ population and clones and cultivars representing the breeding parents. The phenotypes (except for resistance to late blight) are adjusted per location by the means of five cultivars used as checks. Two full-sib families (T₁-C and T₁-D) are separated by color, as these are used in later cross- and within-family predictions and comparisons therewith may be of interest.