

Supplementary Data S1. A. Sequence alignment of the genic region OG08220 for *Tilletia walkeri* and *T. indica* isolates sequenced by Nguyen et al. [43]. Highlighted regions correspond to the qPCR primer sequences (grey) and the probe sequence (yellow).

	241	250	260	270	280	290	300
T_walkeri_DAOMC_230849	G	G	T	G	A	A	T
T_walkeri_DAOMC_236422	G	G	T	G	A	A	T
T_indica_DAOMC_236408	G	G	T	G	A	A	T
T_indica_DAOMC_236414	G	G	T	G	A	A	T
T_indica_DAOMC_236416	G	G	T	G	A	A	T
	301	310	320	330	340	350	360
T_walkeri_DAOMC_230849	G	G	T	G	A	A	T
T_walkeri_DAOMC_236422	G	G	T	G	A	A	T
T_indica_DAOMC_236408	G	G	T	G	A	A	T
T_indica_DAOMC_236414	G	G	T	G	A	A	T
T_indica_DAOMC_236416	G	G	T	G	A	A	T
	361	370	380	390	400	410	420
T_walkeri_DAOMC_230849	G	T	C	A	G	A	G
T_walkeri_DAOMC_236422	G	T	C	A	G	A	G
T_indica_DAOMC_236408	G	T	C	A	G	A	G
T_indica_DAOMC_236414	G	T	C	A	G	A	G
T_indica_DAOMC_236416	G	T	C	A	G	A	G

Supplementary Data S1. B. Sequence alignment of the isolates sequenced by Nguyen et al. [43] presenting part of the region OG01193 unique to *Tilletia walkeri* and *T. indica* used for the qPCR assay design. Highlighted regions correspond to the qPCR primer sequences (grey), and the probe sequence (yellow). Differences with the non-target species in the alignment are highlighted in cyan.

	121	130	140	150	160	170	180
T_caries_DAOMC_238032	C	T	A	C	C	G	C
T_laevis_ATCC_42080	C	T	A	C	C	G	C
T_laevis_DAOMC_238040	C	T	A	C	C	G	C
T_controversa_DAOMC_236426	C	T	A	C	C	G	C
T_controversa_DAOMC_238052	C	T	A	C	C	G	C
T_indica_DAOMC_236414	C	T	A	C	C	G	C
T_indica_DAOMC_236416	C	T	A	C	C	G	C
T_indica_DAOMC_236408	C	T	A	C	C	G	C
T_walkeri_DAOMC_236422	C	T	A	C	C	G	C
T_walkeri_DAOMC_230849	C	T	A	C	C	G	C
	181	190	200	210	220	230	240
T_caries_DAOMC_238032	A	A	C	T	T	C	G
T_laevis_ATCC_42080	A	A	C	T	T	C	G
T_laevis_DAOMC_238040	A	A	C	T	T	C	G
T_controversa_DAOMC_236426	A	A	C	T	T	C	G
T_controversa_DAOMC_238052	A	A	C	T	T	C	G
T_indica_DAOMC_236414	A	A	C	T	T	C	G
T_indica_DAOMC_236416	A	A	C	T	T	C	G
T_indica_DAOMC_236408	A	A	C	T	T	C	G
T_walkeri_DAOMC_236422	A	A	C	T	T	C	G
T_walkeri_DAOMC_230849	A	A	C	T	T	C	G
	241	250	260	270	280	290	300
T_caries_DAOMC_238032	T	G	C	T	G	C	C
T_laevis_ATCC_42080	T	G	C	T	G	C	C
T_laevis_DAOMC_238040	T	G	C	T	G	C	C
T_controversa_DAOMC_236426	T	G	C	T	G	C	C
T_controversa_DAOMC_238052	T	G	C	T	G	C	C
T_indica_DAOMC_236414	T	G	C	T	G	C	C
T_indica_DAOMC_236416	T	G	C	T	G	C	C
T_indica_DAOMC_236408	T	G	C	T	G	C	C
T_walkeri_DAOMC_236422	T	G	C	T	G	C	C
T_walkeri_DAOMC_230849	T	G	C	T	G	C	C
	301	310	320	330	340	350	360
T_caries_DAOMC_238032	A	G	A	T	T	C	G
T_laevis_ATCC_42080	A	G	A	T	T	C	G
T_laevis_DAOMC_238040	A	G	A	T	T	C	G
T_controversa_DAOMC_236426	A	G	A	T	T	C	G
T_controversa_DAOMC_238052	A	G	A	T	T	C	G
T_indica_DAOMC_236414	A	G	A	T	T	C	G
T_indica_DAOMC_236416	A	G	A	T	T	C	G
T_indica_DAOMC_236408	A	G	A	T	T	C	G
T_walkeri_DAOMC_236422	A	G	A	T	T	C	G
T_walkeri_DAOMC_230849	A	G	A	T	T	C	G