

# Comparative genomic analysis of monosporial and monoteliosporic cultures for unraveling the complexity of molecular pathogenesis of *Tilletia indica* pathogen of wheat

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## Supplementary Data 1

Supplementary Data 1: The frequency of the most common motif appears predominately is displayed for each developmental case.

<b>Predominant repeats</b>	<b>monoteliospori c TiK_1</b>	<b>Monosporidial PSWKBGH_1</b>	<b>Monosporidial PSWKBGH_2</b>	<b>Dikaryon PSWKBGD_1_3</b>
<b>AG/CT</b>	1131	1217	1163	1388
<b>A/T</b>	668	1049	963	1130
<b>C/G</b>	641	1113	1192	1763
<b>AGC/CTG</b>	516	600	537	620
<b>AGG/CCT</b>	494	562	536	640
<b>AC/GT</b>	412	416	472	487
<b>ACC/GGT</b>	337	347	376	378
<b>AAC/GTT</b>	263	272	270	321
<b>AAG/CTT</b>	223	253	252	298
<b>CCG/CGG</b>	203	259	197	245
<b>ATC/ATG</b>	198	199	200	261
<b>ACG/CGT</b>	190	277	227	268
<b>CG/CG</b>	52	64	46	58
<b>ACTC/AGTG</b>	50	55	59	68
<b>AAGG/CCTT</b>	27	32	30	41
<b>ACT/AGT</b>	22	19	33	31
<b>AT/AT</b>	18	18	12	20
<b>AGGG/CCCT</b>	18	35	27	18
<b>AACCCT/AGGGTT</b>	12	39	73	15
<b>AAAG/CTTT</b>	8	10	44	22
<b>ACAG/CTGT</b>	8	50	14	13

## Supplementary Data 2

Supplementary Data 2: Protein family annotation shows the distribution of most abundant protein class assigned to *T. indica* genes.

<b>Category name (Accession)</b>	<b>Genes</b>	<b>Percent of gene hit against total genes</b>	<b>Percent of gene hit against total Protein Class hits</b>
extracellular matrix protein (PC00102)	4	0.10%	0.20%
cytoskeletal protein (PC00085)	58	1.90%	2.80%
transporter (PC00227)	148	4.80%	7.20%
transmembrane receptor regulatory/adaptor protein (PC00226)	9	0.30%	0.40%
transferase (PC00220)	281	9.10%	13.70%
oxidoreductase (PC00176)	197	6.40%	9.60%
lyase (PC00144)	60	1.90%	2.90%
cell adhesion molecule (PC00069)	1	0.00%	0.00%
ligase (PC00142)	98	3.20%	4.80%
nucleic acid binding (PC00171)	408	13.20%	19.90%
signaling molecule (PC00207)	14	0.50%	0.70%
enzyme modulator (PC00095)	125	4.00%	6.10%
calcium-binding protein (PC00060)	27	0.90%	1.30%
defense/immunity protein (PC00090)	1	0.00%	0.00%
hydrolase (PC00121)	332	10.70%	16.20%
transfer/carrier protein (PC00219)	45	1.50%	2.20%
membrane traffic protein (PC00150)	69	2.20%	3.40%
transcription factor (PC00218)	81	2.60%	3.90%
chaperone (PC00072)	25	0.80%	1.20%
cell junction protein (PC00070)	2	0.10%	0.10%
structural protein (PC00211)	2	0.10%	0.10%
isomerase (PC00135)	40	1.30%	1.90%
receptor (PC00197)	24	0.80%	1.20%

#### Supplementary Data 4

Supplementary Data 4: Virulence associated genes (VAGs) belonging to *T. indica* genome sequence producing high-scoring segments pairs.

<b>S.No.</b>	<b>Gene phenotype</b>	<b>Number of VAGs</b>
1	loss_of_pathogenicity	33
2	unaffected_pathogenicity	50
3	reduced_virulence	90
4	lethal	22
5	increased_virulence (hypervirulence)	4
6	resistance_to_chemical	1
7	multiple outcome	20
	<b>Total VAGs</b>	<b>220</b>

## Supplementary data 5

Supplementary data 5: The PHI-base accessions assigned to *T. indica* genes hits to other pathogenic fungal organism.

<b>Organisms</b>	<b>No. of hits of <i>T. Indica</i></b>
Fusarium_graminearum	58
Magnaporthe_oryzae	34
Cryptococcus_neoformans	24
Ustilago_maydis	20
Aspergillus_fumigatus	19
Candida_albicans	12
Parastagonospora_nodorum	8
Colletotrichum_gloeosporioides	6
Cryptococcus_gattii	4
Colletotrichum_lindemuthianum	3
Edwardsiella_ictaluri	3
Leptosphaeria_maculans	3
Saccharomyces_cerevisiae	3