Table S1. Soil characteristics of the experimental field, average values of minimal (T_{min}) and maximal (T_{max}) temperature, and rainfall during the sampling period of Odisseo and Saragolla durum wheat.

Soil characteristics	
Soil texture	Slimy-loam (36% sand, 40% silt and 24% clay)
Preceding crop	Barley
Soil nutrient supply before seeding	Total nitrogen 0.9%, nitrates 4.37 ppm
Weeding	On March 13th, 2014, with tribenuron and tifensulfuron
Fungicidal treatment	On May, 5th, 2014, with trifloxystrobin

Climatic trend during crop

Enviromental conditions	April			May			June			July
	1st decade	2nd decade	3rd decade	1st decade	2nd decade	3rd decade	1st decade	2nd decade	3rd decade	1st decade
	(Tillering)	(Stem elongation)	(Booting)		(Saragolla flowering)	(Odisseo flowering)	(Saragolla milk development)	(Odisseo milk development)	(Saragolla physiological maturity)	(Odisseo physiological maturity)
T_{min} (°C)	7.4	5.8	8.9	10.5	9.7	11.3	12.6	16.5	16.2	16.9
T_{max} (°C)	17.5	15.5	18.4	22.5	21.3	22.9	25.5	28.5	28.8	29.6
Rainfall (mm)	25.2	51.9	26.2	42.7	13.0	26.6	28.5	114.8	0.4	57.8

Table S2. Biodiversity measures of endophytic (END) and epiphytic (EPI) *Firmicutes* (16S rRNA) found in hypogeous (roots, H) and epigeous organs (leaves and spikes, E) and processed grain of Odisseo (O) and Saragolla (S) durum wheat. Samples are encoded by using the phenological stage (tillering, T; stem elongation, SE; booting, B; flowering, F; milk development, MD; and physiological maturity, PM).

	Odisseo	T	SE	B	F	MD	PM	Grain	Flour	Chaff	Bran
OTU	END.H	218	198	216	171	212	126	-	-	-	-
	EPI.H	202	83	218	155	153	150	-	-	-	-
	END.E	28	23	26	81	47	56	20	130	-	-
	EPI.E	36	76	34	64	36	55	81	-	98	97
Shannon	END.H	3.17	3.04	2.88	2.18	2.90	0.76	-	-	-	-
	EPI.H	3.17	2.98	3.35	2.13	2.82	2.01	-	-	-	-
	END.E	1.21	2.63	1.35	1.41	0.76	0.98	1.30	2.75	-	-
	EPI.E	2.14	3.09	0.38	1.87	0.78	0.67	1.80	-	1.16	1.14
Simpson	END.H	0.91	0.89	0.85	0.64	0.87	0.27	-	-	-	-
	EPI.H	0.93	0.90	0.92	0.73	0.86	0.62	-	-	-	-
	END.E	0.50	0.90	0.53	0.51	0.45	0.55	0.62	0.89	-	-
	EPI.E	0.76	0.93	0.13	0.76	0.51	0.29	0.72	-	0.55	0.52
ACE	END.H	236	226	239	188	237	146	-	-	-	-
	EPI.H	246	114	243	171	166	182	-	-	-	-
	END.E	41	30	38	103	54	85	34	146	-	-
	EPI.E	44	97	38	79	39	61	96	-	120	118
Chao	END.H	238	235	241	192	238	151	-	-	-	-
	EPI.H	251	99	235	174	164	183	-	-	-	-
	END.E	46	30	71	112	52	108	32	141	-	-
	EPI.E	51	97	49	82	38	59	98	-	119	116

Table S2. (continued)

	Saragolla	T	SE	B	F	MD	PM	Grain	Flour	Chaff	Bran
OTU	END.H	150	202	172	232	187	207	-	-	-	-
	EPI.H	159	189	218	252	189	125	-	-	-	-
	END.E	40	29	45	42	77	68	52	92	-	-
	EPI.E	133	69	60	45	51	62	57	-	127	126
Shannon	END.H	3.53	2.26	3.32	3.69	2.18	2.89	-	-	-	-
	EPI.H	2.30	3.05	3.27	3.58	3.51	3.16	-	-	-	-
	END.E	2.52	2.27	0.31	0.33	1.45	0.94	1.30	2.75	-	-
	EPI.E	2.23	2.62	1.66	1.81	1.09	0.73	1.80	-	1.16	1.11
Simpson	END.H	0.94	0.74	0.92	0.96	0.65	0.89	-	-	-	-
	EPI.H	0.81	0.91	0.91	0.94	0.94	0.93	-	-	-	-
	END.E	0.86	0.84	0.10	0.11	0.63	0.48	0.65	0.89	-	-
	EPI.E	0.80	0.87	0.69	0.75	0.44	0.43	0.72	-	0.55	0.50
ACE	END.H	179	231	211	262	208	242	-	-	-	-
	EPI.H	174	209	244	273	228	273	-	-	-	-
	END.E	57	53	47	47	92	84	70	106	-	-
	EPI.E	154	79	78	55	39	79	64	-	154	152
Chao	END.H	199	251	228	290	213	248	-	-	-	-
	EPI.H	175	214	249	270	224	270	-	-	-	-
	END.E	56	62	46	46	86	82	64	109	-	-
	EPI.E	167	77	75	52	38	74	64	-	152	149

Table S2. (continued)

	Commercial durum wheat grain	T	SE	B	F	MD	PM	Grain	Flour	Bran
OTU	END.H	-	-	-	-	-	-	-	-	-
	EPI.H	-	-	-	-	-	-	-	-	-
	END.E	-	-	-	-	-	-	45	60	-
	EPI.E	-	-	-	-	-	-	52	-	54
Shannon	END.H	-	-	-	-	-	-	-	-	-
	EPI.H	-	-	-	-	-	-	-	-	-
	END.E	-	-	-	-	-	-	0.54	0.23	-
	EPI.E	-	-	-	-	-	-	0.56	-	0.38
Simpson	END.H	-	-	-	-	-	-	-	-	-
	EPI.H	-	-	-	-	-	-	-	-	-
	END.E	-	-	-	-	-	-	0.23	0.07	-
	EPI.E	-	-	-	-	-	-	0.24	-	0.14
ACE	END.H	-	-	-	-	-	-	-	-	-
	EPI.H	-	-	-	-	-	-	-	-	-
	END.E	-	-	-	-	-	-	50	72	-
	EPI.E	-	-	-	-	-	-	69	-	60
Chao	END.H	-	-	-	-	-	-	-	-	-
	EPI.H	-	-	-	-	-	-	-	-	-
	END.E	-	-	-	-	-	-	51	75	-
	EPI.E	-	-	-	-	-	-	120	-	66

OTU, number of Operational Taxonomic Units found in a given sample; Shannon, Shannon diversity index (H') is calculated using: $H' = -\Sigma_{i=1}^{R} p_i \ln(p_i)$, where R is richness and p_i is the relative abundance of the ith OTU; Simposn, Simpson diversity index (D) is calculated using: $D = \Sigma n(n-1)/N(N-1)$, where n is the total number of a given OTU and N is the total number of OTU; ACE, ACE richness estimator; Chao, Chao richness estimator (S_{chao1}) is calculated using: $S_{chao1} = S_{obs} + F_1^2/2F_2$, where S_{obs} is the number of OTU in the sample, F_1 is the number of singletons (i.e., the number of OTU with only a single occurrence in the sample) and F_2 is the number of doubletons (the number of OTU with exactly two occurrences in the sample).

Table S3. Relative abundance (%) of endophytic (END) and epiphytic (EPI) lactic acid bacterium genera/species found in hypogeous (roots, H) and epigeous organs (leaves and spikes, E) and grain of Odisseo (O) and Saragolla (S) durum wheat. Species are encoded by: A.v., *Aerococcus viridans*; C. m., *Carnobacterium maltaromaticum*; G. sp., *Granulicatella* sp.; E. f., *Enterococcus faecalis*; E. sp., *Enterococcus* sp.; L. b., *Lactobacillus brevis*; L. f., *Lactobacillus fermentum*; L. g., *Lactobacillus gasseri*; L. i., *Lactobacillus iners*; L. p., *Lactobacillus plantarum*; L. sp., *Lactobacillus*; W. sp., *Weissella* sp.; Lc. g., *Lactococcus garviae*; Lc. l., *Lactococcus lactis*; Lc. sp., *Lactococcus* sp.; S. sp., *Streptococcus* sp.
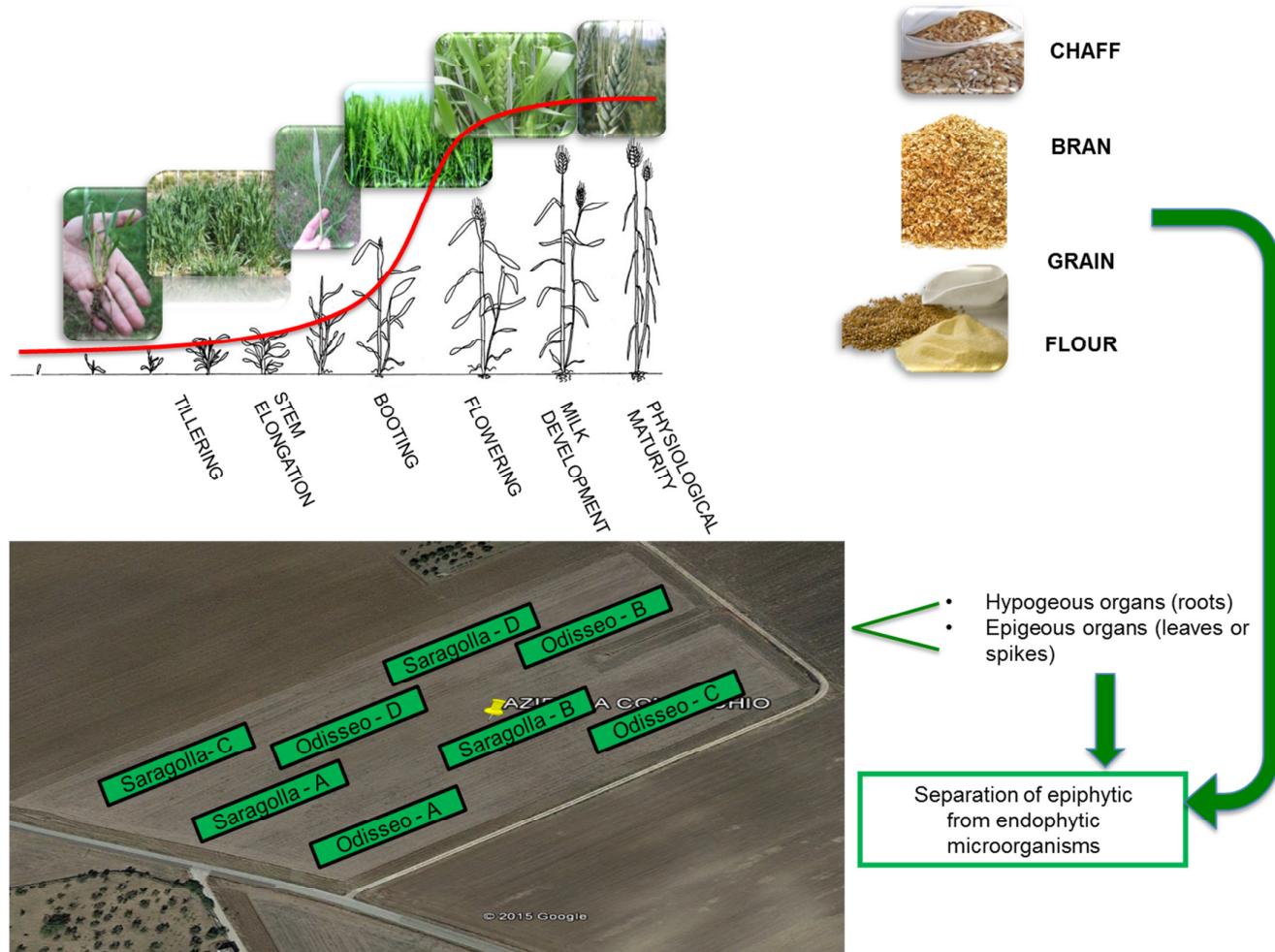
	A. v.	C. m.	C. sp.	G. sp.	E. f.	E. sp.	L. b.	L. f.	L. g.	L. i.	L. p.	L. sp.	W. sp.	Lc. g.	Lc. l.	Lc. sp.	S. sp.
Tillering END, H, O[a]	0.006	0.004	0	0	0.047	0.004	0.025	0.047	0	0	3.004	0.504	0.175	0	0	0.052	0.919
Tillering EPI, H,O	0	0.010	0	0	0	0	0.002	0	0	0	8.456	0.972	0.755	0	0	0.030	1.803
Tillering END, E, O	0	0	0	0	0	0.054	0	0	0	0	6.728	0.917	0.358	0	0	0.015	0.224
Tillering EPI, E, O	1.102	0	0	0	0.412	0	0	0	0	0	7.407	1.631	2.160	0	0	0	7.745
Tillering END, H, S	0	0.002	0	0	0	0.002	0.024	0	0	0.019	0.163	0.167	0.004	0	0	0.049	0.056
Tillering EPI, H, S	0	0	0	0	0	0	0.005	0	0	0.025	0.030	0.117	0.015	0	0	0.020	0.081
Tillering END, E, S	0	0	0	0	0	0	0.016	0	0	0	0.149	0.659	0.052	0	0	0.086	0.287
Tillering EPI, E, S	0	0.026	0	0	0.090	0.039	0	0	0	0	0.134	0.160	0.072	0	0	0.026	0.327
Stem elongation END, H, O	0	0	0	0.008	0.004	0	0.021	0.008	0	0	0.421	0.433	0.088	0	0	0.017	4.508
Stem elongation EPI, H, O	0	0	0	0	0	0	0	0	0	0	0	0.120	0	0	0	0.598	0.359
Stem elongation END, E, O	0	0	0	0	0	0.002	0	0	0	0	0.017	0.006	0.001	0	0	0.001	0.018
Stem elongation EPI, E, O	0.073	0.224	0	0.713	0	0.594	0	0	0	0.310	0.839	2.694	5.117	0	0	1.585	6.662
Stem elongation END, H, S	0	0.003	0	0	0	0	0	0	0	0	0.063	0.073	0.013	0	0	0.026	0.065
Stem elongation EPI, H, S	0	0	0	0	0	0	0	0.087	0	0	0	0.010	0	0	0	0.322	0.215
Stem elongation END, E, S	0	0	0	0	0	0.002	0	0	0	0.270	0.111	0.134	0.020	0	0	0.034	0.116
Stem elongation EPI, E, S	0	0	0	0	0	0	0	0	0	0	0.124	0.825	0.154	0	0	0.056	0.286

Booting END, H, O	0	0.932	0	0.181	0	0	0	7.794	0.028	0	0.018	0.192	0	0	0	0.007	1.156
Booting EPI, H, O	0	0	0.007	0.436	0	0.036	0	0	0	0	0.029	0.524	0.044	0	0.015	8.370	5.258
Booting END, E, O	0	0	0	0.003	0	0.012	0	0.009	0	0	0.015	0.158	0	0	0	0	0.533
Booting EPI, E, O	0	0	0	0	0	0	0	0	0	0	0.026	0.154	0.030	0	0	0.020	0.228
Booting END, H, S	0	0.005	0	0.262	0	0.570	0	0	0	0	0.103	0.005	0	0	0	0.087	3.180
Booting EPI, H, S	0	0	0	0.132	0	0	0	0	0	0	0.003	0.076	0	0	0	0.022	1.828
Booting END, E, S	0	0	0	0.089	0.006	0	0	0	0	0.027	0.037	0.019	0	0	0	0.037	0.704
Booting EPI, E, S	0	0.004	0	1.778	0	0.129	0.469	0	0	0	1.007	5.266	0	0	0	0.260	54.123
Flowering END, H, O	0	0.007	0	0.233	0	0.048	0	0	0	0	0.828	60.501	0	0	0	0.129	3.554
Flowering EPI, H, O	0	0.040	0	0.015	0	0	1.160	0	0	0	29.969	24.489	0	0	0	0.055	1.995
Flowering END, E, O	0	0.002	0	0.109	0.079	0.034	0	0.005	0	0	1.720	55.413	0	0	0	0.175	10.294
Flowering EPI, E, O	0	0	0	0.129	0	0.058	0.143	0.138	0	0	0.517	1.805	0	0	0	0.058	19.555
Flowering END, H, S	0	1.982	0.014	0.050	0.036	0	0	0	0	0	0.163	0.262	0	0	0	0.045	0.643
Flowering EPI, H, S	0	0	0	0.050	0	0.032	0	0	0	0	0.195	0.355	0	0	0	0.805	5.175
Flowering END, E, S	0	0.062	0	0	0	0.045	0	0.005	0	0	0.045	0.086	0	0	0	0.021	0.133
Flowering EPI, E, S	0	0	0	0	0	0.002	0	0	0	0	0.422	0.005	0	0	0	0.322	5.468
Milk development END, H, O	0	0.004	0	0	0	0.089	0	0	0	0	0.122	0.030	0	0	0	0.070	0.093
Milk development EPI, H, O	0.261	0.040	0	0	0	0.008	0	0	0	0.080	0.285	0	0	0	0	0	0.542
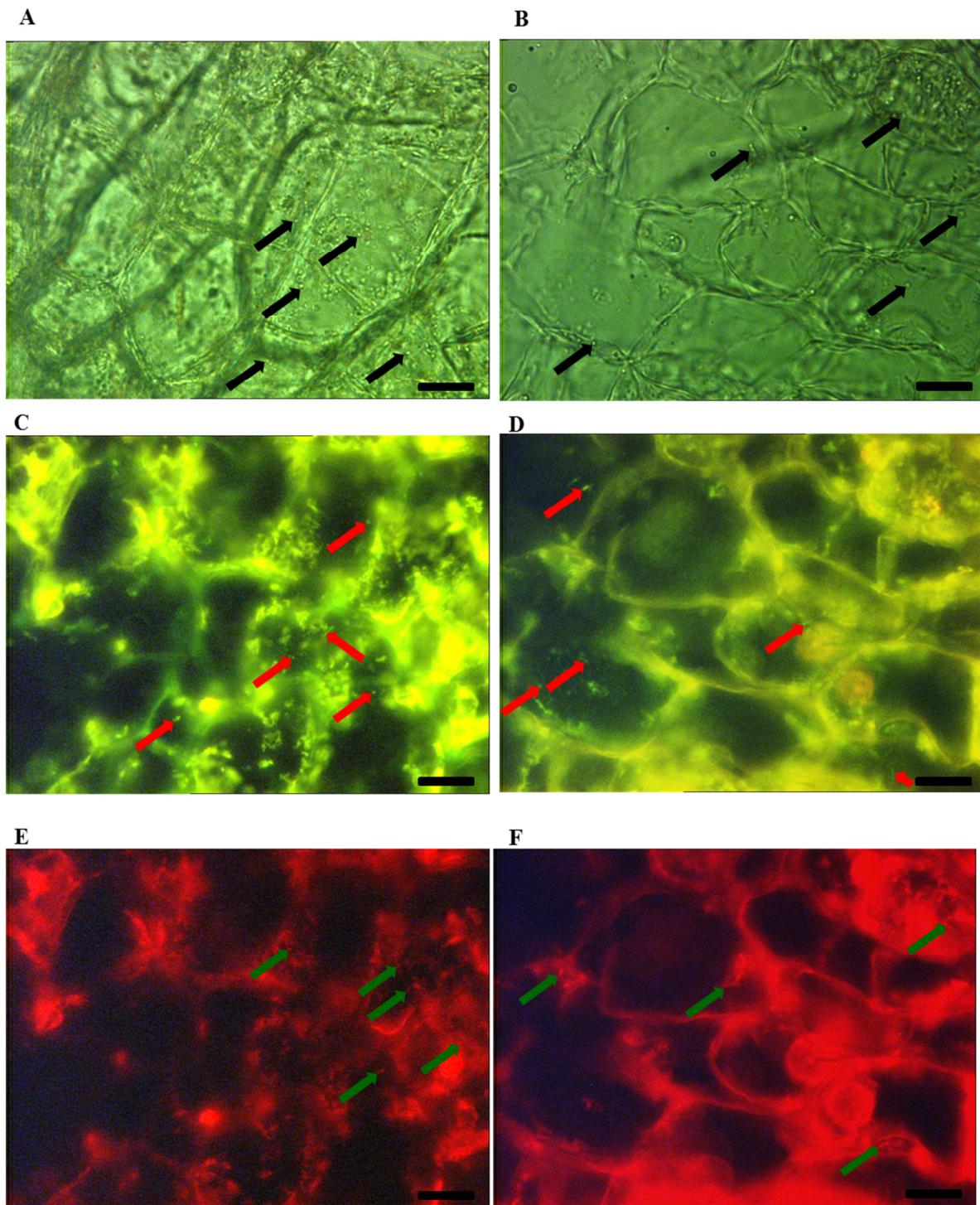
Milk development END, E, O	0	0	0	0	0	1.181	0.017	0	0	0	0.016	0.031	0	0	0	0.015	0.137
Milk development EPI, E, O	0	0	0	0	0	0.130	0	0	0	0	0.009	0.026	0	0	0	0.001	0.037
Milk development END, H, S	0	0	0	0	0	0.036	0	0	0	0	0.077	0.004	0	0	0	0.105	0.093
Milk development EPI, H, S	0	0.084	0	0.451	0	0	0	0	0	0	0.149	0.258	0.060	0	0	0	1.994
Milk development END, E, S	0	0.375	0	0.302	0	0.041	1.832	0	0	0	25.558	0.214	0	0	0.006	1.369	2.306
Milk development EPI, E, S	0	0	0	0.975	0	0	0	0	0	0	0.441	0.159	0	0	0	0	7.269
Physiological maturityEND, H,O	0.008	0.009	0	0.011	0	0.754	0	0.006	0	0	0.028	0.017	0	0	0.041	84.997	0.648
Physiological maturity EPI, H, O	0.160	0	0	0	0	0	0	0	0	0	0.456	0.453	0	0	0.030	60.706	2.413
Physiological maturity END,E,O	0.004	0	0	0	0	0.002	0.002	0	0	0	0.011	0.007	0	0	0.002	46.995	0.105
Physiological maturity EPI, E, O	0	0.003	0	0.009	0	3.768	0	0	0	0	0.012	0.012	0	0	0	1.714	0.168
Physiological maturity END,H,S	0	0.007	0	0.025	0.014	0.098	0.018	0	0	0	0.007	0.049	0	0	0	0.049	0.119
Physiological maturity EPI, H, S	0	0	0	0	0	0	0	0	0	0	0.460	10.587	0	0	0	0.097	0.453
Physiological maturity END,E, S	0	1.305	0.021	0	0	0.003	0.009	0	0	0	0.026	0.009	0	0	0	0.017	0.037
Physiological maturity EPI, E, S	0	0.004	0	0.002	0	0.015	0.002	0	0	0.008	0.006	0.043	0	0	0	0.008	0.053
Grain END, O	0	0	0	0	0	0.008	0	0	0	0	0	0.199	0	0	0	0.008	0
Grain EPI, O	0	0	0.007	0	0	1.275	0	0	0.022	0	0.048	0.067	0.007	0	0	0.163	0.641
Flour O	0.004	0.328	0	1.204	0.001	0.514	0.084	0	0	0.017	0.187	8.346	0	0.070	0.090	19.141	20.352
Bran O	0.003	0.321	0	1.202	0.003	0.520	0.081	0	0	0.015	0.180	8.220	0	0.065	0.086	19.132	20.111
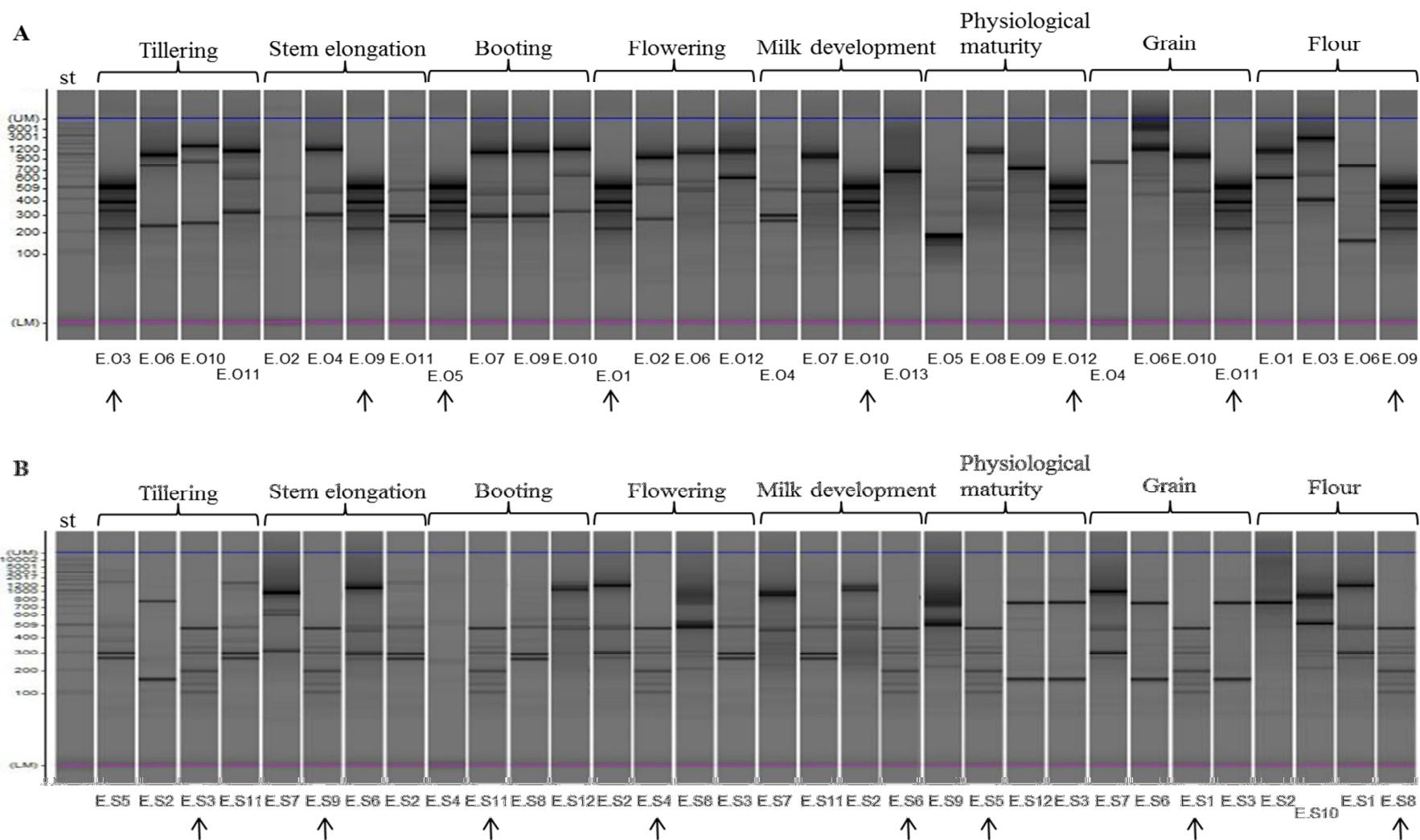
Chaff O	0	0.169	0.005	0.007	0	2.419	0.005	0	0	0	0.055	0.023	0	0	0	0.030	0.039
Grain END, S	0	0.004	0	0.012	0	22.296	0	0	0	0	0.023	0.012	0	0	0	0	0.070
Grain EPI, S	0	0	0	0.014	0	12.523	0	0	0	0	0.007	0.082	0	0	0	0.011	0.039
Flour S	0	0.291	0.002	0.161	0	8.207	0	0.019	0	0	0.469	0.230	0.008	0	0	0.372	1.302
Bran S	0	0.258	0.001	0.153	0	8.307	0	0.013	0	0	0502	0.224	0.006	0	0	0.371	1.283
Chaff S	0	6.170	0.039	0.021	0.239	3.188	0.025	0	0	0	0.080	0.011	4.636	0.062	0	0.003	0.109
Control grain, END	0	0	0	0	0	0.148	0.014	0	0	0	0.012	0.033	0	0	0	70.452	0.093
Control grain, EPI	0	0	0	0	0	0.006	0.024	0	0	0	0.014	0.026	0	0	0.002	74.234	0.104
Control flour	0	0	0	0	0	0.195	0	0	0	0	0.014	0.008	0	0.061	0.006	89.021	0.161
Control bran	0	0	0	0	0	0.0789	0.009	0	0	0	0.033	0.254	0.007	0.007	0.002	85.124	0.289

Figure S1. Schematic representation of experimental plan showing the phenological phases of *Triticum turgidum* subsp. *durum* corresponding to the time of analysis of hypogeous (roots) and epigeous (leaves and/or spikes) organs and the allotments where the wheat was cultivated and sampled.
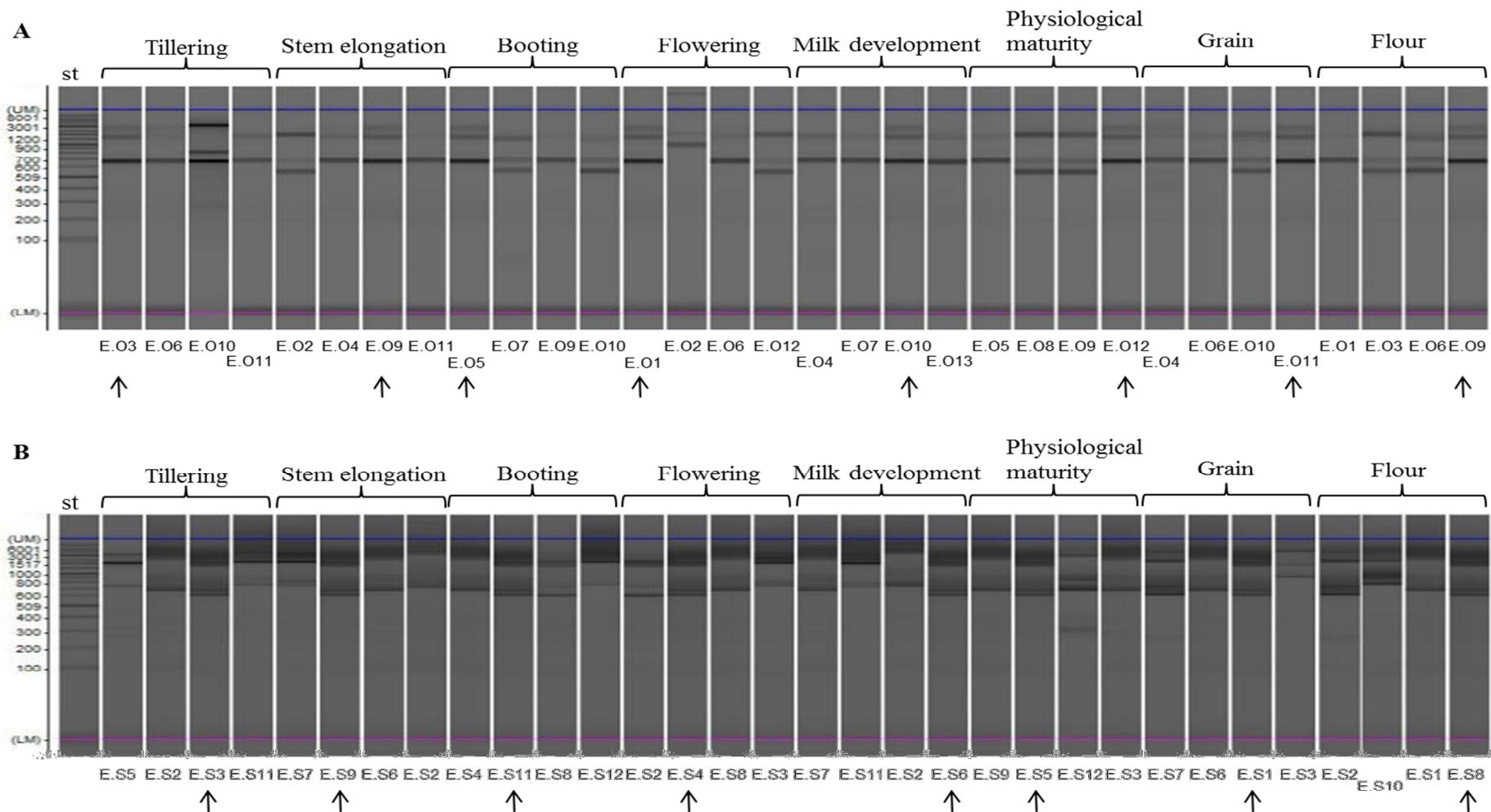
Figure S2. Cross sections of roots (panels A, C, and E) and leaves (panels B, D, and F) of durum wheat (Odisseo) sampled at the stem elongation stage, showing bacterial cells (indicated by arrows). Panels A and B show non-fluorescent sections of durum wheat organs. Metabolically active and dead/damaged bacterial cells are stained green (panels C and D) and red (panels E and F), respectively. Spacebar is 500 µm.

FIG S3 Representative Randomly Amplified Polymorphic DNA-PCR (RAPD-PCR) profiles of *Lactobacillus plantarum* isolated from leaves/spikes, grain, or flour of Odisseo (A) and Saragolla (B) durum wheat. Primer P7 was used for RAPD-PCR analysis. 2-Log DNA Ladder (0.1-10.0 kb) was used as molecular size standard (st). Capillary electrophoretic profiles were singly acquired by MultiNA. Strains isolated from different phenologial stages and processed wheat, and showing similar RAPD-PCR profiles are indicated by arrows.

FIG S4 Representative Randomly Amplified Polymorphic DNA-PCR (RAPD-PCR) profiles of *Lactobacillus plantarum* isolated from leaves/spikes, grain, or flour of Odisseo (A) and Saragolla (B) durum wheat. Primer P4 was used for RAPD-PCR analysis. 2-Log DNA Ladder (0.1-10.0 kb) was used as molecular size standard (st). Capillary electrophoretic profiles were singly acquired by MultiNA. Strains isolated from different phenologial stages and processed wheat, and showing similar RAPD-PCR profiles are indicated by arrows.

Figure S5. Score plot of the two principal components (PC) after principal component analysis (PCA) of environmental temperature, water activity of the wheat organs, cell density of presumptive lactic acid bacteria on selective media, and lactic acid bacterium OTU (genus level) found on hypogeous organs (roots), epigeous organs (leaves and spikes) and processed wheat (grain, chaff, bran and flour) of Odisseo and Saragolla. Hypogeous and epigeous organs were analyzed at tillering, stem elongation, booting, flowering, milk development and physiological maturity stages.