

| 1 | Genetic relationship | between maize | resistance to c | orn borer attack | and yield |
|---|----------------------|---------------|-----------------|------------------|-----------|
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12 Abstract - Selection for reduced stalk tunnel length by the Mediterranean corn borer (MCB, 13 Sesamia nonagrioides Lef.), while maintaining yield under infestation, has already been evaluated. 14 Significant reductions for tunnel length were reported, but yield showed a non significant 15 tendency to decrease with selection that could be due to increased inbreeding or significant 16 genetic correlation between yield and resistance. Simultaneously, the presence of major QTLs for resistance in chromosome 4 has been suggested. In the present study, we investigated the genetic 17 18 relationship between yield and stalk tunneling resistance by conducting one generation of 19 selection each for yield alone, resistance alone, and yield and resistance combined in a broad-20 based population. In addition, we tested the effectiveness of marker assisted selection at two 21 markers on chromosome 4 for reducing tunnels by MCB. Evaluations were made for two years at 22 two locations under MCB infestation. Unfavorable genetic correlation between stalk tunnel 23 length and yield has been confirmed and could prevent detection of major QTLs for tunnel 24 length by using selection mapping. Markers phi076 and umc1329 could be linked to QTLs for plant height, but are not useful markers for reducing tunnel length and hence damage caused by 25 26 borers. Finally, results advise against selection for reduced tunnel length by MCB or any index involving yield and tunnel length. 27

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29 Keywords: Maize, Sesamia nonagrioides, Resistance, Yield, Breeding

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31 Introduction

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Host plant resistance has been presented as one of the main strategies for arthropod pest 33 management in organic farming which is one of the fastest growing sectors of agriculture due to 34 35 the increasing demand for organically produced food and feed (Zehnder et al. 2007). Varieties 36 with partial pest resistance may not be cost effective in conventional farms where pesticides and GMO organisms are currently used, but are advisable to maintain low-level pest densities that 37 support natural enemy populations. In the Mediterranean area the Mediterranean corn borer 38 39 (MCB, Sesamia nonagrioides Lef.), also named pink stem borer or West African pink borer, is the main pest threat for maize cultivation and non-Bt resistant cultivars appear as one promising 40 41 control method for organic farming. Our group developed a maize synthetic (EPS7) intercrossing four local Spanish landraces which showed resistance to stalk tunneling by the Mediterranean 42 corn borer (Ordás 1991; Malvar 1993; Vales et al. 2001) and a selection program was initiated to 43 44 improve resistance to MCB, while maintaining high yield during selection, using the breeding 45 population EPS12 derived from EPS7 (Butrón et al 2005). The breeding scheme used has been presented in detail by Sandoya et al. (2008). Following three cycles of S₁ recurrent selection, 46 molecular changes during selection were monitored (Butrón et al. 2005) and direct and indirect 47 responses to selection were determined (Sandoya et al. 2008; 2010). In the evaluations, crop yield 48 49 showed a non significant tendency to decrease with selection, while stalk tunneling significantly decreased (-1.8 cm cycle⁻¹), as well as days to silking and plant height. Accompanying the 50 51 agronomic changes, allele frequencies for two SSR molecular markers located on chromosome 4 showed directional changes due to selection suggesting the presence of QTLs for resistance to 52 tunneling by MCB in this region. 53

Sandoya et al. (2009) also concluded that selection could continue for more cycles 54 because no reduction of additive variance for tunnel length was observed after three cycles of 55 56 recurrent selection. However, effects on yield would be unpredictable because no information on additive correlation between yield and the length of tunnels made by MCB could be estimated as 57 additive variance for yield did not significantly differ from zero. The non significant tendency of 58 yield to decrease with selection could be due to increased inbreeding or to significant genetic 59 60 correlation between yield and tunnel length. Inbreeding could be avoided using alternative breeding schemes in which the number of families selected is increased. High genetic correlation 61 between yield and tunnel length by MCB, however, would misadvise efforts to increase resistance 62 63 to MCB attack except when performing marker-assisted selection with markers linked to important QTLs for resistance and unlinked to QTLs for yield. In order to study the genetic 64 relationship between yield and resistance, we compared three alternative breeding methods: (1) 65 66 Selection for reduced tunnel length (L), (2) Selection for increased yield under artificial infestation (Y), and, (3) Selection for reduced tunnel length while maintaining yield (T), as done during the 67 68 previous four cycles of selection. Simultaneous to the phenotypic selection for improved resistance to MCB, one cycle of divergent marker-assisted selection was carried out in EPS12 69 70 using those markers for which allele frequency changes due to selection were significant. The 71 goal was to confirm if those markers were indeed linked to major QTLs for tunnel length and 72 unlinked to QTLs for yield.

In the present study, we investigated the genetic relationship between yield and stalk
tunneling resistance by conducting one generation of selection each for yield alone, resistance
alone, and yield and resistance combined in a broad-based population. In addition, we tested the
effectiveness of marker assisted selection at two markers on chromosome 4 for reducing tunnel
length by MCB.

79 Materials and methods

EPS12(T)C2, EPS12(T)C3, and EPS12(T)C4 were derived from EPS12 through S₁ recurrent 81 selection. The 10% families with the least tunnel length and higher yield than the average yield of 82 families evaluated were selected (Sandoya et al. 2008). Synthetics EPS12(L)C1, EPS12(Y)C1, and 83 84 EPS12(T)C5 were obtained following one cycle of S₁ recurrent selection in EPS12(T)C4 for 85 reduced tunnel length, increased yield under infestation or simultaneous selection for both traits, respectively. In 2005, S₁ families were obtained from EPS12(T)C4 and, in 2006, 90 families were 86 evaluated in a simple lattice 9 x 10 under infestation with MCB. In this selection trial, 87 88 heritabilities and genotypic and phenotypic correlation coefficients were computed following 89 Holland (2003, 2006). The estimated heritabilities on a family mean basis (± standard error) for 90 yield and tunnel length were 0.78 (\pm 0.05) and 0.32 (\pm 0.15), respectively. The genotypic and phenotypic correlation coefficients (\pm standard error) between both traits were 0.41 (\pm 0.24) and 91 $0.22 (\pm 0.08)$, respectively. In 2007, ten families with the highest yield or shortest tunnel length 92 93 were recombined to constitute EPS12(Y)C1Syn 1 and EPS12(L)C1Syn1, respectively. Seed of 94 each selected progeny was sown in a 15-plant row. In each row, five plants were used as males and another five plants as females. Bulked pollen from the 50 male plants was used to pollinate 95 the five female plants in each row. The resulting ears contributed equally to the bulk of 1,000 96 seeds named EPS12(Y)C1Syn1 and EPS12(L)C1Syn1. Similarly, EPS12(T)C5Syn1 was the result 97 of recombining 10 families with the shortest tunnel length and higher yield than the average yield 98 99 of families. In 2008, a second recombination was made within each population 100 [EPS12(Y)C1Syn1, EPS12(L)C1Syn1, and EPS12(T)C5Syn1] in order to reach linkage equilibrium: 300 seeds were planted from each population, thinned to 150 plants, and crosses 101 were made using each plant only once as male or female. At harvest, at least 50 ears were 102 obtained from each population and an equilibrated bulk of 1,000 seeds was collected establishing 103

the synthetics EPS12(Y)C1, EPS12(L)C1, and EPS12(T)C5, respectively. In the same year,
EPS12, EPS12(T)C2, EPS12(T)C3, and EPS12(T)C4 were multiplied to obtain homogeneous
seed for evaluations.

107 In a previous work, marker *phi076* segregated for three alleles, arbitrarily coded as 1, 2, 108 and 3; and umc1239 segregated for two alleles, coded 1 and 2; and frequencies of alleles 1 and 3 at 109 marker phi076 and alleles 1 and 2 at marker umc1329 showed directional changes due to selection (Butrón et al., 2005). In order to check whether markers *phi076* and/or *umc1329* could be useful 110 111 markers for marker-assisted selection toward reducing tunnel length by MCB, five individuals carrying a determined combination of alleles at both markers were selected in EPS12 and 112 intercrossed to constitute populations EPS12-1111, EPS12-1112, EPS12-1122, EPS12-1311, 113 114 EPS12-1312, EPS12-1322, EPS12-3311, EPS12-3312, and EPS12-3322 (first two digits after 115 dash refer to *phi076* alleles and the other two to *umc1329* alleles, presence of both alleles at a 116 determined maker does not mean all individuals are heterozygote but each allele is present at a frequency equal to 0.5). The genotypes at other loci were not controlled because marker-assisted 117 118 selection would only be effective if these markers are linked to major QTLs and genetic background should not obscure effects of major QTLs. 119

120 Genotypes were evaluated using triple-lattice designs at Pontevedra (42°24' N, 8°38' W, 20 m above sea level), and Zaragoza (41° 44' N, 0° 47' W, 230 m above sea level) in Spain in 2009 121 122 and 2010. In Pontevedra, the experiment was hand-planted and consisted of two rows spaced 0.80 m. apart with 29 plants within each row spaced 0.21 m. apart. Plots were overplanted and 123 thinned to obtain a final population density of about 60,000 plants ha⁻¹. In Zaragoza, plots were 124 125 machine-planted and consisted of two rows spaced 0.70 m apart with 25 plants within each row spaced 0.20 m apart. Plots were overplanted and thinned to a final population density of 70,000 126 plants ha-1. At flowering, ten adjacent and competitive (equally spaced apart from adjacent 127 plants)plants per plot were infested by placing egg masses of about 40-50 eggs between the upper 128

ear and the stem. The MCB rearing method used has been described by Eizaguirre & Albajes(1992).

Observations were recorded for days to pollen shed (days from planting when 50% of 131 132 plants had shed pollen), days to silking (days from planting to when 50% of plants had silks 133 emerged), plant height (recorded in Pontevedra on ten competitive plants as the distance from the ground to the top of the plant), stem height (recorded in Zaragoza on ten competitive plants 134 as the distance from the ground to the flag leaf), stem lodging (percentage of plants in the plot 135 136 with the stem broken below the main ear), root lodging (percentage of plants in the plot leaning more than 45° to the vertical), kernel moisture (g of water in 100g of kernels), yield (Mg ha⁻¹ of 137 kernels at 140 g H₂O kg⁻¹), tunnel length (total length in cm per plant of stem tunnels made by 138 borers), and visual ratings for kernel, shank, and cob damages (on a 9 point subjective scale 139 determined as follows: 1 > 90% damage, 2 = 81 to 90% damage, 3 = 71 to 80% damage, 4 = 61140 to 70% damage, 5 = 41 to 60% damage, 6 = 31 to 40% damage, 7 = 21 to 30% damage, 8 = 1 to 141 20% damage, and 9 = no damage). 142

143 Combined analysis of variance was done considering genotypes as fixed effects and
144 environments (each location-year combination was considered an environment) as random (SAS
145 2007). The relationship between *phi076* and *umc1329* markers and agronomic traits was computed
146 considering environments as random effects and markers as fixed effects. Mean comparisons
147 were made using Fisher's protected LSD.

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149 Results and discussion

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151 The combined analyses of variance showed significant differences among genotypes for days to152 anthesis and silking, stem and root lodging, kernel moisture, plant and stem heights, yield and

tunnel length (Table 1). In our experiments, significant differences among EPS12, EPS12(T)C2, 153 EPS12(T)C3, EPS12(T)C4, and EPS12(T)C5 were not detected for tunnel length (Table 2), but 154 155 there was a tendency for decreasing tunnel length with selection, agreeing with results obtained 156 previously (Sandoya et al. 2008, 2009). The non-significant tendency to reduce yield during the first three cycles of selection became significant in the following two cycles with plant height 157 changes also becoming undesirable. These undesirable changes could be the result of inbreeding 158 depression due to genetic drift or consequence of negative correlation between resistance to stem 159 160 tunneling and yield. Comparisons among EPS12(L)C1, EPS12(Y)C1, and EPS12(T)C5 161 developed from EPS12(T)C4 using three alternative breeding criteria [tunnel length, yield or both traits (applying more selection pressure on tunnel length)] confirmed that resistance to stem 162 tunneling and yield could be genetically related. As new genetic variability has not been 163 introduced, changes due to increased inbreeding would not be recovered, but original yield and 164 165 plant height were recovered after one cycle of selection made exclusively for yield, suggesting that inbreeding increase due to genetic drift was not responsible for yield and plant height reductions. 166 167 In addition, one cycle of selection made exclusively for yield tended to increase tunnel length, meanwhile one cycle of selection made exclusively for tunnel length reduced tunnel length, 168 resulting in EPS12(L)C1 that was the only cycle significantly different from EPS12 for tunnel 169 170 length. These results give enough evidence for a strong and negative genetic correlation between 171 yield and resistance to stem tunneling, although the estimated genetic correlation coefficient between yield and tunnel length (0.41 ± 0.24) was not significantly different from 0. Previously, 172 Ordás et al (2010) co-localized QTLs of small effect for increased yield and stalk tunneling by 173 MCB in a population of recombinant inbred lines derived from the cross EP39 x EP42, although 174 175 they did not detect significant genetic correlation between both traits. Genetic linkage between yield and stalk tunneling by another stem borer, Ostrinia nubiblalis Hübner (European corn borer), 176 seems to be a common phenomenon (Schulz et al. 1997; Kreps et al. 1998) and this negative 177 association has made that selection for reduced tunnel length resulted in significant yield 178

reductions (Klenke et al. 1986). In addition, minor improvement for resistance to European corn
borer has achieved when selection is done simultaneously for agronomic performance and
resistance to borers (Bohn et al. 2003).

182 One cycle of selection for yield significantly increased productivity of EPS12(T)C4, while 183 one cycle of selection for reduced tunnel length did not significantly change EPS12(T)C4 184 resistance as expected based on estimated heritabilities for yield (0.78 ± 0.05) and tunnel length 185 (0.31 ± 0.15).

186 Marker-assisted selection has proved an useful tool for improving resistance to the European corn borer (Flint-Garcia et al. 2003) using the bi-parental mapping approach. The 187 QTL mapping approach (selection mapping) used by Butrón et al. (2005) identified alleles whose 188 frequencies significantly changed with selection and Wisser et al. (2008) has suggested that this 189 190 kind of mapping identifies the loci responsible for the strongest selection response and allow the discovery of superior alleles at these loci. However, as genotypic classes for markers phi076 and 191 umc1329 did not significantly differ for tunnel length (Table 3), markers phi076 and umc1329 were 192 193 totally discarded as useful markers for marker-assisted selection for improving resistance to tunneling by MCB. The homozygote '33' for *phi076* was significantly taller than the homozygote 194 195 '11' [Butrón et al. (2005) reported that allele '1' was fixed in EPS12(T)C3] and the homozygote '22' for umc1329 was significantly (at 0.10 probability level) less productive and tended to be 196 197 smaller than '11' [Butrón et al. (2005) reported that allele '2' was fixed in EPS12(T)C3]. Therefore 198 QTLs linked to umc1329 could contribute to the yield reduction trend observed during selection 199 and markers phi076 and umc1329 could be used to partially explain the indirect responses in traits 200 such as stem height that was significantly reduced within the first three cycles of the recurrent selection program. These results agree with the fact that previously reported additive genetic 201 202 correlation between plant height and tunnel length depends on the environment, Sandoya et al. (2009) reported a correlation coefficient close to zero in one year and higher than 0.7 in another 203

year. Therefore, markers potentially linked to plant height and/or stem height such as *phi076* and
 umc1329 could have some effect on tunnel length under determined conditions and become
 irrelevant for resistance to stem tunneling under other conditions.

207 In conclusion, unfavorable genetic correlation between stalk tunnel length by MCB and 208 yield has been confirmed and could prevent detection of major QTLs for resistance to stalk 209 tunneling when selection mapping has performed in a selection program using both traits as selection criteria. Markers phi076 and umc1329 could be linked to QTLs for plant height, but are 210 not useful markers for reducing tunnel length and hence damage caused by borers. Finally, results 211 advise against selection for reduced tunnel length by MCB or any index involving yield and 212 213 tunnel length. Selection for increased yield under infestation with MCB is recommended to increase maize tolerance to MCB attack. In the future, phenotypic selection could be combined 214 215 with marker-assisted selection for reduced tunnel length, once makers linked to important QTLs for resistance and unlinked to QTLs for yield are identified. 216

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Table 1. Mean squares (MS) and degrees of freedom (DF) of the combined analysis of variance of maize breeding varieties evaluated in four

environments.

| Source | Source | | Days to | | | | | | | | | | |
|-----------|----------------|---------|----------|---------|---------|----------|--------|--------|--------|--------|--------|--------|--------|
| of | | Days to | pollen | Stem | Root | Kernel | Plant | Stem | | Ear | Shank | Cob | Tunnel |
| variation | n [†] | silking | shedding | lodging | lodging | humidity | height | height | Yield | damage | damage | damage | length |
| G | MS | 31.36** | 39.78** | 126** | 112** | 27.85** | 391** | 309** | 4.24** | 0.33 | 0.48 | 0.86 | 75** |
| | DF | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 |
| GE | MS | 3.13** | 2.40** | 60** | 41** | 6.97** | 71* | 24 | 0.40** | 0.22* | 0.49* | 0.50** | 49 |
| | DF | 44 | 64 | 64 | 64 | 64 | 20 | 20 | 64 | 44 | 44 | 20 | 44 |
| Error | MS | 0.48 | 0.36 | 27 | 24 | 0.30 | 35 | 21 | 0.08 | 0.14 | 0.30 | 0.19 | 36 |
| | DF | 134 | 170 | 185 | 158 | 212 | 91 | 79 | 182 | 152 | 152 | 106 | 134 |

276 † G refers to genotype and GE to genotype x environment

277 *. ** Significant at 0.05 and 0.01 probability level, respectively

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| | | Days to | | | | | | | |
|---------------------------|---------|----------|---------|---------|----------|--------|--------|---------------------|---------------------|
| | Days to | pollen | Stem | Root | Kernel | Plant | Stem | | Tunnel |
| | silking | shedding | lodging | lodging | humidity | height | height | Yield | length [†] |
| Genotype | Days | Days | % | 0/0 | 0/0 | cm | cm | Mg ha ⁻¹ | cm |
| Phenotypic selection | | | | | | | | | |
| EPS12 | 65 | 63 | 28 | 24 | 20 | 234 | 135 | 6.1 | 33.1 |
| EPS12(T)C2 | 68 | 64 | 22 | 14 | 22 | 234 | 127 | 5.4 | 29.7 |
| EPS12(T)C3 | 67 | 64 | 21 | 16 | 20 | 225 | 121 | 5.2 | 30.7 |
| EPS12(T)C4 | 64 | 62 | 19 | 19 | 19 | 217 | 118 | 4.8 | 27.0 |
| EPS12(T)C5 | 64 | 62 | 16 | 16 | 20 | 196 | 105 | 3.5 | 26.4 |
| EPS12(L)C1 | 64 | 62 | 16 | 11 | 19 | 209 | 112 | 4.4 | 23.2 |
| EPS12(Y)C1 | 65 | 63 | 27 | 10 | 19 | 230 | 132 | 5.6 | 31.9 |
| Marker-assisted selection | | | | | | | | | |
| EPS12-1111 | 64 | 64 | 30 | 20 | 21 | 216 | 113 | 5.9 | 31.1 |

| 280 | Table 2. Mean | comparison amo | ong breeding p | opulations f | for agronomic | traits evaluated | at two location | ns for two years. |
|-----|---------------|----------------|----------------|--------------|---------------|------------------|-----------------|-------------------|
| | | | | | | | | |

| EPS12-1112 | 65 | 63 | 32 | 17 | 20 | 217 | 126 | 5.5 | 34.2 |
|-------------------------|----|----|----|----|----|-----|-----|-----|------|
| EPS12-1122 | 64 | 63 | 33 | 20 | 20 | 217 | 126 | 5.9 | 36.1 |
| EPS12-1311 [‡] | 67 | 65 | 32 | 20 | 22 | 241 | 135 | 6.4 | 31.2 |
| EPS12-1312 | 66 | 64 | 28 | 18 | 19 | 226 | 122 | 5.9 | 40.0 |
| EPS12-1322 | 65 | 63 | 27 | 25 | 21 | 226 | 129 | 5.2 | 38.2 |
| EPS12-3311 | 68 | 66 | 24 | 25 | 22 | 250 | 135 | 5.6 | 34.7 |
| EPS12-3312 | 65 | 63 | 21 | 26 | 21 | 238 | 130 | 5.8 | 36.0 |
| EPS12-3322 | 66 | 64 | 29 | 15 | 19 | 246 | 132 | 5.1 | 32.3 |
| LSD (0.05) | 3 | 2 | 12 | 10 | 2 | 19 | 9 | 1.0 | 9.7 |
| | | | | | | | | | |

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282 [†]Total length in cm of stem tunnels made by borers.

²⁸³ [‡] Presence of both alleles at a determined maker does not mean all individuals are heterozygote but each allele is present at a frequency equal to 0.5.

Table 3. Differences in agronomic traits among genotypic classes for SSR markers *phi076* and $umc1329^{\dagger}$.

| | | | | | Days to | | | |
|---------|---------------------|--------|---------------------|---------|----------|----------|--------|--------|
| | | Tunnel | | Days to | pollen | Kernel | Plant | Stem |
| | | length | Yield | silking | shedding | humidity | height | height |
| Marker | Allele [‡] | cm | Mg ha ⁻¹ | Days | Days | 0⁄0 | cm | cm |
| phi076 | 33 | 34.1 a | 5.4 a | 66 a | 64 a | 20 a | 245 a | 133 a |
| | 13 | 36.5 a | 5.8 a | 66 a | 64 a | 21 a | 231 b | 129 ab |
| | 11 | 33.8 a | 5.7 a | 64 b | 63 b | 20 a | 216 c | 122 b |
| | | | | | | | | |
| umc1329 | 11 | 32.3 a | 6.0 a [§] | 66 a | 65 a | 22 a | 236 a | 128 a |
| | 12 | 36.8 a | 5.7 ab | 65 a | 63 b | 20 b | 225 a | 125 a |
| | 22 | 35.5 a | 5.4 b | 65 a | 63 b | 20 b | 229 a | 129 a |

286 [†]For each marker and trait, means followed by the same letter did not differ at 0.05 probability
287 level

[‡]Butrón et al. (2005) reported that frequency of allele '1' increased at marker *phi076* and

decreased at marker *umc1329* during the first three cycles of selection for reduced tunnel length,

290 while maintaining yield. Presence of both alleles at a determined maker does not mean all

individuals are heterozygote but each allele is present at a frequency equal to 0.5

292 [§] Differences were significant at 0.10 probability level.