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1	Molecular characterization of storage proteins for selected durum wheat
2	varieties grown in different environments
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12	Keywords: HMW-GSy to HMW-GSx ratio, HMW-GS to LMW-GS ratio, Protein variability,
13	ExGxF interaction.
14	Abbreviations: CE, capillary electrophoresis; CIMMYT, International Maïze and Wheat
15	Improvement Center; E, environment; F, fertilizer; G, genotype; HMW-GS, high molecular weight
16	glutenin subunit; ICARDA, International Center for Agricultural Research in the Dry Areas; INRAT,
17	Institut National de Recherches Agronomiques de Tunis; K, potassium; LMW-GS, low molecular
18	weight glutenin subunit; N, nitrogen; P, protein content; SA, semi-arid; SDS-PAGE, sodium dodecyl
19	sulfate polyacrylamide gel electrophoresis; SH, sub-humid.

# 21 ABSTRACT

22 The variations of the amounts of individual high molecular weight glutenin subunits (HMW-GS), of the ratios HMW-GSy to HMW-GSx and HMW-GS to low molecular weight glutenin 23 subunits (LMW-GS) and of protein content were evaluated for eight durum wheat cultivars in 24 two regions using four fertilizer combinations during two successive years. All measured 25 parameters showed significant variation with genotypes (G), environments (E) and fertilizers 26 (F). The interaction ExGxF was highly significant for glutenin amount variation. Amongst 27 cultivars possessing HMW-GS 20, landraces seem to better valorize the N-fertilizer use for 28 the accumulation of HMW-GSy than high yielding cultivars. Both HMW-GSy to HMW-GSx 29 and HMW-GS to LMW-GS ratios were found to be positively correlated (p<0.05) with total 30 protein content. 31

## 33 Introduction

The main storage proteins of cereals are gliadins and glutenins. Glutenins are polymeric 34 fractions composed of high molecular weight and low molecular weight glutenin subunits 35 (HMW-GS and LMW-GS) linked with intermolecular disulfide bonds. The HMW subunits 36 are classified into two types on the basis of their molecular values and sequences: x-type 37 which migrates more slowly on SDS-PAGE and y-type which migrates faster (Shewry and 38 Tatham, 1990). The HMW-GS are the most studied protein fractions because of their 39 relationship to gluten strength and bread-making quality (MacRitchie et al., 1990). The ratios 40 between the different components of proteins have been shown to reflect the qualitative 41 42 changes in durum wheat quality (Flagella et al., 2010; Triboï et al., 2000). A high HMW-GS 43 to LMW-GS ratio has been associated with a better technological performance (Flagella et al., 2010). Fertilization and water availability are considered the most important environmental 44 45 factors affecting protein content and composition. Nitrogen-supply has been shown accompanied with an increase of grain protein content, gliadin and glutenin content and the 46 gliadin to glutenin ratio (Triboï et al., 2000). A water deficit through the growing season was 47 shown accompanied with an increase in protein content and in HMW-GS to LMW-GS ratio 48 (Flagella et al., 2010). 49

The aim of this paper was to assess the glutenin variation of eight durum wheat cultivars in different environments using the ratios HMW-GS*y* to HMW-GS*x* and HMW-GS to LMW-GS.

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# 1. Material and Methods

# 54 1.1.Cultivars and experimental conditions

The experiment was laid out as a randomized 3 block design with a factorial set of treatments that included 8 genotypes and 4 fertilizer treatments of nitrogen and potassium combinations  $(N_0K_0, N_0K_1, N_1K_0 \text{ and } N_1K_1)$ , each block included 32 experimental units. The eight cultivars were composed of 'Chili', 'Biskri', 'Mahmoudi', 'INRAT69' 'Karim', 'Razzak', 'Khiar' and
'Omrabiaa'. The experiment was repeated in two regions of Tunisia: semi-arid (Kef) and subhumid (Bousalem) and during two growing seasons (2007 and 2008).

# 61 **1.2. Glutenin extraction**

A glutenin extraction was carried out on 3 samples from each variety as described by Fu and 62 Kovacs (1999) and Rhazi et al. (2009) with some modifications. Samples of 30 mg of flour 63 were stirred for 15 min at room temperature with 1ml of 0.08 M Tris-HCl buffer (pH=7.5) 64 containing 50% propan-1-ol, then they were centrifuged at 15,900 g for 10 min at 15°C. The 65 supernatant was discarded (eliminating albumins, globulins and gliadins). The pellet was 66 67 added to 600 µl of the buffer containing Tris -HCl 0.2 M (pH=9.2), 2% (w/v) of SDS and 1% of DDT, and dispersed by sonication with amplitude of 40 % for 40 s using a stepped microtip 68 probe of 3 mm diameter (ultrasonic Processor, Sonics, model 75038) then the mixture was 69 70 maintained at a temperature of 60°C for 20 min and centrifuged at 12,500 g for 10 min at 20°C. 71

# 72 **1.3. Separation of glutenin subunits by CE LabChip 90**®

Analysis of the glutenin subunits was carried out on capillary electrophoresis (CE) LabChip 90® plateform as described by Rhazi et al. (2009). The 384 samples (8 genotypes x 4 fertilizer treatments x 4 environments x 3 blocks) were used for quantitation of HMW-GS and estimation of HMW-GS to LMW-GS ratio and HMW-GSy to HMW-GSx ratio. Results were expressed as percentage of the time corrected area of individual HMW-GS to the total HMW-GS area. The cultivar set was analyzed 3 times using multiple Chips.

# 79 **1.4. Protein content evaluation**

80 Grain protein content (P) was determined using the NIRS system (near infrared
81 spectroscopy using a Perten-Inframatic-8600).

82 **1.5. Statistical methods** 

Analysis of variance was carried out using proc anova and option proc mixed of SAS (version 9.1).When first or second order interaction were significant, the option PDMix800 was used to compare means. Proc corr was used to evaluate relationships between protein content and ratios between the different protein components.

#### 87 2. Results and discussion

## 88 2.1. Wheat properties

The durum wheat genotypes used in this study were composed of four landraces 'Chili', 89 'Biskri', 'Mahmoudi' and 'INRAT69' and four high yielding varieties 'Karim', 'Razzak', 90 91 'Khiar' and 'Omrabiaa'. Landraces and high yielding varieties are known for their contrasting qualities (Daaloul Bouacha et al., 2014). Using CE Lab-On-Chip technique, 92 different Glu-B1 HMW-GS patterns were identified: 6+8, 7+8 and 20 (Fig.1). The high 93 yielding varieties 'Karim', 'Razzak' and 'Khiar' possessed the subunits 7+8. 'Biskri' 94 possessed the 6+8 composition and 'Chili', 'Mahmoudi', 'INRAT69' and 'Omrabiaa' 95 96 possessed the HMW-GS 20.

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# 98 2.2. Impact of Genotypes (G), Environments (E), Fertilizers (F) and their 99 interactions on total protein content and quantitative parameters of glutenins

In this study a combination of one region (sub-humid or semi-arid) and one cropping season (2007 or 2008) was considered as a separate environment (E). HMW-GSy and HMW-GSx are complementary and their distribution followed an inverse order of classification amongst cultivars and they were found to be negatively correlated. The strong relationship between these two fractions is due to the fact that they are very tightly linked genes on each locus. Therefore, only the results from HMW-GSy were reported.

# 106 **2.2.1 Genotypic impact**

Genotype was a significant source of variation for individual HMW-GS amounts, for HMW-GS to LMW-GS ratios and for HMW-GSy to HMW-GSx ratios (Table 1). This is in accordance with Luo et al. (2000) indicating that the content of HMW-GS and LMW-GS was genetically controlled. Furthermore, Fuertes-Mendizábal et al. (2010) found that the relative proportions of HMW-GS subunits were strongly conserved by genetic determination.

HMW-GS to LMW-GS ratios showed significant (p<0.05) inter-genotype variations. Karim</li>
showed the highest ratio with a mean of 25.10 followed by Biskri and Khiar with respectively
23.3 and 23.29 (Table 2). Cultivar Chili showed intermediate ratio with a mean of 19.75.
Mahmoudi and INRAT69 were comparable to Chili with similar values (p>0.05). The lowest
HMW-GS to LMW-GS ratio was observed with Omrabiaa. These variations were attributed
to genotype factor which was considered the only significant source for the quantitative
variation of HMW-GS and LMW-GS (Luo et al., 2000).

The HMW-GS relative amounts varied significantly with genotypes (Table 2). Cultivar Biskri
showed the highest amounts of HMW-GSy with a mean of 38.04 %, followed by Mahmoudi,
Karim, Razzak and Khiar with similar values ranging from 21.60 % to 22.14 %. Omrabiaa
showed the lowest amount of HMW-GSy with a mean of 17.22%.

Changes in the relative quantity of HMW-GS were also reflected in the variation of HMW-123 GSy to HMW-GSx ratios. Comparison amongst the HMW-GSy to HMW-GSx ratio means of 124 the eight cultivars according to their HMW-GS composition showed that cultivars possessing 125 126 the 7+8 HMW-GS composition showed similar HMW-GS ratios ranging from 0.27 to 0.28 127 (Table 2). Similarities in the expression of HMW-GS between high yielding cultivars Karim, Razzak and Khiar could be explained by the fact that these three cultivars are lines selected 128 from CIMMYT crosses and could have the same origin. On the other hand, cultivars with 129 HMW-GS 20 showed different (p<0.05) HMW-GS ratios ranging from 0.20 for cultivar 130 Omrabiaa, which is a line selected in ICARDA, to 0.28 for cultivar Mahmoudi, which is a 131

pure line selected from a land variety in INRAT. These results could indicate that possessing the same HMW-GS composition did not translate systematically into the same variability in both HMW-GS types. The observed variability could be explained by the degree of subunit's expression which would be specific for each cultivar.

Protein content varied significantly amongst genotypes from 15.29 % to 18.70%. Table 2 showed that the highest overall protein content mean was found for Mahmoudi, Chili and Biskri, landrace genotypes, while Khiar, high yielding genotype, was the cultivar with the lowest overall protein content mean. These results showed that genotypes with high grain yield were associated with low protein content; this is in accordance with Li et al. (2013).

The present study showed statistically significant variations among genotypes in relation to 141 total protein content and relative quantitative composition of glutenin fraction. It is well 142 known that protein content and protein composition are affected by genotypic (G) factors. The 143 144 G factors control the protein level via a number of major genes and quantitative trait loci (QTLs) (Bogard et al., 2011; Uauy et al., 2006). Protein content might be directly genetically 145 controlled by the presence of certain genes in specific cultivar. For example, it was 146 147 established that NAM gene is an important element to enhance grain protein contents (Hu et al., 2013). In addition, a deletion or a non-functional copy of certain NAM gene is related to 148 149 the low protein amount of wheat (Uauy et al., 2006). However, genes implicated mostly in the protein content are associated with other physiological function of the plant (Habash et al., 150 151 2007). The grain protein content gene is an early regulator of a complex regulatory network 152 that contains hundreds of genes influencing both monocarpic senescence and nutrient remobilization from the leaves to the grain (Cantu et al., 2011). 153

Variation in relative quantitative glutenin subunits could be due to the variation in the controlof the transcription and or the expression of HMW-GS. These differences suggest that HMW

glutenin genes did not share the same regulatory elements. However, Kolster et al. (1993) 156 suggested that glutenin loci share regulatory mechanism which implies common *cis* and *trans* 157 regulators may control the expression of glutenin alleles, regardless of the genotype. In 158 addition, Storlie et al. (2009) suggested that HMW glutenin regulation occurs at various 159 points between gene transcription and protein function; the HMW glutenin probably undergo 160 translational and post-translation control. Therefore, these suggest that regulatory systems did 161 162 not affect expression of glutenin genes in the same way. More investigation would be necessary to elucidate the mechanism of regulation. 163

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## 2.2.2. Fertilizer effect

The application of N and K fertilizers showed significant effects on protein content and 165 166 HMW-GS, while it was of smaller contribution in the variation of HMW-GS/LMW-GS ratios (Table 1). Protein content varied among fertilizer combinations from a mean of 15.67 % to 167 18.20 % (Table 3). Results showed that protein content increased significantly with nitrogen 168 application in both regions, in accordance with previous results (Li et al., 2011; Malik et al., 169 2013). In addition, potassium application appeared to enhance the assimilation and 170 remobilization of other elements like nitrogen, since Zörb et al. (2014) reported that 171 potassium deficiency may restrict the ability to use N. 172

Comparison amongst overall means of fertilizer treatments showed significant differences in HMW-GS (p<0.05) (Fig.2. A<sub>2</sub>).  $K_0N_1$  and  $K_1N_1$  treatments showed significantly higher means of HMW-GSy amounts (23.49 % and 23.94 %, respectively) than  $K_0N_0$  and  $K_1N_0$ combinations (22.24 % and 22.38 %, respectively). Thus nitrogen fertilizer, used alone or in combination with potassium, appeared to affect positively the HMW-GSy amounts. This result was in accordance with previous findings showing that the protein subunits contents increased with the supply of nitrogen (Malik et al., 2013). Nitrogen application appeared to

enhance the y-type HMW-GS expression rather than the x-type HMW-GS (Fig. 2. B<sub>2</sub>). This 180 181 could enhance technological parameters since previous results showed that the accumulation of HMW-GSy was related to quality parameters. The HMW-GS to LMW-GS ratio was 182 significantly (p<0.05) higher for the  $K_1N_1$  treatment. An overall mean of 21.44 was scored for 183 this application, while, this ratio showed similar values for K<sub>0</sub>N<sub>0</sub>, K<sub>1</sub>N<sub>0</sub> and K<sub>0</sub>N<sub>1</sub> 184 combinations ranging from 19.91 to 20.24 (p>0.05) (Fig. 2. C<sub>2</sub>). Changes observed in this 185 186 study suggest that fertilizer treatments affect storage protein distribution. In a previous report applying N fertilizer significantly increased the proportions of LMW-GS and gliadins and 187 decreased the proportions of albumins and globulins but had not significant impact on HMW-188 189 GS (Kindred et al., 2008). However, Tea et al. (2004) showed that monomers, LMW-GS and HMW-GS levels increased significantly; and HMW-GS was the most affected. In addition, 190 other researchers showed that nitrogen impact was influenced by application levels (Fuertes-191 192 Mendizábal et al., 2010), application mode (Luo et al., 2000) and application stage (Yue et al., 2007). 193

The source regulation of the accumulation of storage proteins is also in good agreement with 194 the presence of two regulatory elements in the promoter region of the genes of several grain 195 storage proteins. It is known that the "endosperm motif" acts as a positive element under 196 197 high- N conditions; and the "GNC4-like motif" acts as a negative element under low-N conditions for grains of barley (Müller and Knudsen, 1993). All of these modifications could 198 not be achieved without the direct implication of other plant mechanisms such as assimilation, 199 200 transport, amino acid biosynthesis and remobilization. However, knowledge on the biochemical and molecular mechanisms affected by nitrogen fertilization is still fragmentary. 201

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#### 2.2.3. Environmental effect

Substantial differences in protein content were found among the four environments,characterized by different soil and climatic conditions including rainfall rate and temperature.

Protein content was consistently higher in semi-arid areas than sub-humid areas averaging 18.32% versus 15.81%. In addition, a significant year effect was noted; protein contents were higher during 2008 as compared to 2007, in both regions. Differences observed appeared to be due to rainfall distribution during the grain filling period. Excessive rainfall was scored (129.4 mm in semi-arid area and 108 mm in sub-humid area) in 2007, while during 2008 the amount of available water was limited in both regions (40.8 mm in semi-arid and 53 mm in sub-humid regions).

The HMW-GSy amounts varied also significantly with environments (p<0.05) from a mean of 212 22.19 % in the sub-humid region (during 2008) to a mean of 24.08 % in the semi-arid during 213 214 the same cropping season (Fig. 2.  $A_1$ ). HMW-GSy to HMW-GSx ratio varied significantly from 0.29 in the sub-humid areas during 2008 to 0.32 in the semi-arid areas during the same 215 year (Fig. 2. B<sub>1</sub>). Regarding the HMW-GS to LMW-GS ratio, it varied significantly from 216 217 18.75 during the sub-humid areas in 2007 to 22.73 in the semi-arid areas during 2008 (Fig. 2. C1). HMW-GS to LMW-GS ratios seemed to be increased in water limitation conditions of 218 semi-arid areas during a normal rainfall distribution. However, this ratio appeared to decrease 219 with the water availability conditions of the sub-humid areas during a year of excessive 220 221 rainfall.

222 In this study, we showed that protein contents were affected by environmental conditions. These variations attributed to environment might be due to differential effects of high 223 temperature and low precipitation on protein and starch deposition, and was accompanied 224 225 with differences in protein distribution. Malik et al. (2013) showed that temperature before anthesis was found to affect grain protein concentration substantially, while temperature after 226 227 anthesis was of less importance. This could be explained by the fact that increased temperature reduces the vegetative cycle of plant and thus leads to lower assimilation of 228 carbohydrates (Bertholdsson, 1999). As a consequence, plants accumulate less starch and 229

thereby have a higher protein content (Savin and Nicolas, 1996). Increase of protein content 230 231 was also observed in case of water limitation. When water stress occurred throughout the growing season an increase in grain protein concentration was found (Flagella et al., 2010). 232 However, when high rainfall or irrigation occurred during grain filling an increase of protein 233 content was observed due to an increase of nitrogen uptake (Gooding et al., 2003). In 234 addition, our investigation showed that environment influenced glutenin distribution. In 235 236 general, it was found that drought promoted HMW-GS accumulation in the early grain filling (Dai et al., 2013). Zhang et al. (2013) showed that concentration of HMW-GS in grains were 237 up-regulated by the single early drought, the early drought combined with late heat and the 238 239 double drought stress treatments, while it was found to be down-regulated by early heat and 240 double heat stress events. In literature, water regime showed significant increase of glutenin, HMW-GS, LMW-GS and HMW-GS to LMW-GS ratio (Flagella et al., 2010). Variations in 241 242 protein fraction composition due to temperature factor were observed (Triboï et al., 2003). Changes in glutenin and glutenin subunits were associated to general increases in total protein 243 content (Flagella et al., 2010). Qualitative and quantitative protein regulation might be related 244 to mechanisms involved in reserves remobilization during abiotic stress. 245

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#### 2.2.4. Effect of interactions between Environment, Fertilizer and Genotype

Interactions E x G, G x F, E x F and E x G x F were highly significant for all parameters
except for GxF and ExGxF interactions which did not have a significant effect on protein
content (Table 1).

Regarding the interaction between environments and fertilizers, protein content showed a better expression in the semi-arid areas with low input of fertilizers. However, similar values were obtained in sub-humid areas with high fertilizer input while in the semi-arid region, means of protein content of 15.29 and 18.84 % during 2007 and 2008 respectively, using

 $K_0N_0$  were noted. In addition, in the sub-humid region similar protein values were obtained under N and NK fertilizer treatments (Table 3).

Comparison of protein means according to genotype x environment interaction showed that 256 protein content was expressed differently amongst cultivars in the four considered 257 environments; for example, cultivars Chili, Biskri and Omrabiaa showed significant 258 differences in protein values between the sub-humid and the semi-arid areas, however cultivar 259 260 Karim showed similar protein values in SH07, SH08 and SA07 and a significantly different protein mean in SA08. On the other hand, we can conclude that cultivars known for their 261 contrasting quality could present similar protein contents in different environments; cultivars 262 263 Razzak, Karim and Khiar in SA08 showed similar (p>0.05) protein contents to cultivar Mahmoudi in SH07 and cultivar INRAT69 in SH08. These results stipulated that the degree 264 of protein accumulation in the grain was strongly influenced by genotype x environment 265 266 interaction

According to E x F x G interaction, HMW-GS relative quantity varied significantly (p<0.05) intra-genotypes. When comparing the overall means of HMW-GS, the behavior of each cultivar changed from one environment to another. For some varieties, nitrogen fertilization increased the HMW-GSy amounts whereas for others quite the contrary. Differences between environments and some cultivars could be due to differences in rainfall distribution between 2007 and 2008, especially since Dai et al. (2013) found that irrigated and rainfed conditions had different influences on the glutenin subunits.

In water availability conditions, the nitrogen fertilization sometimes led to increase the HMW-GS amounts. Concerning the group of cultivars carrying the HMW-GS 20, nitrogen fertilization appeared to increase the HMW-GSy amount for landraces Chili, INRAT69 and Mahmoudi in sub-humid and semi-arid regions in 2007 and in semi-arid regions during 2008, but not for the high yielding cultivar Omrabiaa in the same environments. These differences

could be explained by a better adaptation of landraces to valorize nitrogen during excessive
rainfall conditions than high yielding cultivar (Omrabiaa). The stability of HMW-GS
expression appeared to be a function of the genotypic effect. Such a result was found by
Triboï et al. (2000) for bread wheat cultivars.

Variations in the HMW-GS to LMW-GS ratio for each genotype according to ExGxF 283 interaction, was influenced by fertilizer treatments under specific conditions. Cultivar Biskri 284 285 showed similar values (p>0.05) of HMW-GS to LMW-GS ratio in the sub-humid region in a year of excessive rainfall with all fertilizer treatments, while in semi-arid region the nitrogen 286 fertilizer increased this ratio in 2007. For Chili and INRAT69 cultivars, the sub-humid areas 287 288 allowed the nitrogen and potassium fertilizer to increase the HMW-GS to LMW-GS ratio. 289 These two cultivars appeared to be more adapted to excessive rainfall distribution and better valorized the use of fertilizers in sub-humid areas. Regarding Karim cultivar, this ratio was 290 291 increased only with nitrogen fertilizer and especially in sub-humid area. However, HMW-GS to LMW-GS ratio for Razzak cultivar was increased with fertilizer treatment in all 292 environments. Fertilizer use and environmental condition combinations did not affect the 293 HMW-GS to LMW-GS ratio for Omrabiaa cultivar. 294

295 Our investigation showed that individual factors (G, E and F) alone presented a larger impact 296 on protein characteristics which is in agreement with previous studies (Li et al., 2011). 297 However, Malik et al. (2013) reported that interactions such as variation in temperature before and after anthesis, N amount and timing, soil and starter fertilizer showed a higher influence 298 299 than factors studied separately. In this study, we were interested in the evaluation of impact of various factors on total protein content, HMW-GS, LMW-GS, HMW-GS/LMW-GS ratio. In 300 the previous study (Malik et al., 2013), mainly formation of glutenin polymers were 301 evaluated. Therefore, changes observed herein due to different factors and their interactions 302 could certainly influence gluten protein polymer structure. Malik et al. (2013) found that 303

304 glutenin proteins extractable and unextractable in SDS were affected differently depending on305 factors and their interactions.

306 Much more work on molecular and biochemical regulation of grain protein accumulation 307 remains to be done. The roles of hormones and other growth regulating compounds in 308 endosperm development are still uncovered. The implications of signal transduction pathways 309 that coordinate the response to the environment are also to elucidate.

## 310 **2.3.** Relationship between protein content and glutenins composition

Variations in HMW-GSy to HMW-GSx ratio were related to protein content. A highly 311 significant positive correlation was found between total protein content and HMW-GSy to 312 313 HMW-GSx ratio ( $r=0.30^{**}$ ). This is in agreement with previous report (Triboï et al., 2000). 314 This relationship was evaluated for the four environments and in each fertilizer combination by class of cultivars according to their HMW-GS composition (Fig.3). Concerning the 20x-315 316 20y composition, a positive significant correlation was observed in sub-humid region during the two seasons with both fertilizer treatments. Nitrogen and potassium fertilizers could affect 317 positively the relationship between HMW-GSy to HMW-GSx ratio and total protein content (r 318 =0.86 \*\* and 0.66\* with  $K_0N_1$  and r = 0.67 \*\* and 0.93\*\* with  $K_1N_0$  during 2007 and 2008, 319 320 respectively). Whereas, association of this ratio to protein content was only significant in the semi-arid area during 2007 ( $r = 0.77^{**}$  for K<sub>0</sub>N<sub>1</sub> and  $r = 0.69^{*}$  for K<sub>1</sub>N<sub>1</sub> fertilizer treatments). 321 During 2008, the semi-arid area showed that the use of fertilizers did not affect the 322 relationship between HMW-GSy to HMW-GSx ratio and protein content. This result could be 323 324 explained by the high value of protein content obtained without fertilizer treatment, when compared to the other environments (sub-humid 2007 and 2008) (Table 3). For the group of 325 6-8 composition, including only one cultivar in this study, no significant variation was 326 observed for HMW-GSy to HMW-GSx ratio in relation to protein content, except, in semi-327 arid region during 2007 where a slightly significant negative correlation was observed with 328

nitrogen-fertilizer application. Regarding the 7+8 composition class, HMW-GSy to HMW-GSx ratio variation with protein content was restricted to some specific conditions. A positive association was established in the semi-arid region during 2008 with K<sub>1</sub>N<sub>1</sub> fertilizer combination ( $r = 0.72^*$ ) and a highly significant negative correlation was found in the same region during 2007 without fertilizer application ( $r = -0.86^{**}$ ).

The sub-humid area and the semi-arid area in a year of excessive rainfall during grain filling 334 335 period showed an increase in protein content accompanied with an increase in the HMW-GSy to HMW-GSx ratio, when using fertilizers. In conditions of water availability during the grain 336 filling period, nitrogen and potassium fertilizers affected positively the relationship between 337 338 HMW-GSy to HMW-GSx ratio and total protein content. However, in cases of water shortage (in semi-arid region during 2008 a year of conventional rainfall conditions) the fertilizer use 339 did not affect the relationship between protein content and HMW-GSy to HMW-GSx ratio. 340 341 These results stipulate that increased protein content did not translate systematically a remaining gluten quality. Therefore, increased protein quality could be associated with higher 342 amounts of x-type or y-type, which could reflect different gluten qualities. It was shown that 343 increasing HMW-GS y-type could contribute in ameliorating flour quality thanks to the 344 345 greater potential polymer resulting from inter and intra- molecular disulfide bonds, since it 346 was established that y-type contains more cysteine residues than x-type.

In addition, variation in HMW-GS to LMW-GS ratio was related to protein content. A significant positive correlation was found between these two parameters ( $r=0.12^*$ ). This relationship was considered a function of the class of genotype according to their HMW-GS composition. For genotype with 6+8 composition, the correlation between HMW-GS to LMW-GS ratio and total protein content was significant at p<0.05 ( $r=0.30^*$ ). Whereas, for cultivars with HMW-GS 20 and 7+8, this correlation was significant at p<0.01 ( $r = 0.30^{**}$ for both classes). Association between HMW-GS to LMW-GS ratio and total protein content was compared for overall fertilizers use. Using K<sub>0</sub>N<sub>0</sub>, protein content and HMW-GS to LMW-GS ratio were positively associated ( $r = 0.31^{**}$ ), whereas, no such association was established (p>0.05) when nitrogen or potassium fertilizer combinations were used.

# 358 **Conclusions**

Our study has permitted to confirm that environment, fertilizer and genotypes were very 359 important source of variation for protein content and composition. Significant differences 360 361 were observed between landraces and high yielding cultivars for the expression of protein content. The identification of HMW-GS amongst the eight genotypes showed three different 362 patterns. Consistently, the group of varieties carrying the 7+8 subunits, showed the same 363 relative percentages of HMW-GSy and HMW-GSx distribution while the group of varieties 364 carrying the HMW-GS 20 showed a much larger variability in the individual HMW-GS 365 366 amounts. HMW-GSy to HMW-GSx ratio could be considered as an indicator of the variation of HMW-GS amounts amongst cultivars. Comparison between landraces and high yielding 367 cultivars possessing the same HMW-GS composition (20 showed different behaviors when N-368 369 fertilizer was applied; landraces seemed to be more adapted to valorize N-fertilizer's use for the accumulation of HMW-GSy than high yielding cultivars (Omrabiaa). This could support a 370 better ability of these landrace cultivars to be adapted to pasta manufacturing. Such a 371 relationship between glutenin subunits and technological quality would be important to 372 elucidate. 373

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- 464 Revised Figures



468 Fig.1. Gel image overlay of glutenin subunits from cultivars Karim, Omrabiaa, Razzak, Khiar, Chili,

Biskri, Mahmoudi and INRAT69, respectively: 1, 2, 3, 4, 5, 6, 7 and 8, separated by EC LabChip 90.

 $\mathbf{A}_{\mathbf{1}}$ 

 $A_2$ 









492 Fig.3. Relationship between HMW-GSx to HMW-GSy ratio and total protein content in the four
493 environments (Env11; SH07, Env 12; SH08, Env 21; SA07 and Env 22; SA08) with the four fertilizer

- 494 combination for the 3 classes of cultivars according to their HMW-GS composition at Glu-B1:20, 6+8
- 495 and **7+8** (**a**, **b** and **c**, respectively).