Table S1. Permanova tests for the effects of soil history, soil water content and genotype, and their interactions on rhizosphere-associated microbial communities.

Bacterial communities				
	Relative		Quantitative	
Factor	F	Р	F	Р
SWC	0.15	0.001	0.21	0.018
Genotype	0.13	0.001	2.13	0.001
Soil history	3.52	0.001	3.69	0.001
Block	0.04	0.490	0.20	0.011
SWC × Soil history	0.07	0.012	0.16	0.082
SWC × Genotype	0.04	0.307	0.12	0.147
Genotype × Soil history	0.08	0.014	0.73	0.001
SWC × Genotype × Soil history	0.05	0.229	0.13	0.133
Fungal communities				
_	Relative		Quantitative	
	F	Р	F	Р
swc	0.25	0.001	0.39	0.009
Genotype	0.26	0.001	1.69	0.001
Soil history	9.84	0.001	4.66	0.001
Block	0.08	0.190	0.15	0.721
SWC × Soil history	0.13	0.006	0.26	0.103
SWC × Genotype	0.09	0.042	0.45	0.001
Genotype × Soil history	0.16	0.007	1.44	0.001
SWC × Genotype × Soil history				

^a Soil water content (SWC) refers to: high water content (50% soil water holding capacity, SWHC); moderate water content (30% and 20% SWHC) and low water content (5-8% SWHC).

^b Genotype refers to AC Nass (*Triticum aestivum*), AC Walton (*Triticum aestivum*), AC Barrie (*Triticum aestivum*), Strongfield (*Triticum turgidum* subsp. *durum*)

^c Soil history refers to soils with either an history of water stress (NI: non-irrigated soils from Saskatchewan) or with no recent history of water stress (IR: irrigated soils from Saskatchewan).

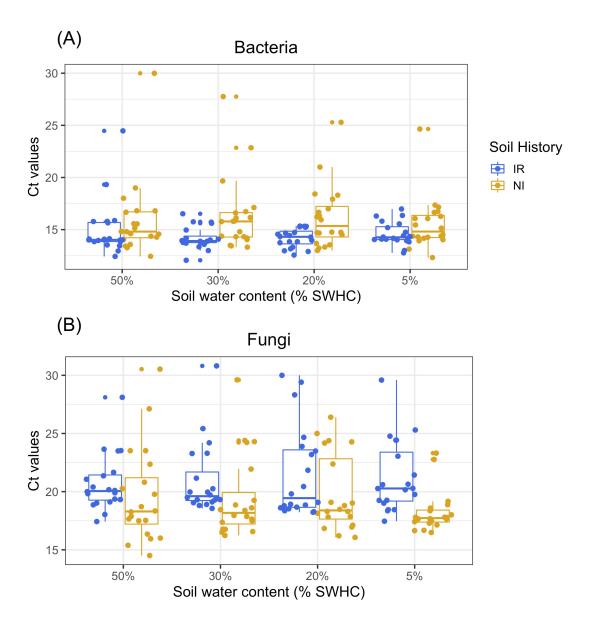


Fig S1. The Ct (cycle threshold) of qPCR data for (A) bacterial and (B) fungi in the rhizosphere of four wheat genotypes grown in soil with two contrasting stress histories (Soil history) under different contemporary water stress (SWHC).

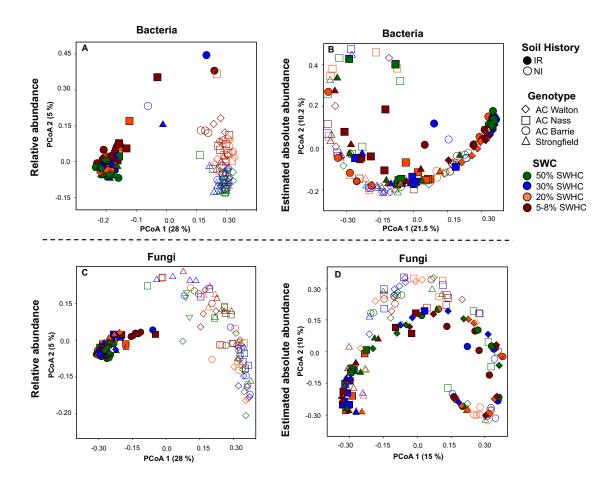


Fig. S2. Principal coordinate analyses (PCoA) of Bray–Curtis dissimilarity for relative abundance (A, C) and estimated absolute abundance (B, D) visualizing the impact of each of the experimental factors (Soil history, SWC, and wheat genotype) on bacterial and fungal communities associated with the rhizosphere.