

Table S3. Percentages of sequence similarities among *Fusarium* spp. KP4L proteins and with the *Ustilago maydis* KP4 (UmKP4) protein. (A) Intraspecific variability was calculated by pairwise alignment between proteins from different isolates of the same species. (B) Interspecific variability was calculated among proteins from different species considering proteins of either all *Fusarium* spp., only species belonging to the FHBSC, or only species outside the FHBSC. (C) Intergeneric variability was calculated by pairwise alignments between the UmKP4 protein and the consensus sequence derived from the alignment of KP4L proteins from either all *Fusarium* spp., only species belonging to the FHBSC, or only species outside the FHBSC.

A	Intraspecific	KP4L-0	KP4L-1	KP4L-2	KP4L-3	KP4L-4	KP4L-4 D1	KP4L-4 D2	TEF-1
	<i>F. graminearum</i>	.	100	100	100	95	95	95	100
	<i>F. avenaceum</i>	.	98	96	97	98	98	99	99.8
	<i>F. culmorum</i>	.	100	100	100	100	100	100	99.9
	<i>F. oxysporum</i> *	99	99	100	99.8

B	Interspecific	KP4L-0	KP4L-1	KP4L-2	KP4L-3	KP4L-4	KP4L-4 D1	KP4L-4 D2	TEF-1
	<i>Fusarium</i> spp.	56	94	93	92	70	66	78	92.8
	FHBSC	.	99	97	98	83	79	91	95.4
	Outside FHBSC	56	.	.	.	70	66	73	96.7

C	Intergeneric	KP4L-0	KP4L-1	KP4L-2	KP4L-3	KP4L-4	KP4L-4 D1	KP4L-4 D2
	<i>Fusarium</i> spp.	33	39	36	41	.	36	37
	FHBSC	.	39	36	41	.	36	37
	Outside FHBSC	33	37	35	39	.	30	32

* Fo47, NRRL32931, *F. oxysporum* f. sp. *melonis*, *F. oxysporum* f. sp. *lycopersici*