

Supplementary Tables for

Genic introgression from an invasive exotic fungal forest pathogen increases the establishment potential of a sibling native pathogen

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Table S1. Statistics of reads mapping of the nine *Heterobasidion* hybrid genotypes to reference genome.

ID Genotype	136SE	41NB	150EA	115OG	118NB	51ED	144SE	45EH	49OE
Paired End Reads sequenced	8038987	8026990	8028932	8035436	8019832	8028281	8021231	8020438	8025321
Mapped Reads	7327574 (91.15%)	7054626 (87.89%)	7176330 (89.38%)	7280041 (90.60%)	6667878 (83.14%)	7336365 (91.38%)	6226031 (77.62%)	6111281 (76.20%)	6335056 (78.94%)
Properly mapped Reads	7000741 (87.08%)	6750729 (84.10%)	6864707 (85.50%)	6961685 (86.64%)	6361712 (79.32%)	6926108 (86.27%)	5750147 (71.69%)	5642827 (70.36%)	5899279 (73.51%)
Singletons	49135	53328	74249	52032	102334	63817	207614	198319	151301

Table S2. Virulence assay results; for each *Heterobasidion* genotype the rapidity to death (average and min-max range among replicates), expressed as the number of days elapsed since pathogen inoculation (DPI mortality - Days Post Inoculation), was reported.

ID Genotype	Species	DPI mortality (average, days)	Range days (min-max, days)
48NB	<i>H. irregulare</i>	25	14-35
9OA	<i>H. irregulare</i>	44	28-56
49SA	<i>H. irregulare</i>	18	11-28
137OC	<i>H. annosum</i>	14	10-19
136SE	Hybrid (<i>H. irregulare</i>)	14	12-16
41NB	Hybrid (<i>H. irregulare</i>)	14	11-22
150EA	Hybrid (<i>H. irregulare</i>)	13	12-15
115OG	Hybrid (<i>H. irregulare</i>)	13	11-17
118NB	Hybrid (<i>H. annosum</i>)	16	12-28
51ED	Hybrid (<i>H. irregulare</i>)	37	28-49
144SE	Hybrid (<i>H. annosum</i>)	14	10-17
45EH	Hybrid (<i>H. annosum</i>)	12.5	8-16
49OE	Hybrid (<i>H. annosum</i>)	39	30-49

Mock	-	-	-
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Table S3. Saprobiic assay results; for each *Heterobasidion* genotype the *in vitro* growth rate was reported. The radial growth of fungal cultures was measured every 48 hours for 10 days along two perpendicular lines.

ID Genotype	Species	Radius of fungal colony (mm)
48NB	<i>H. irregulare</i>	20.35 ±0.70
90A	<i>H. irregulare</i>	40.00 ±0.55
49SA	<i>H. irregulare</i>	25.55 ±0.25
137OC	<i>H. annosum</i>	24.90 ±0.75
136SE	Hybrid (<i>H. irregulare</i>)	24.65 ±0.20
41NB	Hybrid (<i>H. irregulare</i>)	20.90 ±0.20
150EA	Hybrid (<i>H. irregulare</i>)	18.95 ±0.45
115OG	Hybrid (<i>H. irregulare</i>)	19.00 ±0.35
118NB	Hybrid (<i>H. annosum</i>)	25.15 ±0.15
51ED	Hybrid (<i>H. irregulare</i>)	18.35 ±0.15
144SE	Hybrid (<i>H. annosum</i>)	31.20 ±0.85
45EH	Hybrid (<i>H. annosum</i>)	29.95 ±0.70
49OE	Hybrid (<i>H. annosum</i>)	32.90 ±0.25

Table S4. List of *Heterobasidion* hybrid genotypes showing genome admixture based on AFLP markers (Gonthier and Garbelotto 2011). Molecular identification based on Gonthier et al. (2007) is also included.

ID	Geographic origins	Nuclear marker (Ef1-α)	Mitochondrial marker
136SE	Italy, Circeo North East	<i>H. annosum</i>	<i>H. annosum</i>
41NB	Italy, Circeo Central West	<i>H. annosum</i>	<i>H. annosum</i>
150EA	Italy, Circeo North	<i>H. irregulare</i>	<i>H. annosum</i>
115OG	Italy, Circeo North	<i>H. irregulare</i>	<i>H. irregulare</i>
51ED	Italy, Anzio	<i>H. irregulare</i>	<i>H. irregulare</i>
118NB	Italy, Circeo North	<i>H. annosum</i>	<i>H. irregulare</i>
45EH	Italy, Circeo Central West	<i>H. annosum</i>	<i>H. annosum</i>
144SE	Italy, Circeo Central West	<i>H. annosum</i>	<i>H. annosum</i>
490E	Italy, Circeo Central West	<i>H. annosum</i>	<i>H. annosum</i>