

Table S3. Genera of fungal strains isolated and identified ($n = 424$) from 1080 pieces of wheat (W) and oilseed rape (O) residue collected from the wheat monoculture plot (W_M) and the two wheat-oilseed rape rotation plots (W_R and O_R) in 2015-2016 and 2016-2017. Molecular typing of the strains was performed with the ITS1-5.8S-ITS2 region. Data for the three sampling periods (October, December and February) were pooled for each cropping season. The genera not detected by metabarcoding in the study by Kerdraon *et al.* (2019b) are indicated by *.

	2015-2016			2016-2017		
	W_M	W_R	O_R	W_M	W_R	O_R
<i>Actinomucor</i> *	0	0	0	0	0	1
<i>Alternaria</i>	1	13	1	0	0	8
<i>Boeremia</i> *	0	0	0	0	0	3
<i>Botrytis</i> *	0	0	0	0	0	1
<i>Chaetomium</i>	3	0	0	0	0	4
<i>Cladorrhinum</i>	0	2	5	1	0	0
<i>Cladosporium</i>	0	0	1	0	1	7
<i>Epicoccum</i>	3	6	7	9	10	13
<i>Fusarium</i>	18	15	13	58	68	38
<i>Laetisaria</i>	0	0	0	0	0	0
<i>Lophodermium</i>	0	0	0	0	0	0
<i>Leptosphaeria</i>	2	0	0	1	0	0
<i>Microdochium</i>	0	2	0	1	3	0
<i>Mortierella</i> *	6	5	20	5	4	6
<i>Mucor</i>	8	2	6	5	1	12
<i>Neurospora</i> *	0	0	0	0	1	0
<i>Nigrospora</i>	0	9	0	0	0	0
<i>Phaeosphaeria</i>	1	0	0	1	0	0
<i>Septoriella</i>	0	0	0	0	0	0
<i>Stagonosporopsis</i> *	0	0	0	0	0	1
<i>Trichoderma</i>	0	5	0	1	0	2
<i>Waitea</i>	0	1	0	0	0	0
NI	1	2	0	0	0	0
Total number of strains	43	62	53	82	88	96
Total number of genera identified	8	10	7	9	7	12