SUPPLEMENTAL MATERIAL.

Supplemental Results S1. Partial repeat of Experiment 1 on *D. seguieri.*

Additional methodological details: The final sample size of the *D. seguieri* treatment in Experiment 1 was small, we therefore repeated it with a subset of 10 of the 19 isolates used in the full Experiment 1 inoculation trail (See Table S1 below). We also inoculated a smaller number of *D. pavonius* plants at the same time, but only 23 of these flowered and could be scored for disease, so we did not analyze the results further (infections occurred in all *D. pavonius* treatments except Lineage 2 where only two plants flowered).

Table S1 Number of *D. seguieri* and *D. pavonius* plants that flowered and were scored for disease in the partial repeat of Experiment 1.

		Lineage 1	**Lineage 2**	**Lineage 3**	**Lineage 4**
Host species	**Host population**	(6,7)	(2,3, 13, 15)	(9,10)	(11, 17,20)
D. seguieri	Val Maira	93	187	52	112
	Valle Corsaglia	42	76	18	70
D. pavonius	Valle Pesio	9	2	3	9

Supplemental material S2.

Table S2. Effect of host species treatment and pathogen lineage on infection success in Experiment 1 when isolates 12 and 15 (potential hybrids) were excluded from the analysis.

Source	**Chi^2 Deviance**	**df**	**p**
Host species	154.52	2	<0.000 1
Pathogen Lineage	9.003	3	0.0292
Host*Lineage	34.45	6	<0.0001

Supplemental Results S3. Comparing the infection rates between populations within host species in Experiment 1. **A)** Results of overall test for host population (across all lineages). For *D. pavonius* and *D. seguieri* the test statistic is from a mixed model that included pathogen isolate. For *D. furcatus*, a simple fisher-exact test was used, by summing across lineages. **B)** Results of individual fisher exact tests examining the variation between host populations from the same species infected by the same pathogen lineage.

A)

Host species	Population	D	H	test-statistic	p
D. pavonius	Valle Pesio	168	13		
	Ferrere	78	15	1.115	1
D. seguieri	Val Maira	23	44		
	Valle Corsaglia	24	16	0.705	0.401
D. furcatus	Alberghi	2	16		
	Valle Grana	2	17	2.68	0.012

B)

Host species	Host. Pop.	Lineage	Num. Diseased	Number Healthy	Fisher odds ratio	p
D. pavonius	Valle Pesio	L1	27	3		
	Ferrere		13	2	1.37	1
	Valle Pesio	L2	75	6		
	Ferrere		29	7	2.98	0.11
	Valle Pesio	L3	16	1		
	Ferrere		5	3	8.59	0.08
	Valle Pesio	L4	50	3		
	Ferrere		31	3	0.67	0.67
D. seguieri	Val Maira	L1	0	8		
	Valle Corsaglia		0	2	0	1
	Val Maira	L2	22	7		
	Valle Corsaglia		21	3	0.46	0.32
	Val Maira	L3	0	3		
	Valle Corsaglia		1	6	0	1
	Val Maira	L4	1	26		
	Valle Corsaglia		2	5	0.11	0.10
D. furcatus	Alberghi	L1	0	3		
	Valle Grana		0	3	0	1
	Alberghi	L2	2	3		
	Valle Grana		1	3	1.85	1
	Alberghi	L3	0	2		
	Valle Grana		1	3	0	1
	Alberghi	L4	0	8		
	Valle Grana		0	8	0	1

Supplemental Results S4. Variation among pathogen isolates within Lineages.

We were able to carry out two contrasts to compare the effect of isolate locality while holding lineage and host-of-origin constant. We found no significant effect of location among isolates of Lineage 2 that had been collected from *D. seguieri* in either Val Maira or Rio Freddo (F=2.15, df=1 p=0.1519). Similarly, there was no effect of location among isolates of Lineage 4 from *D. seguieri* collected from either San Bernardo di Mendatica or Lago di Osiglia (F=7.587, df=1, p=0.387).

Eight pairs of replicate *Microbotryum* isolates were assigned to the same lineage and collected from the same host-of-origin and location. After correcting for multiple comparisons, none of these pairs showed evidence of significant variation in overall infection rate (Table S4 below).

Table S4. Results of Fisher-exact tests comping the infection rate between replicate pairs of strains from the same pathogen lineage and geographic location in experiment1.

Lineage	Pathogen strain	Total Number	Number Diseased	Fisher-exact test
1	7	18	8	
	8	21	18	0.3022
2	3	28	20	
	4	24	19	0.8348
2	13	19	14	
	14	19	16	0.8116
2	15	32	28	
	16	28	24	1.0
3	9	25	14	
	10	18	9	1.0
4	11	28	13	
	12	26	16	0.6467
4	17	27	20	
	18	25	17	1.0
4	19	11	2	
	20	20	16	0.0947

Supplemental Results S5. Variation in flowering rates between inoculated and control plants.

A total of 420 (out of 735) inoculated plants and 69 control plants (out of 179) flowered in the first year of the experiment. Two out of the *D. pavonius* control plants were infected, but none of the other two species had infected controls. Flowering rates in the first year differed significantly among host species (X^2=97.90, p<0.0001) and between control and inoculated treatments (X^2=20.03, df=1, p<0.0001). The flowering rate was highest in *D. pavonius* (69%) and lowest in *D. furcatus* (24%). In *D. pavonius*, the flowering rate was higher among inoculated plants (71%) than among control plants (57%; X^2=3.56, p=0.06). There was a similar trend of higher flowering in the inoculated treatment of *D. seguieri* (53% versus 38%) but the effect was not significant (X^2=1.52, p=0.22). Pathogen lineage did not have a significant effect on flowering rate in any species (results not shown).

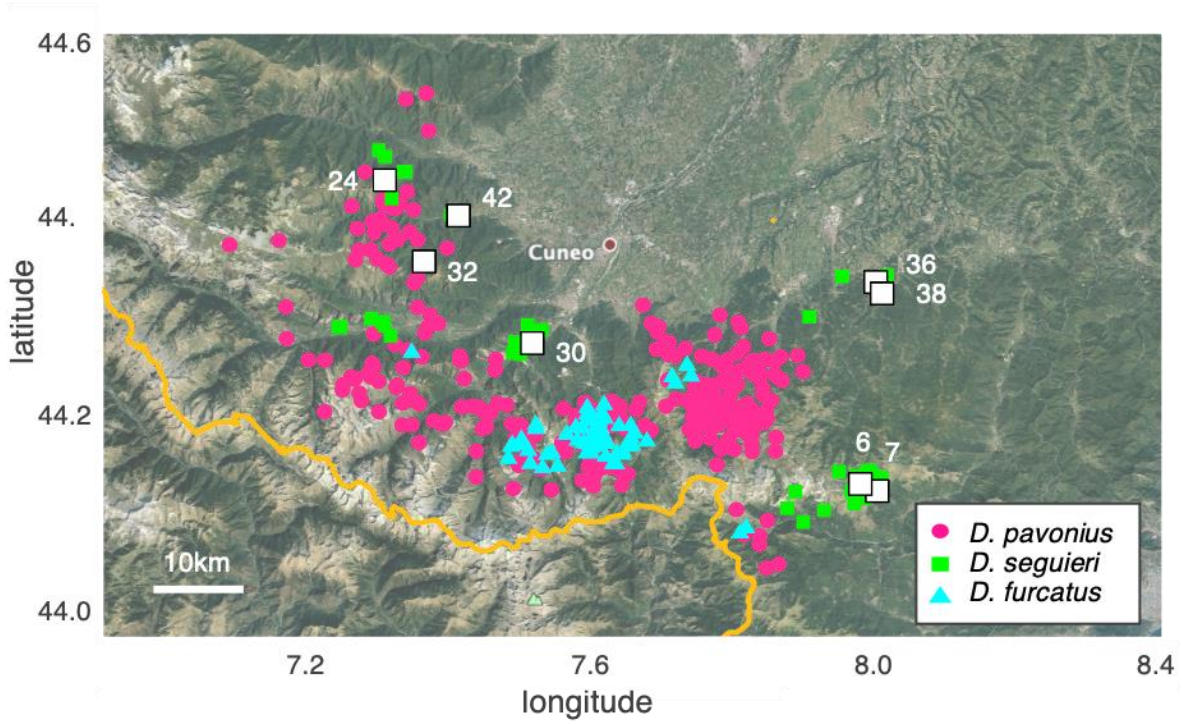

Fig. S1. Location of eight additional *D. seguieri* host populations sampled for Experiment 2 (White numbered boxes). The distribution of the three host species is shown for reference. Points have been randomly jittered to minimize overlap. The yellow line indicates the border with France.

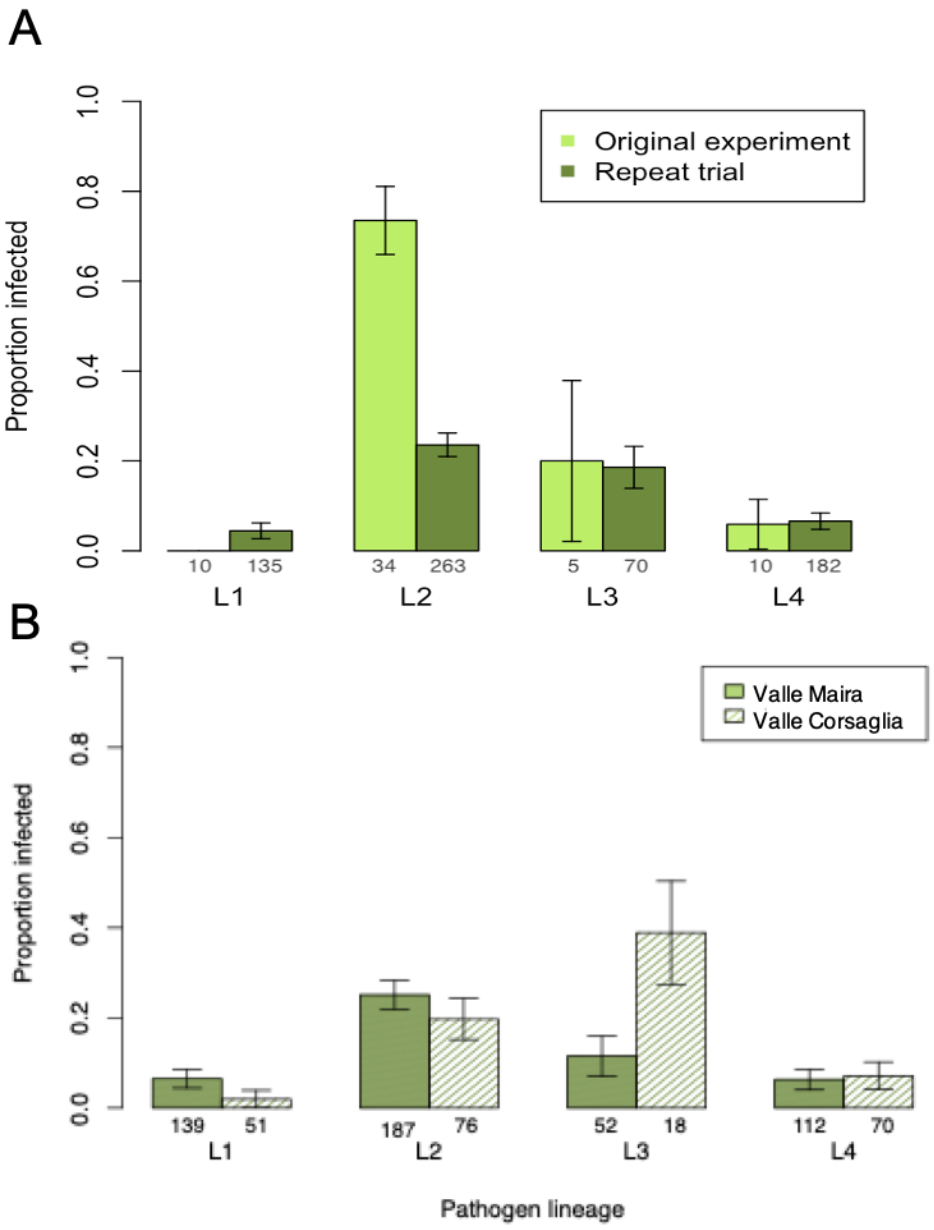

Figure S2. A) Comparison of infectivity of four pathogen lineages on *D. seguieri* in the original inoculation experiment (light green bars) and the repeat inoculation experiment (dark green bars). For consistency, the infection rates for the original experiment shown above (light green bars) were calculated using only the subset of 10 isolates that were used in in the repeat inoculation trial. B) The variation in infection rate among the two *D.* seguieri population in the partial repeat experiment of Experiment 1. In both A and B numbers indicate sample size and error bars are 1 SEM.

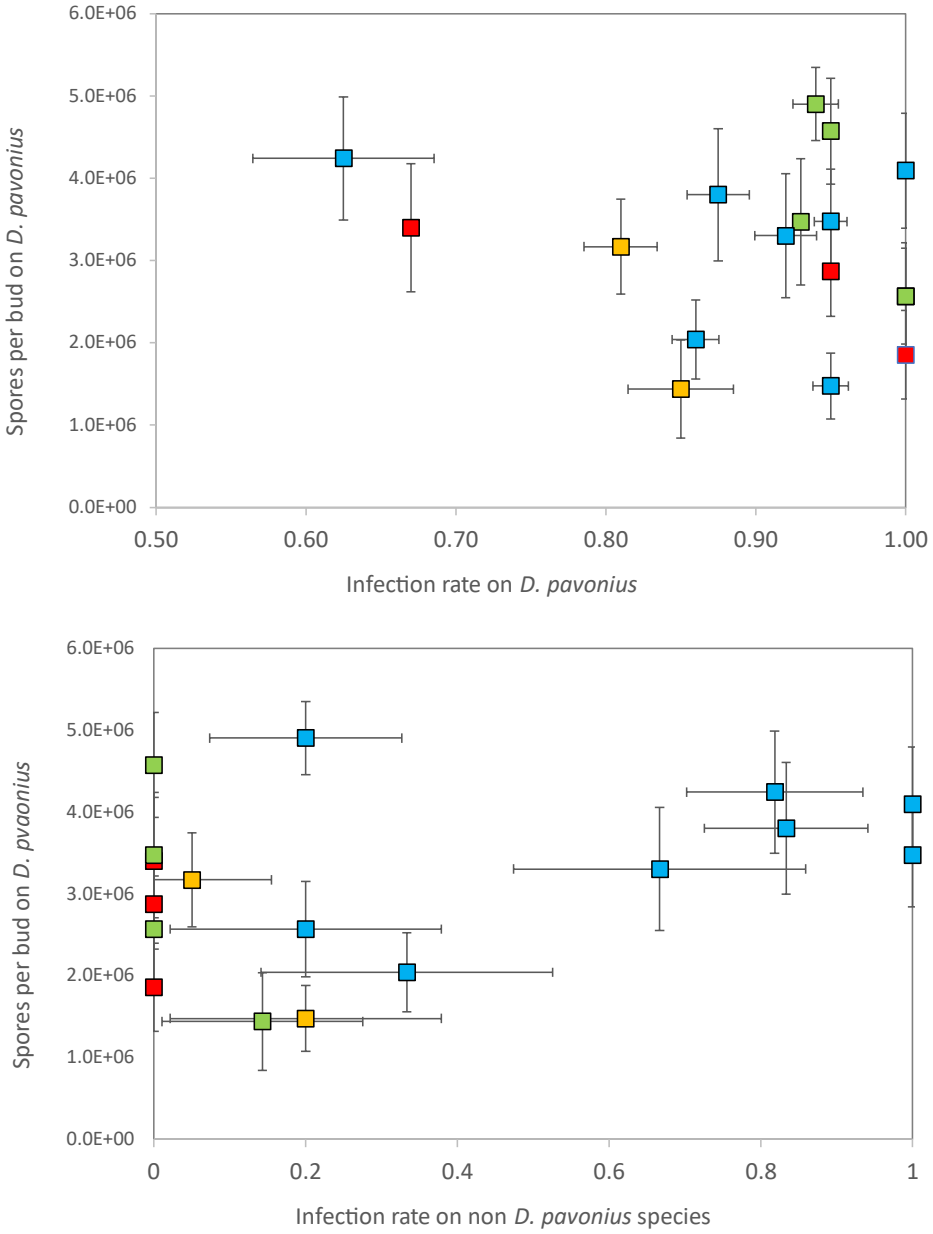

Fig S3. Relationship between infection rate on **Top)** *Dianthus pavonius* and **Bottom)** Other *Dianthus* species *(*not *D. pavonius*), and average spore production on *D. pavonius.* Each square is an individual *Microbotryum* isolate. Colors indicate lineage: *Red*-L1, *Blue*-L2, *Yellow*-L3, and *Green*-L4. Error bars are 1 SEM. Note that the x-axis starts at 0.5 in the top plot because all isolates were highly infectious on *D. pavonius.* We did not find any evidence of a significant negative relationship that would indicate a trade-off between infectivity and spore production (see main text for details.