

TABLE S1. Estimated molecular mass range (kDa) and pI of polypeptides found in flours from *Triticum turgidum* spp. *durum*, cultivar Senatore Cappelli, under conventional and organic farming^a

Cluster (kDa)	C _{ONV}		O _{MAN}		O _{LEG}		NO _{INPUT}	
Gliadins	N _o of spots	Spot area	N _o of spots	Spot area	N _o of spots	Spot area	N _o of spots	Spot area
I (>45)	7 ^a	1.24 ^b	5 ^b	1.51 ^a	7 ^a	1.28 ^b	3 ^c	0.82 ^b
II (30-45)	51 ^b	10.53 ^a	62 ^a	10.8 ^a	56 ^b	9.64 ^b	48 ^b	7.13 ^c
III (<30)	9	2.31 ^a	9	2.33 ^a	11	2.58 ^a	10	1.81 ^b
Tot. N _o	67 ^b	14.08 ^a	76 ^a	14.64 ^a	74 ^a	13.5 ^b	61 ^c	9.76 ^c
Glutenins								
I (70-140)	15 ^b	1.53 ^b	20 ^a	2.0 ^a	12 ^b	1.76 ^b	25 ^a	2.25 ^a
II (30-70)	47 ^b	5.67 ^a	46 ^b	4.83 ^b	44 ^b	5.03 ^b	53 ^a	4.98 ^b
HMW/LMW		0.27 ^c		0.41 ^a		0.35 ^b		0.45 ^a
III (<30)	47 ^b	3.11 ^b	41 ^c	3.03 ^b	38 ^c	2.96 ^b	56 ^a	3.49 ^a
Tot. N _o	109 ^b	10.58 ^b	107 ^b	10.27 ^b	94 ^c	10.1 ^b	134 ^a	11.17 ^a

^aTreatments were set according to a completely randomized design with three field replicates. C_{ONV}, conventional system; O_{MAN}, organic system with cow manure; O_{LEG}, organic system with green manure; NO_{INPUT}, without inputs (control). Further details were included in Material and methods.

Analyses were carried out with Image Master software (Amersham Pharmacia Biotech, Uppsala, Sweden). Spot designation corresponds to those of the gels in Fig. 1.

The data are the means of three independent experiments ± standard deviations (n = 3).

^{a-c}Values in the same raw with different superscript letters differ significantly (P<0.05). Number and intensity of the spots were analyzed separately.

TABLE S2. Concentration of free amino acids and their derivatives (mg kg⁻¹) of doughs (after mixing and before fermentation) and mature sourdoughs (after ten refreshments) from *Triticum turgidum* spp. *durum*, cultivar Senatore Cappelli under conventional and organic farming^a. Three-letters amino acid code (IUPAC) is used

Amino acids (mg kg ⁻¹)	C _{ONV}		O _{MAN}		O _{LEG}		NO _{INPUT}	
	Dough	Sourdough	Dough	Sourdough	Dough	Sourdough	Dough	Sourdough
Cysteic acid	2.92	0.61	3.00	1.06	3.00	1.16	2.81	1.16
Asp	60.14	117.14	57.00	111.75	53.92	106.93	55.47	119.41
Thr	7.22	27.34	7.77	22.56	8.17	24.96	7.98	28.02
Ser	65.72	31.30	64.13	52.97	64.63	57.26	65.62	19.93
Glu	34.92	41.30	33.57	45.48	36.15	53.04	33.43	71.51
Gly	29.24	33.15	26.14	23.84	26.56	29.31	28.86	33.08
Ala	25.97	74.27	24.11	56.61	24.78	54.41	26.42	64.52
Cys	2.23	23.04	21.21	20.67	20.22	20.07	17.87	22.14
Val	23.58	65.74	23.03	56.31	22.35	61.23	15.77	71.49
Met	2.85	28.74	3.28	24.97	2.85	26.93	2.16	29.21
Ile	6.90	34.09	6.79	27.28	6.94	31.20	7.35	38.09
Leu	15.64	122.38	15.66	111.54	15.77	118.82	15.90	138.81

TABLE S2. Continued

Amino acids (mg kg ⁻¹)	C _{ONV} ^a		O _{MAN} ^a		O _{LEG} ^a		NO _{INPUT} ^a	
	Dough	Sourdough	Dough	Sourdough	Dough	Sourdough	Dough	Sourdough
Tyr	10.08	43.51	10.46	39.25	10.53	40.02	10.24	44.75
Phe	10.39	62.11	10.57	55.55	10.74	55.88	10.68	66.51
His	21.76	29.40	20.64	25.29	21.53	26.96	20.89	29.27
Trp	66.58	102.80	64.33	101.65	58.59	94.71	57.59	95.80
Orn	19.03	108.49	13.98	98.91	15.79	94.30	16.60	99.15
Lys	20.10	103.94	19.35	92.04	19.02	100.76	19.17	98.57
Arg	55.11	9.69	52.85	19.55	56.83	35.89	52.61	21.34
Pro	38.40	65.71	37.93	59.88	36.72	61.15	37.61	66.44
GABA	32.44	60.21	26.23	48.12	28.58	52.72	31.54	53.20
Total	551.22±25 ^d	1184.96±41 ^{ab}	542.03±27 ^d	1095.28±30 ^c	543.67±32 ^d	1147.69±20 ^b	536.56±24 ^d	1212.40±35 ^a

^aTreatments were set according to a completely randomized design with three field replicates. C_{ONV}, conventional system; O_{MAN}, organic system with cow manure; O_{LEG}, organic with green manure; NO_{INPUT}, without inputs (control). Further details were included in Material and methods.

The data are the means of three independent experiments ± standard deviations (n = 3).

^{a-d}Values in the same column with different superscript letters differ significantly (P<0.05).

TABLE S3. Sequencing results from excised PCR-DGGE-DNA bands

Closest relative and identity (%)^a	Nearest accession no.
<i>Triticum</i> sp. (100%)	AY049041.1
<i>Saccharomyces cerevisiae</i> (100%)	JX141338.1
<i>Candida</i> sp. (99%)	KC425313.2
<i>Saccharomyces bayanus/Kazachstania</i> sp. (99%)	AY048156.1/FJ437053.1
<i>Rhodotorula glacialis</i> (100%)	EF151261.1
<i>Candida humilis/Kazachstania barnettii</i> (100%)	KC481701.1/FN393991.1
<i>Alternaria</i> sp. (98%)	AB808158.1

^aSpecies showing the highest identity (%). The percentage of identity was that shown by performing multiple sequence alignments in BLAST.

TABLE S4. Number of sequences analyzed, observed diversity, and estimated sample coverage for 16S rRNA amplification from doughs (after mixing and before fermentation, 0 days) and mature sourdoughs (after 10 days of propagation) from *Triticum turgidum* spp. *durum*, cultivar Senatore Cappelli under conventional and organic farming^a

Samples	No. of OTUs	Chao1 richness	Shannon diversity index	ESC (%)
C _{CONV} - 0	114	127.14	3.00	99
O _{MAN} - 0	84	89.57	2.57	95
O _{LEG} - 0	97	110.57	2.96	99
NO _{INPUT} - 0	87	91.71	2.63	99
C _{CONV} - 10	24	31.50	2.12	99
O _{MAN} - 10	27	29.00	2.06	99
O _{LEG} - 10	20	20.50	1.89	99
NO _{INPUT} - 10	40	42.00	2.70	99

^aTreatments were set according to a completely randomized design with three field replicates. C_{CONV}, conventional system; O_{MAN}, organic system with cow manure; O_{LEG}, organic system with green manure; NO_{INPUT}, without inputs (control). Further details were included in Material and methods.

^bAbbreviations: OTU, operational taxonomic unit; ESC, estimated sample coverage. Chao1 richness, Shannon diversity, and ESC were calculated with Qiime at the 3% distance level.

Figure S1. Principle Coordinate Analysis (PCoA) based on weighted UniFrac analysis of all RNA samples directly extracted from doughs (after mixing and before fermentation) and mature sourdoughs (after 10 days of propagation) from *Triticum turgidum* spp. *durum*, cultivar Senatore Cappelli. C_{ONV}, conventional system; O_{MAN}, organic system with cow manure; O_{LEG}, organic system with green manure; and NO_{INPUT}, without inputs. Further details were included in Material and methods.

