Supplementary Results

Summary of the main findings according to each class of PCWDE.

Cutinases

All six cutinase genes found in *Z. tritici* were confirmed in *Z. pseudotritici* and Z. *ardabiliae* and four were found in *Z. passerinii* (supplementary table S1). All cutinases were functionally assigned to the CAZy family Carbohydrate Esterases 5 (CE5). Estimated neutrality indices from the MKTs did not deviate significantly from neutral expectations for the pooled CE5 data set (supplementary table S3b). But at the level of individual genes, two of the six genes had neutrality indices significantly different from zero (fig. 3). CE5-ProtID-99331 was identified as being under significant diversifying selection ($-\log_{10}NI = 0.356$, p = 0.011; alpha = 0.559) while CE5- ProtID-18212 exhibited significant purifying selection (supplementary table S3a).

On the lineage specific level, we found a significant five-fold increase in dN / dS for CE5-ProtID-18212 of *Z. tritici* compared to its ancestors, indicating an increase in diversifying selection between species (supplementary table S4). All other cutinases showed dN /dS values not significantly different from the single rate model.

Cellulases

All eleven cellulase genes were confirmed in *Z. tritici*, *Z. pseudotritici* and Z. *ardabiliae* and nine were found in *Z. passerinii* (supplementary table S1). The cellulases were assigned to five different CAZy families. Two of these families, Glycoside Hydrolases 5 (GH5) and GH61, were multi-gene families with six and two members, respectively. The individual members of these two families as well as the pooled data sets did not deviate from neutral expectations in the MKTs. GH45-ProtID-76589 was the only cellulase undergoing significant diversifying selection ($-\log_{10}NI = 0.390$, p < 0.001, alpha = 0.593). None of the cellulases showed evidence for significant purifying selection (fig. 3; supplementary tables S3a and S3b).

Hemicellulases

Eighteen hemicellulase genes belonging to seven CAZy families exist in *Z. tritici*. Sixteen of the genes were confirmed in all species, but six could not be detected in *Z. passerinii* (supplementary table S1). CAZy families GH10, GH43 and GH51 were

multigene families with two, nine and three members, respectively. Multilocus MKTs on the pooled members resulted in evidence of significant purifying selection for CAZy family GH51, GH10 was neutral and no multilocus MKT could be calculated for GH43 because of heterogeneity among all pairwise comparisons (fig. 3; supplementary table S3b).

At the individual gene level, however, three of the nine GH43 genes (ProtIDs-73095, 98714, and 84076) and one of the three GH51 genes (ProtID-40215) were identified as being under significant purifying selection. Purifying selection was also indicated for the gene GH54-ProtID-70396. GH62-ProtID-68922 was the only hemicellulase gene showing significant diversifying selection ($-\log_{10}NI = 0.686$, $p < 0.001$, alpha = 0.794; fig. 3; supplementary table S3a).

The HYPHY analyses indicated widespread heterogeneity in selection pressure in this class of PCWDEs. Six of the 18 hemicellulases of *Z. tritici* showed significantly reduced dN / dS values compared to their ancestors, indicating increased purifying selection, e.g. due to substrate optimization on the new wheat host.

Pectinases

Among the 13 pectinase genes in *Z. tritici*, all were confirmed in *Z. pseudotritici*, 11 were found in *Z. ardabiliae* and eight were found in *Z. passerinii*. The pectinases were distributed among eight CAZy families; five of these families included two members each (supplementary table S1). MKTs on the pooled members of CAZy families detected significant purifying selection for GH88 (fig. 3; supplementary table S3b). The pectinases are dominated by purifying selection and are the only class of enzymes without a gene showing significant diversifying selection. Eleven out of the 13 individual genes had negative NIs with five showing significant evidence of purifying selection (ProtIDs-77196, 25958, 33711, 50077, 65051, and 27839; fig. 3; supplementary table S3a).

On the phylogenetic level, one gene (GH115-ProtID-65051) showed a significant threefold reduction in dN /dS for *Z. tritici* (fig. 4; supplementary table S4).

Supplementary table S1: Identification of homologues and orthologues gene sequences coding for cell wall degrading enzymes in 19 whole genome assemblies of *Zymoseptoria tritici* and its closest relatives. BLAST searches used search-algorithms of > 50% nucleotide identity and >50% sequence length identity with respect to 48 annotated CWDEs from the *Z. tritici* isolate IPO323 genome. Number of amino acids and average amino acid identity (AA_ID) are given with respect to IPO323. Genes are listed by enzymatic families according to the Carbohydrate-Active EnZymes database (CAZy) and the protein identification number (Prot_ID) from the Joint Genome Institute (JGI).

	CAZy	JGI PROT_ID	IPO323 amino acids	*Z. tritici* amino acids	(N=9) % AA_ID	*Z. pseudotritici* amino acids	(N=5) % AA_ID	*Z. ardabiliae* amino acids	(N=4) % AA_ID	*Z. passerinii* amino acids	(N=1) % AA_ID
Cutinases	CE5	77282	231	231	99.00	231	96.20	231	94.00	231	88.00
	CE5	68483	216	216	99.00	216	97.00	216	97.00	214	82.00
	CE5	35055	108	108	98.00	108	97.00	108	87.50	-	-
	CE5	99331	239	239	99.00	239	94.20	141	87.65	-	-
	CE5	43394	232	232	99.33	232	98.60	232	96.00	232	90.00
	CE5	18212	202	202	99.89	202	99.00	202	95.00	202	84.00
Cellulases	GH5	71664	495	495	99.78	495	95.20	495	93.00	495	88.00
	GH5	88889	418	418	98.89	418	98.00	418	98.00	418	92.00
	GH5	106779	417	417	99.78	417	98.00	417	96.50	-	-
	GH5	83843	616	616	98.56	616	98.00	616	94.50	616	86.00
	GH5	92097	364	364	98.86	364	89.59	364	87.81	363	81.73
	GH5	111224	1085	1085	99.98	1085	93.45	1085	92.89	1084	85.27
	GH7	100252	444	444	100.00	444	99.00	444	98.00	444	94.00
	GH12	105871	246	246	98.78	246	92.40	246	91.00	245	80.00
	GH45	76589	240	240	99.44	240	90.20	240	85.25	187	77.00
	GH61	33254	320	320	98.50	320	92.00	284	89.50	-	-
	GH61	103512	390	390	97.44	390	95.00	390	92.50	390	87.00
Hemi-cellulases	GH10	94846	370	370	99.00	370	96.00	370	94.00	369	84.00
	GH10	61141	348	348	99.81	348	90.49	348	88.76	-	-
	GH11	60105	225	167	100.00	167	94.00	167	91.00	-	-
	GH43	98714	324	324	98.56	324	96.00	324	94.00	324	94.00
	GH43	105323	319	319	98.56	319	95.00	319	95.00	-	-
	GH43	96505	385	385	87.56	385	83.00	385	82.50	385	77.00
	GH43	84076	545	545	97.00	535	95.00	545	93.00	545	86.00
	GH43	75584	294	294	100.00	294	97.00	294	93.00	294	82.00
	GH43	96947	679	679	96.91	679	91.85	679	89.61	-	-
	GH43	73095	322	322	99.58	322	96.57	322	92.51	322	86.60
	GH43	30121	297	222	98.94	225	90.28	222	87.68	-	-
	GH43	105728	341	341	98.90	341	90.22	341	90.45	344	81.84
	GH51	71466	633	633	99.71	633	95.85	633	93.11	633	85.64
	GH51	111130	691	691	96.75	691	92.70	687	88.87	690	85.47
	GH51	40215	503	503	98.87	503	95.52	503	92.80	503	85.79
	GH54	70396	502	502	98.22	502	96.40	502	94.00	502	88.00
	GH62	68922	321	321	99.89	321	98.00	321	90.75	321	88.00
	GH93	95102	417	416	99.62	416	91.98	414	88.83	-	-
Pectinases	CE8	66866	330	330	99.30	330	95.00	330	94.00	330	82.00
	GH28	86032	416	416	99.22	416	97.00	416	93.00	416	86.00
	GH28	77196	491	491	99.78	491	88.00	491	92.00	491	78.00
	GH53	25958	332	332	98.78	332	97.60	-	-	-	-
	GH53	51381	342	342	99.67	342	97.00	342	90.50	-	-
	GH78	33711	798	798	99.27	798	94.27	798	94.15	-	-
	GH78	69329	680	680	99.76	680	95.05	-	-	-	-
	GH88	50077	380	380	97.72	380	94.20	380	93.23	380	78.28
	GH88	57259	388	388	97.49	388	96.05	388	94.33	388	79.38
	GH115	65051	1024	1024	99.17	1024	93.49	1024	91.84	1024	82.50
	PL1	42327	342	342	98.11	342	91.80	342	91.00	342	83.00
	PL1	85457	324	324	94.78	324	90.00	324	91.00	-	-
	PL3	27839	215	215	100.00	215	96.40	215	95.50	215	89.00
Average					98.65		94.47		92.10		84.77

Supplementary table S2: Transcription data for the 48 identified plant cell wall degrading enzymes (PCWDEs) of *Zymoseptoria tritici* sorted by CAZy families and function. For each of the three life cycle stages (biotroph, necrotroph and saprotroph) transcription reads of biological triplicates are standardized to RPKM values and formatted using a 3-color scale (red: RPKM=0, yellow: RPKM=25 and green: RPMK=50). Average RPKM values at each life cycle stage are reported with the corresponding standard deviations.

Cazy	Function	Protein ID	Chr	7dpi_1_RPKM	7dpi_2_RPKM	7dpi_3_RPKM	13dpi_1_RPKM	13dpi_2_RPKM	13dpi_3_RPKM	56dpi_1_RPKM	56dpi_2_RPKM	56dpi_3_RPKM	7dpi - Means	7dpi - Stdev	13dpi - Means	13dpi - Stdev	56dpi - Means	56dpi - Stdev
CE5	Cutinase	43394	Chr6	18.477	6.934	10.792	24.141	52.289	25.525	44.358	54.398	62.864	12.068	5.876	33.985	15.867	53.873	9.264
CE5	Cutinase	77282	Chr12	3.548	2.219	4.145	82.614	90.814	70.640	134.630	187.636	163.626	3.304	0.986	81.356	10.146	161.964	26.542
CE5	Cutinase	68483	Chr2	13.246	10.357	5.803	238.530	507.182	228.740	61.311	57.528	59.730	9.802	3.753	324.817	158.008	59.523	1.900
CE5	Cutinase	99331	Chr2	0.000	8.841	10.319	130.811	199.266	97.629	26.959	25.885	24.141	6.387	5.580	142.569	51.828	25.662	1.422
CE5	Cutinase	18212	Chr9	93.774	263.950	117.011	16.422	16.852	38.101	6.070	11.895	11.357	158.245	92.278	23.792	12.394	9.774	3.219
CE5	Cutinase	35055	Chr1	0.000	0.000	0.000	1.323	3.287	1.000	53.838	38.577	36.158	0.000	0.000	1.537	1.654	42.858	9.586
GH5	Cellulase	106779	Chr1	297.634	203.268	435.491	23.656	21.171	21.595	11.122	11.230	13.798	312.131	116.789	22.141	1.329	12.050	1.515
GH5	Cellulase	88889	Chr1	16.439	32.134	9.602	8.950	8.980	12.524	10.661	10.466	8.985	19.392	11.553	10.151	2.055	10.037	0.916
GH5	Cellulase	83843	Chr1	7.777	15.983	12.329	2.791	2.774	4.514	2.034	2.868	1.670	12.030	4.111	3.360	1.000	2.191	0.614
GH5	Cellulase	71664	Chr4	15.066	15.707	17.600	29.444	27.520	29.248	4.768	5.489	4.689	16.124	1.317	28.737	1.059	4.982	0.441
GH5	Cellulase	92097	Chr3	558.239	125.764	51.119	85.982	111.241	153.775	6.978	9.076	9.696	245.041	273.794	116.999	34.261	8.584	1.425
GH5	Cellulase	111224	Chr11	32.822	38.674	46.367	32.732	38.756	29.153	22.130	22.366	19.243	39.287	6.793	33.547	4.853	21.246	1.739
GH7	Cellulase	100252	Chr5	20.427	0.000	3.254	15.864	19.321	15.090	17.190	18.243	28.545	7.893	10.975	16.758	2.253	24.659	6.470
GH12, I	Cellulase	105871	Chr10	0.000	4.710	39.587	151.796	141.036	139.731	125.636	230.472	272.857	14.766	21.624	144.188	6.621	209.655	75.786
GH45	Cellulase	76589	Chr10	4.929	6.167	4.319	63.994	82.574	53.077	49.393	56.573	104.403	5.138	0.942	66.548	14.914	70.123	29.903
GH61	Cellulase	33254	Chr1	0.000	0.000	0.000	0.449	0.000	0.000	0.546	0.561	0.367	0.000	0.000	0.150	0.259	0.491	0.108
GH61	Cellulase	103512	Chr2	0.000	1.135	0.000	13.379	11.709	7.375	139.783	204.525	362.125	0.378	0.656	10.821	3.099	235.478	114.357
GH10, I	Hemi-cellulases	94846	Chr7	58.020	85.648	77.265	12.051	13.039	7.544	6.846	10.201	13.794	73.644	14.165	10.878	2.930	10.280	3.475
GH10, I	Hemi-cellulases	61141	Chr7	4.120	9.019	4.812	521.702	588.081	488.768	147.097	178.629	225.870	5.984	2.651	532.851	50.586	183.865	39.647
GH11, I	Hemi-cellulases	60105	Chr6	3.444	8.617	10.058	55.960	116.101	43.380	57.808	56.225	90.825	7.373	3.478	71.814	38.866	68.286	19.536
GH43	Hemi-cellulases	73095	Chr6	0.000	4.451	12.469	48.870	45.902	36.622	56.461	61.725	56.880	5.640	6.319	43.798	6.389	58.355	2.925
GH43	Hemi-cellulases	96947	Chr12	2.536	3.966	3.703	9.134	10.027	6.698	5.934	9.731	10.050	3.402	0.761	8.620	1.723	8.572	2.290
GH43	Hemi-cellulases	30121	Chr4	26.091	29.014	15.239	52.932	63.342	90.699	3.834	5.663	4.952	23.448	7.258	68.991	19.507	4.816	0.922
GH43	Hemi-cellulases	105728	Chr9	55.118	34.477	48.290	23.921	25.546	33.593	59.383	105.749	110.746	45.962	10.516	27.687	5.179	91.959	28.322
GH43	Hemi-cellulases	98714	Chr1	46.964	9.792	64.005	15.734	17.917	12.721	18.314	16.019	21.569	40.254	27.723	15.457	2.609	18.634	2.789
GH43	Hemi-cellulases	105323	Chr8	2.244	1.404	9.175	66.537	71.449	72.034	88.805	117.739	154.396	4.274	4.265	70.007	3.019	120.313	32.871
GH43	Hemi-cellulases	96505	Chr11	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
GH43	Hemi-cellulases	84076	Chr1	9.462	5.918	1.842	3.962	4.266	3.204	7.540	5.501	7.434	5.741	3.813	3.811	0.547	6.825	1.148
GH43	Hemi-cellulases	75584	Chr9	9.462	5.918	1.842	3.962	4.266	3.204	7.540	5.501	7.434	5.741	3.813	3.811	0.547	6.825	1.148
GH51	Hemi-cellulases	71466	Chr4	9.521	16.165	10.328	6.380	5.661	6.632	5.811	6.833	5.297	12.005	3.626	6.224	0.504	5.980	0.782
GH51	Hemi-cellulases	111130	Chr10	0.000	0.779	5.094	1.461	2.074	4.556	1.394	3.303	4.171	1.958	2.744	2.697	1.639	2.956	1.421
GH51	Hemi-cellulases	40215	Chr4	8.559	6.424	12.997	25.806	20.303	21.561	19.328	19.585	16.139	9.327	3.353	22.557	2.883	18.351	1.920
GH54	Hemi-cellulases	70396	Chr3	328.567	313.021	66.430	81.287	57.327	80.100	1.286	2.645	1.209	236.006	147.063	72.904	13.504	1.713	0.808
GH62	Hemi-cellulases	68922	Chr2	7.772	3.241	1.513	409.247	469.034	404.226	112.274	123.634	178.244	4.176	3.233	427.502	36.055	138.051	35.269
GH93	Hemi-cellulases	95102	chr8	6.194	6.458	2.412	24.557	24.491	33.558	3.361	1.585	2.116	5.021	2.264	27.535	5.216	2.354	0.912
CE8	Pectinases	66866	Chr1	0.000	0.000	5.922	307.421	372.401	257.486	143.372	148.377	182.535	1.974	3.419	312.436	57.622	158.095	21.314
GH28, I	Pectinases	86032	Chr5	12.389	2.583	4.824	3.805	3.867	5.034	7.351	9.507	6.489	6.599	5.138	4.235	0.692	7.783	1.555
GH28, I	Pectinases	77196	Chr12	106.752	66.773	26.576	21.986	23.671	36.264	4.807	3.174	4.543	66.700	40.088	27.307	7.803	4.175	0.876
GH53	Pectinases	25958	Chr13	5.187	40.555	21.207	3.475	3.238	3.161	5.540	5.066	9.214	22.316	17.710	3.292	0.164	6.607	2.270
GH53	Pectinases	51381	Chr13	15.061	9.421	2.932	6.728	6.791	9.179	16.087	18.214	20.752	9.138	6.069	7.566	1.398	18.351	2.335
GH78	Pectinases	33711	chr1	6.474	1.350	3.781	12.290	14.594	10.960	13.939	13.324	10.246	3.868	2.563	12.615	1.839	12.503	1.979
GH78	Pectinases	69329	chr12	36.720	28.512	50.290	45.389	34.253	44.244	22.541	26.943	23.962	38.507	10.998	41.295	6.126	24.482	2.247
GH88	Pectinases	50077	chr11	0.000	1.417	0.000	2.657	3.772	3.683	2.074	2.529	2.786	0.472	0.818	3.370	0.620	2.463	0.361
GH88	Pectinases	57259	chr3	0.000	2.769	0.000	3.708	7.369	10.792	7.205	6.022	6.502	0.923	1.599	7.290	3.543	6.577	0.595
GH115	Pectinases	65051	chr1	5.045	2.630	2.947	2.958	9.098	2.050	8.810	14.020	13.500	3.540	1.313	4.702	3.834	12.110	2.870
PL1, I	Pectinases	42327	Chr5	0.000	1.570	2.932	4.625	2.612	3.060	44.943	73.730	69.972	1.501	1.467	3.432	1.057	62.882	15.649
PL1, I	Pectinases	85457	Chr3	0.000	0.000	0.000	0.888	1.103	3.229	0.539	0.924	0.724	0.000	0.000	1.740	1.294	0.729	0.193
PL3	Pectinases	27839	Chr1	0.000	2.137	1.996	58.950	95.983	51.365	198.114	221.448	290.155	1.378	1.195	68.766	23.874	236.572	47.848
				BIOTROPH			NECROTROPH			SAPROTROPH			BIOTROPH		NECROTROPH		SAPROTROPH	

Cutinases	Cellulases	Hemi-cellulases	Pectinases

Cutinases

comparison	The Mantel-Haenszel Test of homogeneity:	
	x2	p
Z. tritici- Z. pseudotritici	5.96	0.202
Z. tritici- Z. ardabiliae	8.731	0.068
Z. pseudotritici- Z. ardabiliae	2.667	0.614

C01 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	0.664
Non-Synonymous				-LOG10(NI)	0.043
TOTAL				alpha	0.136
				p=	0.678

Cellulases

comparison	The Mantel-Haenszel Test of homogeneity:		
	x2	p	
Z. tritici- Z. pseudotritici	3.567	0.616	
Z. tritici- Z. ardabiliae	15.056	0.01	**	ns
Z. pseudotritici- Z. ardabiliae	12.197	0.032	*	ns

GH5 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	1.1
Non-Synonymous				-LOG10(NI)	-0.041
TOTAL				alpha	-0.093
				p=	0.699

comparison	The Mantel-Haenszel Test of homogeneity:	
	x2	p
Z. tritici- Z. pseudotritici	0.000	0.987
Z. tritici- Z. ardabiliae	0.101	0.751
Z. pseudotritici- Z. ardabiliae	0.010	0.918

GH11 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	1.239
Non-Synonymous				-LOG10(NI)	-0.093
TOTAL				alpha	-0.239
				p=	0.436

Hemi-cellulases

comparison	The Mantel-Haenszel Test of homogeneity:		
	x2	p	
Z. tritici- Z. pseudotritici	2.354	0.124	
Z. tritici- Z. ardabiliae	0.410	0.51	
Z. pseudotritici- Z. ardabiliae	0.76	0.383	

GH10 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	0.873
Non-Synonymous				-LOG10(NI)	0.059
TOTAL				alpha	0.137
				p=	0.762

comparison	The Mantel-Haenszel Test of homogeneity:		
	x2	p	
Z. tritici- Z. pseudotritici	20.668	0.008 **	ns
Z. tritici- Z. ardabiliae	32.681	0 ***	ns
Z. pseudotritici- Z. ardabiliae	19.207	0.019 *	ns

GH3 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	na
Non-Synonymous				-LOG10(NI)	na
TOTAL				alpha	na
				p=	na

comparison	The Mantel-Haenszel Test of homogeneity:		
	x2	p	
Z. tritici- Z. pseudotritici	7.638	0.021 *	ns
Z. tritici- Z. ardabiliae	5.987	0.05	
Z. pseudotritici- Z. ardabiliae	0.833	0.659	

GH1 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	1.597
Non-Synonymous				-LOG10(NI)	-0.192
TOTAL				alpha	-0.557
				p=	0.002

Pectinases

comparison	The Mantel-Haenszel Test of homogeneity:	
	x2	p
Z. tritici- Z. pseudotritici	3.603	0.057
Z. tritici- Z. ardabiliae	1.675	0.195
Z. pseudotritici- Z. ardabiliae	3.255	0.115

GH28 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	1.970
Non-Synonymous				-LOG10(NI)	-0.296
TOTAL				alpha	-0.979
				p=	0.333

comparison	The Mantel-Haenszel Test of homogeneity:		
	x2	p	
Z. tritici- Z. pseudotritici	6.257	0.039 *	locus missing in Z. ardabiliae
Z. tritici- Z. ardabiliae			locus missing in Z. ardabiliae
Z. pseudotritici- Z. ardabiliae			locus missing in Z. ardabiliae

GH53 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	na
Non-Synonymous				-LOG10(NI)	na
TOTAL				alpha	na
				p=	na

comparison	The Mantel-Haenszel Test of homogeneity:		
	x2	p	
Z. tritici- Z. pseudotritici	0.161	0.687	
Z. tritici- Z. ardabiliae			locus missing in Z. ardabiliae
Z. pseudotritici- Z. ardabiliae			locus missing in Z. ardabiliae

GH78 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	1.513
Non-Synonymous				-LOG10(NI)	-0.180
TOTAL				alpha	-0.338
				p=	0.281

comparison	The Mantel-Haenszel Test of homogeneity:	
	x2	p
Z. tritici- Z. pseudotritici	0.063	0.801
Z. tritici- Z. ardabiliae	0.331	0.86
Z. pseudotritici- Z. ardabiliae	0.062	0.802

GH88 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	2.065
Non-Synonymous				-LOG10(NI)	-0.314
TOTAL				alpha	-1.063
				p=	0.001

comparison	The Mantel-Haenszel Test of homogeneity:	
	x2	p
Z. tritici- Z. pseudotritici	0.184	0.667
Z. tritici- Z. ardabiliae	0.444	0.505
Z. pseudotritici- Z. ardabiliae	2.799	0.094

PL1 combined

	Polymorphism	Divergence	TOTAL		
Synonymous				Mantel-Haenszel	1.336
Non-Synonymous				-LOG10(NI)	-0.116
TOTAL				alpha	-0.306
				p=	0.104

Supplementary table S4: Likelihood ratio test for selection heterogeneity across the phylogeny of *Zymoseptoria tritici* against its ancestors. Four heterogeneity models (M2 - M5) are compared agains the null model (M1) of no heterogeneity in dN/dS ratios. Ratios of dN/dS ≤ 0.01 were regarded as significant and highlighted in red (diversifying selection) or blue (purifying selection), respectively, Models are explained in the text and Figure 4a.

	JGI IPO323_ProtID	CAZy family	M1 Global	M2 Branch	M2 Z.t.+Ancestors	M3 Z. tritici	M3 Ancestor+ Branch	M4 Z.t.+Branch	M4 Ancestor	M5 Z. tritici	M5 Ancestors	M5 Branch	AIC best model	p
Cutinases	77282	CE5	0.080	0.089	0.079	0.091	0.047	0.089	0.025	0.090	0.025	0.090	4	0.046
	68483	CE5	0.138	0.388	0.126	0.123	0.332	0.135	0.252	0.123	0.252	0.390	3	>0.05
	35055	CE5	0.156	0.000	0.156	0.156	0.001	0.156	0.000	0.156	0.000	0.000	1	ns
	99331	CE5	0.150	0.070	0.165	0.175	0.099	0.157	0.118	0.178	0.118	0.068	1	ns
	43394	CE5	0.067	0.044	0.069	0.069	0.059	0.066	0.086	0.069	0.086	0.044	1	ns
	18212	CE5	0.080	0.000	0.097	0.093	0.020	0.079	0.353	0.095	0.358	0.000	2	0.005
Cellulases	71664	GH5	0.060	0.037	0.062	0.061	0.051	0.059	0.078	0.061	0.078	0.037	1	ns
	88889	GH5	0.057	0.048	0.057	0.056	0.060	0.056	0.061	0.056	0.061	0.048	1	ns
	106779	GH5	0.111	0.008	0.128	0.176	0.017	0.144	0.021	0.177	0.022	0.008	3	<0.001
	83843	GH5	0.079	0.041	0.081	0.103	0.038	0.098	0.038	0.103	0.037	0.041	3	<0.001
	92097	GH5	0.132	0.172	0.125	0.135	0.127	0.141	0.108	0.134	0.108	0.170	1	ns
	111224	GH5	0.043	0.043	0.043	0.039	0.060	0.040	0.370	0.039	0.366	0.044	4	0.014
	100252	GH7	0.058	0.025	0.061	0.061	0.016	0.065	0.000	0.065	0.000	0.025	3	>0.05
	105871	GH12	0.136	0.460	0.119	0.113	0.220	0.133	0.154	0.112	0.150	0.458	2	0.007
	76589	GH45	0.116	0.371	0.101	0.150	0.070	0.159	0.033	0.141	0.033	0.333	5	<0.001
	33254	GH61	0.321	0.324	0.321	0.316	0.334	0.318	0.345	0.316	0.345	0.326	1	ns
	103512	GH61	0.104	0.093	0.104	0.096	0.121	0.096	0.130	0.096	0.130	0.093	1	ns
Hemi-cellulases	94846	GH10	0.096	0.040	0.104	0.101	0.062	0.093	6.133	0.101	5.743	0.041	5	0.011
	61141	GH10	0.109	0.147	0.089	0.182	0.105	0.154	0.080	0.182	0.081	0.148	4	>0.05
	60105	GH11	0.116	0.191	0.094	0.113	0.122	0.130	0.000	0.110	0.000	0.187	4	0.036
	98714	GH43	0.079	0.098	0.078	0.046	0.240	0.051	0.313	0.047	0.313	0.101	4	<0.001
	105323	GH43	0.113	0.130	0.111	0.091	0.125	0.100	0.124	0.091	0.124	0.131	1	ns
	96505	GH43	0.165	0.112	0.165	0.171	0.158	0.171	0.158	0.171	0.159	0.101	1	ns
	84076	GH43	0.114	0.038	0.117	0.105	0.139	0.103	0.149	0.106	0.151	0.037	4	>0.05
	75584	GH43	0.083	0.110	0.080	0.080	0.110	0.082	0.000	0.080	0.000	0.110	1	ns
	96947	GH43	0.141	0.044	0.147	0.106	0.168	0.101	0.178	0.108	0.179	0.044	4	0.028
	73095	GH43	0.049	0.000	0.053	0.031	0.279	0.032	0.409	0.034	0.405	0.000	4	<0.001
	30121	GH43	0.085	0.135	0.079	0.107	0.058	0.109	0.038	0.105	0.037	0.128	4	0.027
	105728	GH43	0.052	0.090	0.045	0.015	0.068	0.041	0.063	0.015	0.062	0.089	3	0.003
	71466	GH51	0.062	0.035	0.066	0.077	0.032	0.070	0.030	0.076	0.030	0.035	3	>0.05
	111130	GH51	0.084	0.087	0.087	0.106	0.072	0.094	0.075	0.106	0.075	0.063	3	>0.05
	40215	GH51	0.174	0.069	0.190	0.107	0.272	0.103	0.343	0.110	0.110	0.073	4	<0.001
	70396	GH54	0.122	0.076	0.125	0.087	0.268	0.087	0.330	0.088	0.330	0.077	4	<0.001
	68922	GH62	0.096	0.408	0.090	0.098	0.079	0.101	0.040	0.096	0.040	0.387	5	>0.05
	95102	GH93	0.356	0.639	0.318	0.311	0.522	0.351	0.399	0.308	0.399	0.646	2	>0.05
Pectinases	66866	CE8	0.183	0.144	0.186	0.183	0.182	0.181	0.209	0.183	0.209	0.145	1	ns
	86032	GH28	0.075	0.063	0.076	0.074	0.079	0.074	0.083	0.075	0.083	0.063	1	ns
	77196	GH28	0.142	0.242	0.138	0.135	0.321	0.141	0.741	0.136	0.747	0.247	3	>0.05
	25958	GH53	0.116	0.008	0.157	0.170	0.066	0.112	0.126	0.177	0.125	0.008	2	<0.001
	51381	GH53	0.088	0.076	0.091	0.095	0.070	0.091	0.062	0.095	0.062	0.075	1	ns
	33711	GH78	0.206	0.109	0.220	0.197	0.223	0.186	0.276	0.276	0.200	0.111	2	>0.05
	69329	GH78	0.117	0.108	0.142	0.142	0.110	0.115	0.144	0.142	0.144	0.107	1	ns
	50077	GH88	0.227	0.402	0.213	0.180	0.319	0.203	0.298	0.180	0.296	0.405	3	>0.05
	57259	GH88	0.232	0.000	0.242	0.199	0.269	0.194	0.280	0.207	0.282	0.000	2	>0.05
	65051	GH115	0.090	0.072	0.094	0.066	0.132	0.069	0.194	0.067	0.194	0.075	4	<0.001
	42327	PL1	0.155	0.340	0.146	0.139	0.187	0.150	0.167	0.138	0.165	0.334	2	>0.05
	85457	PL1	0.238	0.251	0.237	0.172	0.280	0.177	0.281	0.172	0.279	0.292	3	>0.05
	27839	PL3	0.086	0.105	0.085	0.086	0.085	0.087	0.000	0.086	0.000	0.105	1	ns

Blue	significantly lower dN/dS ratio
Red	significantly higher dN/dS ratio
Yellow	no heterogenity between *Z. tritici* and its ancestors

ns; not significant, the null model M1 can not be rejected

Supplementary Fig. S1