

## Supporting Information

### **Pattern and causes of the establishment of the invasive bacterial potato pathogen *Dickeya solani* and the maintenance of the resident pathogen *D. dianthicola***

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#### **The following Supporting Information is available for this article:**

- **Supplementary Methods 1 (SM1): definitions and formula for calculating pathological and competitive indexes**
- **Supplementary Methods 2 (SM2): qPCR, RT-qPCR and transcriptomics**
- **Supplementary Figures S1 to S8**
- **Supplementary Tables S1 to S5 (tables S6 to S8 are separate excel files)**
- **References of Supplementary information**

## **Supplementary Methods (SM1): Definitions and formula for calculating disease severity index and competitive index.**

**Virulence:** pathogen's ability to infect a host; in this work, virulence was measured using symptom incidence.

**Symptom incidence:** fraction (%) of plant hosts exhibiting symptoms after plant inoculation; in this work, symptom incidence was measured using the assays with hyacinths and potato plants.

**Aggressiveness:** degree of damage caused by a pathogen on a host; in this work, aggressiveness (also referred as symptom or disease severity) was measured on potato tubers (soft rot assays) using five symptomatic classes.

**Disease severity index** (arbitrary unit, formula in SI): this pathological index uses symptomatic classes, corresponding to increasing damages to the plant, to quantify aggressiveness of a pathogen in a given host; in this work, disease severity index (DSI) was calculated using soft-rot assays on potato tubers.

**Fitness:** ability of an organism to transmit its genes to the next generation, which can have different components for a pathogen, from the ability to infect a host to the ability to proliferate within the hosts and then disperse to other hosts; in our study, it usually means the capacity of the pathogen to proliferate by exploiting the resource of a given host (proliferation was measured by CFU/gram of damaged tissues in mono-infection assays) and by outcompeting another pathogen in case of co-infection (measured by calculating competitive index in co-infection assays).

**Competitive index** (arbitrary unit, formula in SI): this index measures the relative abundance of two pathogens in symptomatic tissues, following inoculation in balanced proportions. In this work, competitive index (CI) values were used to analyze competitions between *D. solani* and *D. dianthicola* strains and between *D. solani* VfmB<sub>Pro</sub> and *D. solani* VfmB<sub>Ser</sub> strains.

**Calculation of the disease severity index.** Five aggressiveness classes were considered according to the severity of the symptoms in each tuber (Figure S2). To each class, we assigned a coefficient, whose value increased with symptom severity (0, 0.25, 0.5, 0.75 and

1). Aggressiveness of the pathogens on tubers was represented as normalized values in a disease severity index (DSI) calculated as follows:

$$\text{Disease severity index} = \frac{\sum(\text{number of tubers per class} \times \text{class coefficient})}{\text{Total of tubers}} \times 100$$

**Calculation of competitive index in competition assays between *Dickeya solani* and *D. dianthicola*.** *Dickeya dianthicola* and *D. solani* abundance in inoculum and plant tissues (potato stems and tubers and hyacinths) were used for the calculation of the competitive index (CI) values (Macho et al., 2010) according to the formula:

$$\text{Competitive index} = \frac{(\textit{D. solani} \div \textit{D. dianthicola}) \textit{symptoms}}{(\textit{D. solani} \div \textit{D. dianthicola}) \textit{inoculum}}$$

CI = 1 indicates similar fitness between *D. solani* and *D. dianthicola*;

CI > 1 indicates a fitness advantage to *D. solani*;

CI < 1 indicates a fitness advantage to *D. dianthicola*.

**Calculation of competitive index (CI) in competition assays between *Dickeya solani* VfmB<sub>Pro</sub> and VfmB<sub>Ser</sub> experimental populations.** *Dickeya solani* VfmB<sub>Pro</sub> and VfmB<sub>Ser</sub> relative abundance in inoculum and plant tissues (potato stems and tubers) were used for the calculation of the competitive index (CI) values (Macho et al., 2010) according to the formula:

$$\text{Competitive Index} = \frac{(\textit{D. solani} \textit{vfmBPro} \div \textit{D. solani} \textit{vfmBSer}) \textit{symptoms}}{(\textit{D. solani} \textit{vfmBPro} \div \textit{D. solani} \textit{vfmBSer}) \textit{inoculum}}$$

CI = 1 indicates an equal fitness between *D. solani* VfmB<sub>Pro</sub> and VfmB<sub>Ser</sub> strains;

CI > 1 indicates a fitness advantage to *D. solani* VfmB<sub>Pro</sub>;

CI < 1 indicates a fitness advantage to *D. solani* VfmB<sub>Ser</sub>.

## Supplementary Methods (SM2): qPCR, RT-qPCR and transcriptomics

### Quantification of *Dickeya solani* and *D. dianthicola* abundance by Taq Man qPCR.

Symptomatic tissues from potato stems (emerging lesions) and tubers (at 5 dpi), as well as hyacinths (emerging lesions), were dissociated in 10 mL phosphate buffer ( $\text{Na}_2\text{HPO}_4$  2,7 g.L<sup>-1</sup>;  $\text{NaH}_2\text{PO}_4$  0,4 g.L<sup>-1</sup>; pH 7.2) under agitation. After elimination of rotten tissues, the macerate was centrifuged 15 min at 4000 rpm and the supernatant discarded. Pellets of cells were stored at -20°C until DNA extraction (MasterPure™ Complete DNA and RNA Purification Kit (Epicentre, Illumina)). *Dickeya dianthicola* and *D. solani* experimental populations were quantified by TaqMan technology using species-specific primers developed by FN3PT/ inov3PT. The TaqMan probes were labelled with the 5'-end reporter dye FAM-6-carboxyfluorescein or Yakima Yellow and 3'-end quencher dye (BHQ-1). For each TaqMan qPCR, 2 µL of the samples were mixed with 18 µL of reaction mix containing 10 µL 2x of FastStart Essential Probe Master (Roche), 0.5 µM of each forward and reverse primer and 0.2 µM of the associated dye. For both TaqMan protocols, the thermal cycling conditions included an initial 2 min incubation at 50 °C and 10 min at 95°C, followed by 40 cycles, consisting in 10 s at 95 °C and an annealing temperature of 62°C for 80 s. Analysis was done by automatic threshold calculation within the LightCycler® 96 software version.

### Comparative expression of virulence genes in *Dickeya solani* and *D. dianthicola* strains.

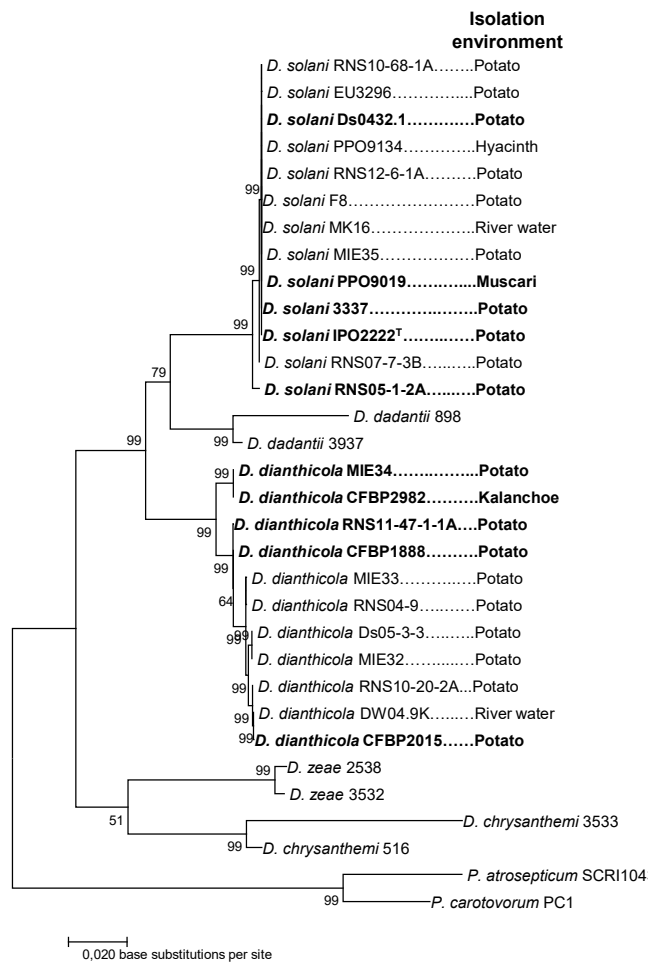
Using RT-qPCR, expression levels of the pectate lyase genes *peIA*, *peID* and *peIE*, and of genes involved in siderophore synthesis (*cbsE* and *acsD*), were measured in *D. dianthicola* RNS1147, CFBP1888, CFBP2982, CFBP2015 and MIE34, and *D. solani* RNS08.23.3.1A (=3337), IPO2222, RNS05.1.2A, Ds0432.1 and PPO9019. RNAs were extracted from cultures of *D. solani* and *D. dianthicola* individuals in TY growth medium (late exponential phase  $\text{OD}_{600} = 0.6$ ) and macerated tissues of potato stems and tubers.

For each of the *D. solani* and *D. dianthicola* strains, 30 tubers were infected by injecting 10<sup>7</sup> CFU. At 5 dpi, internal rotted tissues of ten tubers were homogenized and crushed into 10 mL of GL20 buffer (RNA protect Cell Reagent, Qiagen) containing 20% RNA protect and 80 % buffer  $\text{KPO}_4$  50 mM. Ten potato plants were infected by watering the compost with 10<sup>9</sup> CFU of each of the *D. solani* and *D. dianthicola* strains. The plants were inspected every two days and the symptomatic tissues were sampled immediately when they emerged; hence the collected symptomatic tissues therefore belonged to the same pathological state: emerging lesions. All the macerated stem tissues were collected and immediately frozen in liquid nitrogen. RNA extractions were carried out using the MasterPure™ Complete DNA and RNA Purification Kit (Epicentre, Illumina) according to the manufacturer protocol for cell samples. cDNAs were prepared from 1µg of RNA using RevertAid H Minus First Strand cDNA Synthesis Kit

(Fermentas, Saint-Remy-les-Chevreuse, France) following the manufacturer instructions. RT-qPCRs were performed on a Lightcycler® 96 (Roche) apparatus. Four measurements were performed per condition. Expression values were normalized using *rpoB* and *yafS* as reference genes (Chapelle et al., 2015; Hommais et al., 2011). The comparative cycle threshold method ( $\Delta\Delta CT$ ) was used to measure relative gene expression (Livak & Schmittgen 2001). Primers were designed online using Primer3 (Untergasser et al., 2012) and are listed in **Table S1**.

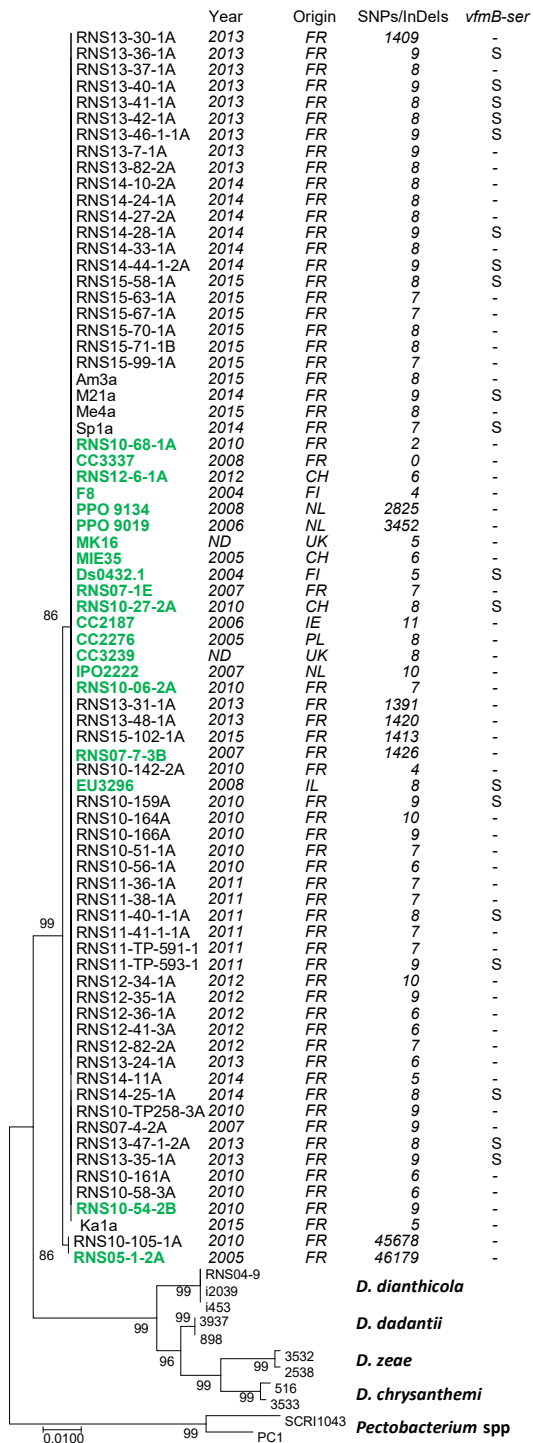
**RNA Extraction for transcriptomics of IPO2222 VfmB<sub>Pro</sub> and Ds0432.1 VfmB<sub>Ser</sub> in potato tubers.** For comparative transcriptomics of the *D. solani* strains IPO2222 and Ds0432.1, tuber inoculation and macerated zone recovery were performed as described above in the presence of the RNA-protect GL20 buffer. Plant tissues and bacteria were separated by a gel gradient using Gentodenz (Centaur, Paris, France) according to the procedure described by Chapelle et al. (2015). Bacterial pellets were suspended into 300  $\mu$ L lysis buffer (sodium acetate 20 mM pH 5.5; SDS 0.5%; EDTA 1 mM pH8.0) and mixed thoroughly. Seven hundreds  $\mu$ L of hot Aquaphenol (60°C) were added and the solutions mixed again. After centrifugation 4 min at 14,000 rpm at room temperature, the aqueous phase was saved and extracted twice as above. Five hundred  $\mu$ L of a chloroform/isoamyl alcohol (24:1) mix were added to the aqueous phases and mixed 3 times 30 sec. After centrifugation 4 min at 14 000 rpm at room temperature, 500  $\mu$ L of aqueous phase were recovered. RNAs were precipitated using sodium acetate 3M and cold 100% ethanol according to standard procedure. Samples were left overnight at -20°C and centrifuged 1 hour at 14 000 rpm at 4°C. The supernatant was eliminated and the pellet dried and then suspended in 50 $\mu$ L of RNase free water. Samples were treated by a RNase free DNase (Ambion) as indicated by the manufacturer.

Quantity and quality of RNAs were checked (Agilent 2100 Bioanalyzer and Qubit Invitrogen). After depletion of the ribosomal RNAs, sequencing was performed by the NextSeq NS500446 using the NextSeq 500 High Output Kit at the I2BC sequencing platform (Gif-sur-Yvette, France). Seventy-five cycles (single-end) were done. At the end, between 25 and 30 million reads were obtained. Reads were mapped on the annotated genome (MaGe <https://www.genoscope.cns.fr/agc/microscope/home/>). Only gene reads mapping on 80% of their length and displaying 90% identity have been retained. Normalization and differential expression analyses were performed using generalized linear models as described in DESeq2 package (Love et al., 2014). An absolute log<sub>2</sub> fold change > 2 and p-value < 0.05 were used to determine differentially expressed genes. RNAseq data were validated by RT-qPCR using the genes *peIE*, *ImpC*, *budA* and *cytA* (the primers are listed in **Table S1**).



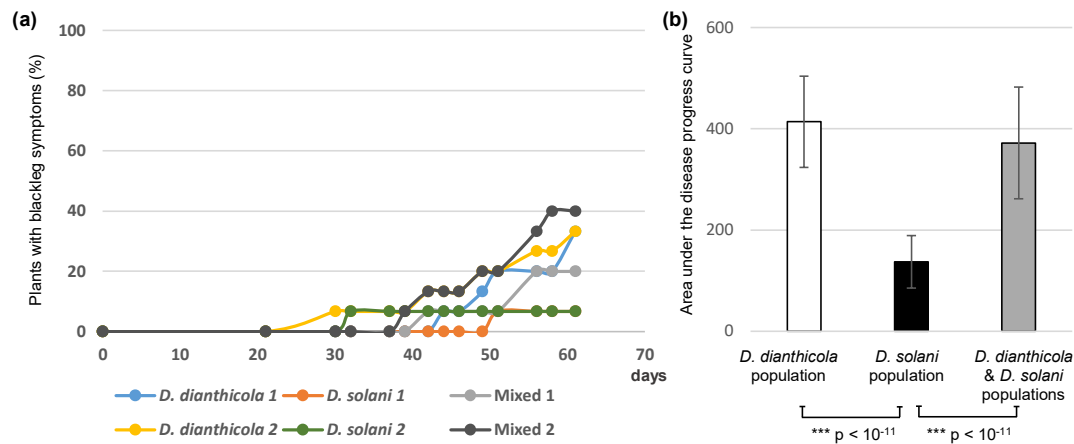
**Fig. S1. *Dickeya solani* and *D. dianthicola* strains used for experimental populations.**

Boldface fonts indicate the strains that have been chosen for the *D. dianthicola* and *D. solani* experimental populations. Multi-locus sequence analysis was performed using 10 concatenated nucleotide sequences of the genes *dnaN*, *dnaX*, *rpoS*, *rpoD*, *gyrA*, *recA*, *fusA*, *gyrB*, *purA* and *gapA*. The Genealogical relationships were inferred by using the maximum likelihood method based on the Tamura-Nei model.



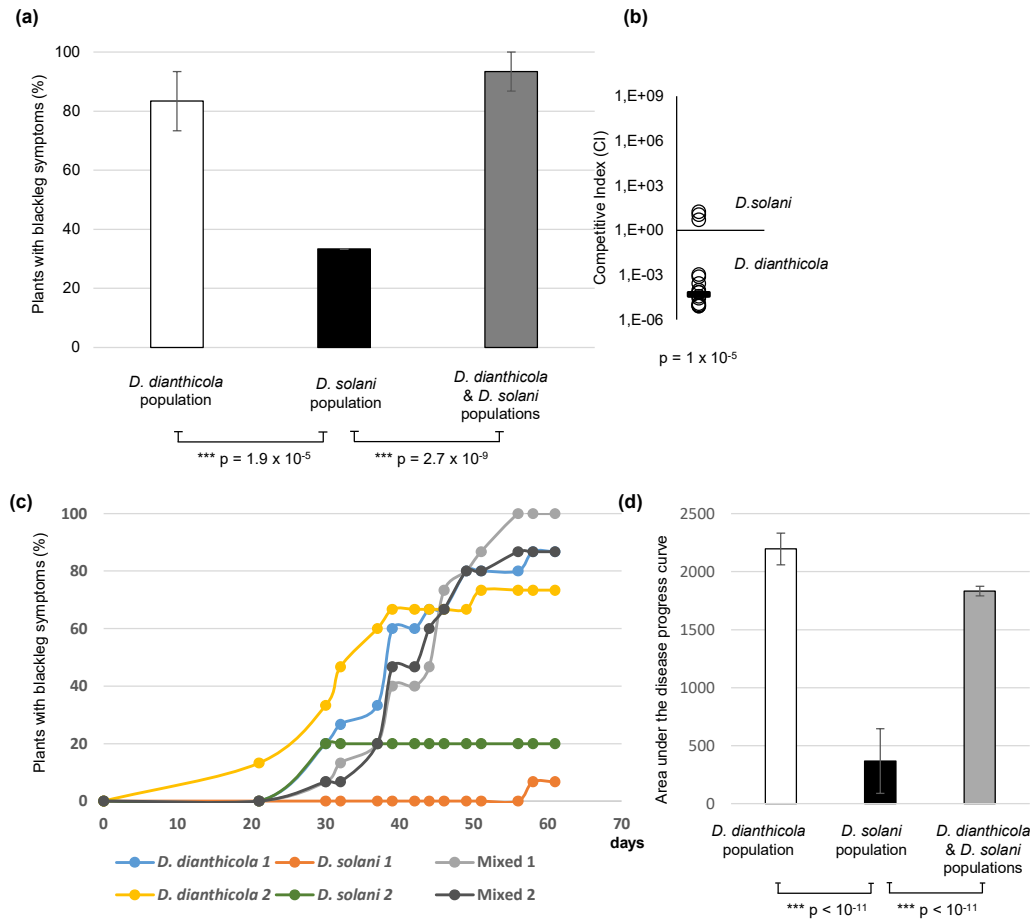
**Fig. S2. Relationships and characteristics of the 67 analyzed *Dickeya solani* strains.**

For each of the analyzed *D. solani* strains, the year and country of isolation, the number of SNPs and InDels in the sequenced genomes compared to the reference *D. solani* strain 3337, and presence of VfmB<sub>ser</sub> (S) or VfmB<sub>Pro</sub> (-) alleles are indicated. The *recA*, *rpoS*, *dnaX*, *gapA* and *gyrB* nucleotide gene sequences were concatenated for building the tree. The genealogical relationships were inferred using the Neighbor-Joining method. Bootstrap supports (1000 replicates) are shown next to the branches. The 20 genomes from Khayi et al. (2015) are indicated in green color, the 47 others were sequenced in this study. ND: not determined.



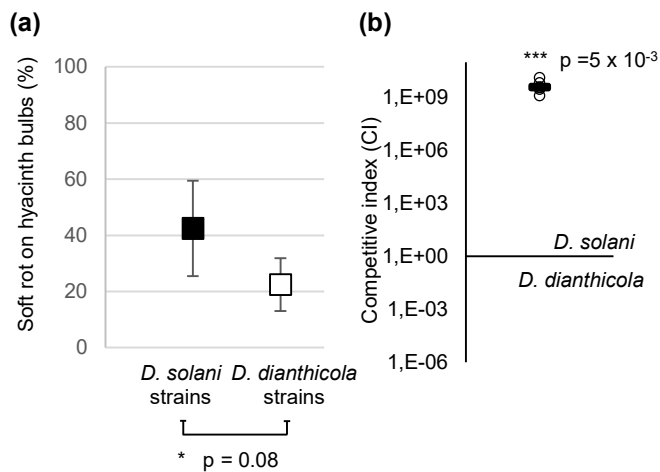
**Fig. S3. Disease progress curves on potato plants.** In **a**, disease (symptom incidence in %) progress curves measured on unwounded potato plants inoculated by *D. dianthicola* and *D. solani* experimental populations and their mix. The two biological replicates (1 & 2) are shown. Fifteen plants were used per replicate. In **b**, mean value and SE between two replicates of the calculated area (arbitrary unit) under the disease progress curves. The p-values of the pairwise comparisons (Post-hoc Tukey test) are indicated below the graph. Legend: \* for 0.05 < p ≤ 0.1; \*\* for 0.01 < p ≤ 0.05 and \*\*\* for p ≤ 0.01.





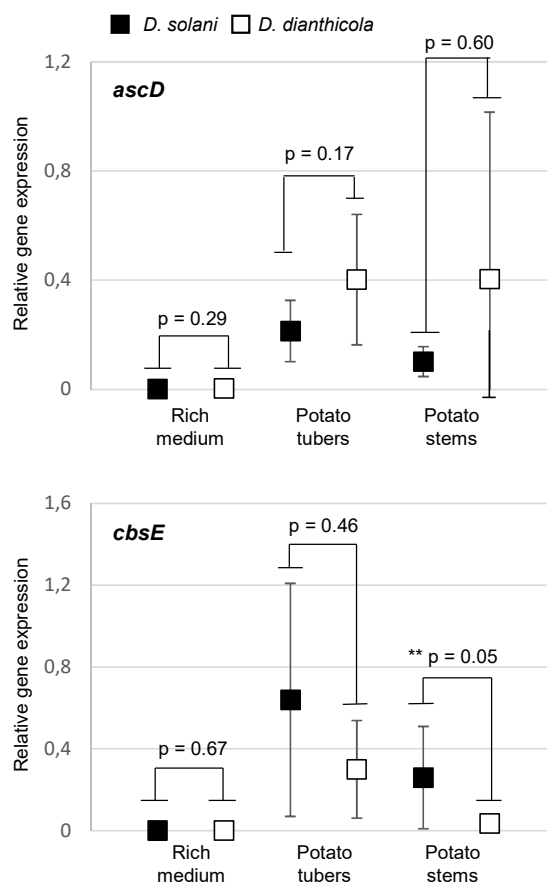
**Fig. S4. Symptoms on wounded potato plants.**

The graphs show data collected either at the end point in **a** or along the complete experimental time in **b-d** from a same plant assay with two replicates per condition and 15 wounded potato plants per replicate. In **a**, mean value and SE between the two replicates of the percentages (%) of plants exhibiting blackleg symptoms which was measured at 61 days post infection on wounded plants inoculated by *D. dianthicola* and *D. solani* experimental populations and their mix. The p-values of the pairwise comparisons (Post-hoc Tukey test) of the symptom classes are indicated below the graph, when  $p \leq 0.1$ . In **b**, competitive index (CI) values between *D. solani* and *D. dianthicola* populations were calculated in 27 emerging lesions of co-infected plants and revealed a competitive advantage of *D. dianthicola*: the median CI ( $= 5.1 \times 10^{-5}$ ) is represented by a thick bar; the p-value resulting from Kruskal-Wallis test testing difference from one is indicated. In **c**, disease (symptom incidence in %) progress curves measured on wounded potato plants inoculated by *D. dianthicola* and *D. solani* experimental populations and their mix. The two biological replicates (1 & 2) are shown. In **d**, mean value and SE between two replicates of the calculated area (arbitrary unit) under the disease progress curves. The p-values of the pairwise comparisons (Post-hoc Tukey test) are indicated below the graph. Legend: \* for  $0.05 < p \leq 0.1$ ; \*\* for  $0.01 < p \leq 0.05$  and \*\*\* for  $p \leq 0.01$ .



**Fig. S5. Symptoms on hyacinths.**

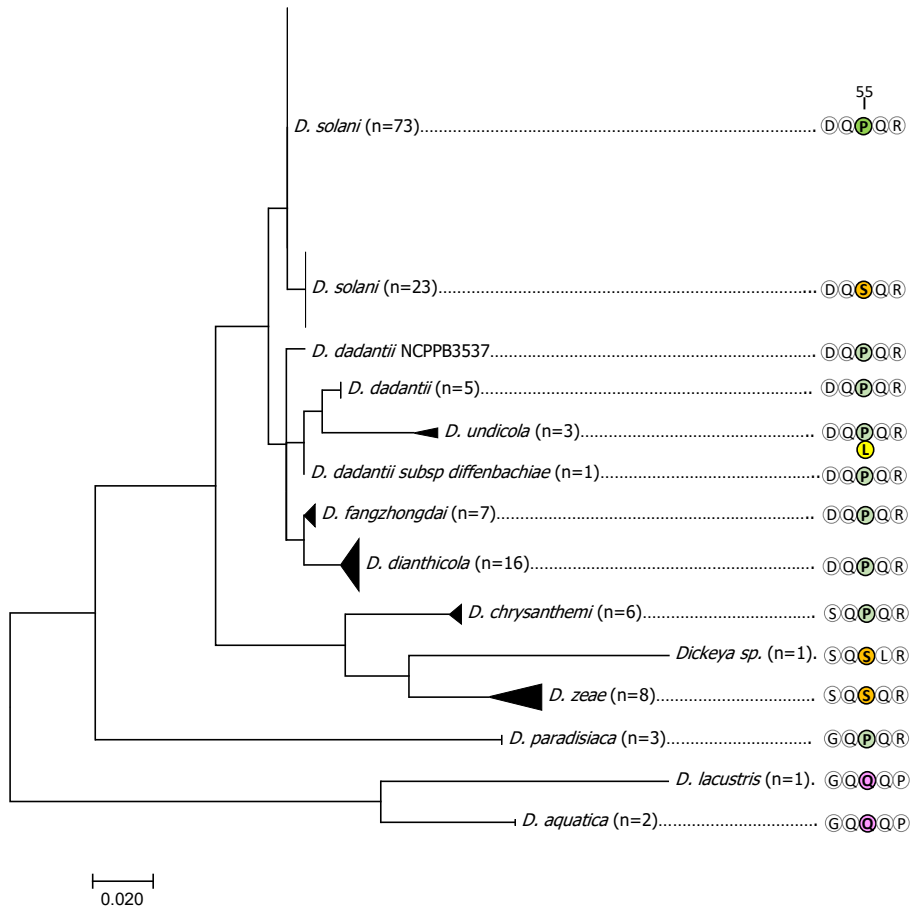
In **a**, mean value and standard error (SE) of the percentage (%) values of plants exhibiting soft rot symptoms, which were measured after inoculation of each of the five *D. solani* strains (3337, IPO2222, RNS05-1-2A, Ds0432.1, PPO9019) and five *D. dianthicola* strains (RNS11-47-1-1A, CFBP1888, CFBP2982, CFBP2015, MIE34) on 8 plants. The p-value of the Kruskal-Wallis test comparing the symptom classes between the two species is indicated below the graph. In **b**, the competitive index (CI) values between *D. solani* and *D. dianthicola* populations were calculated in five emerging lesions of co-infected plants and revealed a competitive advantage of *D. solani*: the median CI (= 4 10<sup>-9</sup>) is represented by a thick bar; the p-value resulting from Kruskal-Wallis tests testing difference from one is indicated. Legend: \* for 0.05 < p ≤ 0.1; \*\* for 0.01 < p ≤ 0.05 and \*\*\* for p ≤ 0.01.



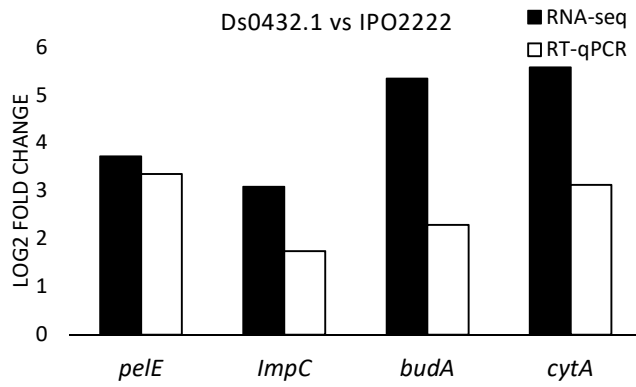
**Fig. S6. Expression of the *ascD* and *cbsE* genes.**

The expression level of the *ascD* and *cbsE* genes was evaluated in each of the five *D. solani* strains (3337, IPO2222, RNS05-1-2A, Ds0432.1, PPO9019) and five *D. dianthicola* strains (RNS11-47-1-1A, CFBP1888, CFBP2982, CFBP2015, MIE34), grown in three conditions: a rich culture medium in the absence of pectin and symptomatic tubers and stems. Relative expression was measured four times and normalized using the *rpoB* and *yafS* gene expression. In the graphs, the mean values and standard error (SE) of gene expression from all strains of a given species are indicated, as well as p-values of the pairwise comparisons by Tukey tests.

Legend: \* for  $0.05 < p \leq 0.1$ ; \*\* for  $0.01 < p \leq 0.05$  and \*\*\* for  $p \leq 0.01$ .



**Fig. S7. Phylogenetic analysis**  
 Phylogeny of the VfmB protein at the position 55 according to the amino acid sequence. The phylogeny was constructed using the Maximum Likelihood method with a matrix-based model. The tree with the lowest likelihood (-1321.46) is shown. Bootstrap values from 1000 heuristic search were obtained using the Neighbor-Join and BioNJ algorithms. Pairwise distances estimated using the Jukes-Cantor model. The tree is drawn to scale, with branch lengths as numbers of substitutions per site. All gaps and missing data were eliminated from the positions in the final dataset.



**Fig. S8. RT-qPCR confirmation of upregulated genes in Ds0432.1 as compared to *Dickeya solani* IPO2222.** Relative gene expression (LOG2 fold change) in *D. solani* strains Ds0432.1 versus IPO2222 measured with RNA-seq (black bars) and RT-qPCR (reverse transcription quantitative polymerase chain reaction) (white bars).

**Table S1. Primers used in this study.**

Name	Sequence	Use	Reference
Dsol-pelA	5'-CTGATCGCTGGCATGATGAC 5'-CTGAGCGCACTGGTGAATC	Gene expression	This work
Dsol-pelD	5'-GCGTGGTCAAGGCGTTTAAAC 5'-CAGACTGGTGGTGGTGGTTTG	Gene expression	This work
Dsol-pelE	5'-AGTGGGATGCGGCAGTAATC 5'-TCCTGCGAGCCATTGTTGTC	Gene expression	This work
Dsol-rpoB	5'-TCATGCCCTGGAACGTTTAC 5'-CTTCCGCACCGATGTAAACG	Gene expression	This work
Dsol-yafS	5'-GCCCTAGCCCAATCAAACCTG 5'-CGATTCCGCATCAGGTCAAC	Gene expression	This work
Dsol-cbsE	5'-GGAGATCGAGAACCCTGCTACTG 5'-CGGTCCGGCAGTTTGTAGTC	Gene expression	This work
Dsol-acsD	5'-AGGGCTGGAATCGCATCATG 5'-GGCGACGGTTGTTTCAGTTC	Gene expression	This work
Ddi-pelA	5'-GCAGCGTCCACAGTTTCAAC 5'-CACCACCTTGACGCTTTG	Gene expression	This work
Ddi-pelD	5'-GCGTCACCTTCCACAACAAC 5'-CTTTGACCACGCTGCATTCC	Gene expression	This work
Ddi-pelE	5'-GCGTCACCTTCCACAACAAC 5'-CTTTGACCACGCTGCATTCC	Gene expression	This work
Ddi-rpoB	5'-TCCGGGATTCTGAGCAAAGC 5'-TTTACCGCACGTTCAACAC	Gene expression	This work
Ddi-yafS	5'-CCAGCACAAACATCCCAGAAG 5'-ACACGTCTGGCTGTCAATCG	Gene expression	This work
Ddi-cbsE	5'-GCGGAAGGACTGGTGAACACTAC 5'-AGTAGCCGCGAAAGGTGTAG	Gene expression	This work
Ddi-acsD	5'-CAGAGCGAGCAGGGATTGTG 5'-GTTGGCGCCGATATGCAATC	Gene expression	This work
impC	5'-AGAGTTCGCCGGACATCAAG 5'-GGGCCTTCAAACACCGATTTTC	Gene expression	This work
budA	5'-GGCCAGCTTTGCACTTCATC 5'-GTTAAGCGCCACCAGTTTAC	Gene expression	This work
cytA	5'-ACAACCAGGTATCCGCCATG 5'-GACCCGGTATCCTGATTAGC	Gene expression	This work
gapA-7-F/gapA-938-R	5'-ATCAAAGTAGGTATCAACG 5'-TCRTACCARGAAACCACT	Taxonomical assignment: <i>Pectobacterium</i> and <i>Dickeya</i> spp	Cigna et al., 2017
ADE1/ADE2	5'-GATCAGAAAGCCCGCAGCCAGAT 5'- CTGTGGCCGATCAGGATGGTTTTGTCGTGC	Taxonomical assignment: <i>Dickeya</i> spp.	Nassar et al., 1996
Y1/Y2	5'-TTACCGGACGCCGAGCTGTGGCGT 5'-CAGGAAGATGTCTGTATCGCGAGT	Taxonomical assignment: <i>Pectobacterium</i> spp.	Darasse et al., 1994
Y45/Y46	5'-TCACCGGACGCCGAACGTGGCGT-3' 5'-TCGCCAACGTTTACGAGAACAAGT-3'	Taxonomical assignment: <i>P. atrosepticum</i>	Fréchon et al., 1998
Br1f/L1r	5'-GCGTGCCGGGTTTATGACCT-3' 5'-CARGGCATCCACCGT-3'	Taxonomical assignment: <i>P. brasiliense</i>	Duarte et al., 2004
PW7011-F/ PW7011-R	5'-CTATGACGCTCGCGGGTTGCTGTT-3' 5'-CGGCGGCGTCTAGTGGAAAGTC-3'	Taxonomical assignment: <i>P. parmentieri</i>	Kim et al., 2012
Pbr-FW1/Pbr- RV1	5'-TGCGGGTTCTGCGTTTC-3' 5'-TGGCGCGTTTCGCAATAT-3' Probe 5'-CAAGGCACGATACG-3'	Taxonomical assignment: <i>P. brasiliense</i>	van der Wolf et al., 2017

**Table S2. Characteristics of the *Dickeya solani* and *D. dianthicola* strains used in experimental populations.** Information about isolation (year, plant host and country) and genomic data (genome accession number and reference) are indicated for the five *D. dianthicola* and five *D. solani* strains used in experimental populations and plant assays.

Species	Strains	Genome accession number	Reference	Year	Plant host	Country
<i>D. dianthicola</i>	RNS11-47-1-1A	VYSC00000000	this work	2011	Potato	France
	CFBP1888	VZQE00000000	this work	1988	Potato	France
	CFBP2982	VZQF00000000	this work	1988	Kalanchoe	France
	CFBP2015	VZQG00000000	this work	1975	Potato	France
	MIE34	VZQH00000000	this work	2013	Potato	Switzerland
<i>D. solani</i>	3337 (=RNS08-23-3-1A)	CP016928.1	Khayi et al., 2018b	2008	Potato	France
	IPO2222	CP015137.1	Khayi et al. 2016	2007	Potato	Netherlands
	RNS05-1-2A	JWMJ01	Khayi et al., 2015	2005	Potato	France
	Ds0432.1	CP017453.1	Khayi et al., 2018a	2004	Potato	Finland
	PPO9019	CM003649.1	Khayi et al., 2018a	2006	Muscari	Netherlands

**Table S3. Characteristics of the *Dickeya solani* strains used in VfmB<sub>Ser</sub> and VfmB<sub>Pro</sub> experimental populations.** Information about isolation (year, plant host and country) and genomic data (genome accession number and reference) are indicated for the VfmB<sub>Pro</sub> and VfmB<sub>Ser</sub> *D. solani* strains used in experimental populations and plant assays.

VfmB allele	Strains	Genome accession number	Reference	Year	Plant host	Country
VfmB <sub>Pro</sub>	3337 (=RNS08-23-3-1A)	CP016928.1	Khayi et al., 2018b	2008	Potato	France
	IPO2222	CP015137.1	Khayi et al. 2016	2007	Potato	Netherlands
	MIE35	VZQI00000000	this work	2005	Potato	Switzerland
	AM3a	VZQK00000000	this work	2015	Potato	France
VfmB <sub>Ser</sub>	Ds0432.1	CP017453.1	Khayi et al., 2018a	2004	Potato	Finland
	RNS10-27-2A	VZQJ00000000	this work	2010	Potato	Switzerland
	Sp1a	VZQL00000000	this work	2014	Potato	France
	M21a	VZQM00000000	this work	2014	Potato	France



**Table S4. Single nucleotide polymorphisms (SNPs) in the *Dickeya solani* strains used in VfmB<sub>Ser</sub> and VfmB<sub>Pro</sub> experimental populations.** The SNP positions according to reference genome *D. solani* 3337 and nature of the variations (nucleotide and absence '-') are indicated for the VfmB<sub>Pro</sub> *D. solani* strains (3337, IPO2222, MIE35 and AM3a) and VfmB<sub>Ser</sub> *D. solani* strains (Ds0432.1, RNS10-27-2A, Sp1a and M21a) used in experimental populations and plant assays. The SNP in *vfmB* gene is indicated in bold face.

SNP position according to the reference genome <i>D. solani</i> 3337	<i>D. solani</i> strains with VfmB <sub>Pro</sub> allele				<i>D. solani</i> strains with VfmB <sub>Ser</sub> allele			
	3337	IPO2222	MIE35	AM3a	Ds0432.1	RNS10-27-2A	Sp1a	M21a
251 348	A	A	G	G	A	A	A	A
373 746	C	C	C	T	C	C	C	C
445 806	G	G	G	C	G	G	G	G
445 810	G	G	G	C	G	G	G	G
445 816	G	G	G	C	G	G	G	G
449 939	C	T	T	T	T	T	T	T
449 939	C	T	T	T	T	T	T	T
542 285	T	T	T	T	C	T	T	T
696 730	A	G	G	A	G	A	A	A
696 730	A	G	G	A	G	A	A	A
696 754	T	T	T	A	C	T	T	T
696 757	G	G	G	T	G	G	G	G
696 766	G	G	G	T	G	G	G	G
696 802	A	A	A	A	A	T	A	A
696 814	A	T	A	A	A	T	A	A
696 814	A	T	A	A	A	T	A	A
696 817	G	T	G	G	G	T	G	G
696 817	G	T	G	G	G	T	G	G
696 856	A	A	A	A	A	T	A	A
696 919	C	A	C	C	C	A	C	C
696 919	C	A	C	C	C	A	C	C
874 452	C	-	C	C	C	C	C	C
874 452	C	-	C	C	C	C	C	C
1 241 485	C	C	C	C	C	C	C	T
2 310 928	C	C	C	C	C	C	C	T
2 581 700	G	C	G	C	G	C	C	C
2 581 700	G	C	G	C	G	C	C	C
2 621 029	T	T	T	T	T	T	T	C
2 680 622	T	A	T	T	T	T	T	T
2 680 622	T	A	T	T	T	T	T	T
2 680 626	-	A	-	-	-	-	-	-
2 680 626	-	A	-	-	-	-	-	-
2 680 628	-	T	-	-	-	-	-	-
2 680 631	G	C	C	C	C	C	C	C
2 680 634	G	C	G	C	G	C	C	C
2 692 264	T	C	C	C	C	C	C	C
2 805 554	C	C	T	C	C	C	C	C
2 850 707	T	T	T	G	T	T	T	T
<b>2 930 940 (<i>vfmB</i>)</b>	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	<b>T</b>	<b>T</b>	<b>T</b>	<b>T</b>
3 073 233	A	A	A	G	A	A	G	G
3 190 835	C	C	C	T	C	C	C	C
3 190 845	C	C	C	C	T	C	C	C
3 190 863	C	T	C	C	C	C	C	C
3 282 696	T	C	T	T	T	T	T	T
3 416 283	-	-	-	-	-	AATACA	-	-
3 776 457	G	G	A	G	G	G	G	G
3 878 996	C	C	C	C	C	A	C	C
4 215 226	A	C	A	A	A	A	A	A
4 266 548	C	C	C	C	T	T	T	T
4 335 313	G	A	G	G	G	G	G	G
4 353 648	G	G	A	G	G	G	G	G
4 700 614	A	G	A	A	A	A	A	A

**Table S5 List of the non-synonymous variations in *Dickeya solani* genomes.** Column1 indicates the number of strains (out of 66 *D. solani* genomes) exhibiting an identical non-synonymous SNP (column2) as compared to the reference genome *D. solani* 3337 (nucleotide in column 3, position in column 4 and putative function of the gene with SNP in column 5).

Number of <i>D. solani</i> strains (out of 66)	Allele in the <i>D. solani</i> strains	Allele in <i>D. solani</i> 3337	Position according to the reference genome <i>D. solani</i> 3337	Putative function according to <i>D. solani</i> 3337 genome annotation
19	T	C	2930940	VfmB
7	A	T	1598282	Putative sugar ABC transport system, permease protein Ytft
5	A	G	1230637	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
5	C	G	1466998	Putative sensory histidine kinase YfhA
4	T	C	373746	Transcriptional regulator, LysR family
4	G	A	4700614	unknown
4	A	G	4889560	Fructose-specific phosphocarrier protein HPr
3	A	C	2934086	Helix-turn-helix transcriptional regulator
3	C	T	3568108	Efflux RND transporter permease subunit
3	A	G	3830681	Transcriptional regulator, TetR family
3	A	T	4036689	ATP-binding component of a transport system
3	C	T	542285	Hemolysin
2	A	T	205872	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase
2	T	C	3815087	DNA gyrase inhibitory protein
2	A	C	542282	Hemolysin
1	T	C	1241485	General secretion pathway protein F
1	C	T	1471940	Phosphoribosylformylglycinamide synthase, synthetase subunit
1	A	C	1704641	RNA polymerase sigma factor RpoS
1	T	C	2042049	Transaldolase
1	T	C	2224192	Flagellar hook-length control protein FliK
1	A	G	2681959	ABC transporter, membrane spanning protein sugar
1	-	G	2754780	rRNA small subunit 7-methylguanosine (m7G) methyltransferase GidB
1	T	C	2829492	Oligopeptidase A
1	G	A	2853950	Formyl-coenzyme A transferase
1	T	C	2937329	hypothetical protein
1	-	G	2938687	Two-component system response regulator
1	A	G	3776457	bacteriophage protein-like
1	A	G	3928372	Aspartyl/Asparaginyl beta-hydroxylase
1	A	G	4094818	Putative membrane protein
1	C	A	4215226	Cytochrome d ubiquinol oxidase subunit I
1	C	T	4239064	Galactokinase
1	A	G	4335313	Rhs-family protein
1	C	G	4371065	Ferrous iron transport permease EfeU
1	T	C	441279	Putative large exoprotein involved in heme utilization or adhesion of ShlA/HecA/FhaA family
1	GT	CC	441285	Putative large exoprotein involved in heme utilization or adhesion of ShlA/HecA/FhaA family
1	A	G	4660131	Malonate decarboxylase alpha subunit
1	A	G	4762009	Biotin synthase
1	A	G	4766262	Excinuclease ABC subunit B
1	T	C	4852455	Oligopeptide transport ATP-binding protein OppF
1	A	G	4889560	Fructose-specific phosphocarrier protein HPr / PTS system, fructose-specific IIA component
1	A	G	521861	Tripeptide aminopeptidase
1	C	T	542255	Hemolysin
1	T	G	590354	Cystine ABC transporter, ATP-binding protein
1	T	A	894568	DNA polymerase III delta prime subunit
1	T	C	952985	Flagellar biosynthesis protein FliC

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