

**Table S1.** Molecular identification of the *Fusarium* sp. isolates based on ITS and  $\beta$ -tubulin sequence analysis.

Isolate	$\beta$ -tub sequence			
	Lineage organism	Nb of hits	Lineage organism *	Nb of hits
3T	<i>F. sambucinum</i> species complex	152	<i>F. pseudograminearum</i>	78
4T	<i>F. sambucinum</i> species complex	152	<i>F. pseudograminearum</i>	78
32T	<i>F. tricinctum</i> species complex	66	<i>F. acuminatum</i>	55
33T	<i>F. tricinctum</i> species complex	64	<i>F. acuminatum</i>	51
Best nr database similarity hit				
	Taxon	E value	ID %	GenBank Accession No.
3T	<i>F. culmorum</i>	4e-100	100	LT598662.1
4T	<i>F. culmorum</i>	5e-99	99.04	LT598662.1
32T	<i>F. acuminatum</i>	5e-68	96.88	MH341248.1
33T	<i>F. acuminatum</i>	8e-92	98.48	MH341248.1
	ITS sequence			
	Lineage organism	Nb of hits	Lineage organism *	Nb of hits
3T	Sordariomycetes	101	<i>F. graminearum</i>	49
4T	Sordariomycetes	101	<i>F. graminearum</i>	56
32T	<i>F. tricinctum</i> species complex	72	<i>F. acuminatum</i>	54
33T	<i>F. tricinctum</i> species complex	95	<i>F. acuminatum</i>	49
Best nr database similarity hit				
	Taxon	E value	ID %	GenBank Accession No.
3T	<i>F. graminearum</i>	0	99.76	MT598163.1
4T	<i>F. graminearum</i>	0	99.76	MT598163.1
32T	<i>F. acuminatum</i>	0	100	MT635295.1
33T	<i>F. acuminatum</i>	0	100	MT635295.1

\* Species with the highest number of hits