

Table S1 Characteristic of 5 pairs of highly similar gene clusters in *Pst* genome

Species	Gene ID	Transcript ID	Similarity (nucleotide)	Similarity (AA)	Signal peptides (aa)	Structure	Sublocation
	PSTG_13661	KNE92947			1-24		apoplactic
	PSTG_13662	KNE92948	80.03%	82.12%	1-24		non-apoplactic, mitochondrial
	PSTG_13644	KNE92928			1-35		apoplactic
<i>Puccinia</i>	PSTG_13645	KNE92929	58.14%	50.57%	1-32		apoplactic
<i>striiformis</i> f. sp.	PSTG_06370	KNF00442			NO	transmembrane region	
<i>tritici PST-78</i>	PSTG_06371	KNF00443	57.86%	47.34%	1-27		Non-apoplactic
(ASM14938v1)	PSTG_06025	KNF00609			1-21		Non-apoplactic
	PSTG_06026	KNF00610	66.91%	63.06%	1-21		Non-apoplactic
	PSTG_03021	KNF03934			NO	transmembrane region	
	PSTG_03021	KNF03935	72.76%	72.77%	NO	transmembrane region	