

List of supplementary data:

Table S1 (supplementary): Mean parental and recombinant inbred values, standard deviation, heritability and significance of genotype effect in the 5 field trials, for different types of measurements describing plant development and growth.

Table S2 (supplementary): QTLs detected for all traits in 5 field environments, by genomic regions. For each QTL, the LOD-value, the variation accounted for by the QTL (R^2), the additive effect of the T  r  se allele, and the QTL position are indicated.

Table S3 (supplementary): Description of experiments used to assess potential and field value for one-seed weight and seed protein content in 8 genotypes

Figure S1 (supplementary): Correlations between each seed trait and all the other traits. Correlations are given for the RIL1 population, for the subgroup of RIL carrying the *Le* allele, and for the subgroup of RIL carrying the *le* allele. Correlations are given for each of the 5 environments and for the mean value over the 5 environments (Dijon 2000 one-row trial: D00row; Dijon 2002 one-row trial: D02row; Dijon 2002 plot trial: D02plot; Chartainvilliers 2000 one-row trial: C00row; Premesques 2000 one-row trial: P00row). Traits: date of beginning of flowering (BegFlo), date of end of flowering (EndFlo), date of harvesting (Harvest), plant height (Height), number of basal branches (NBranch), biomass and nitrogen content of plant at beginning of seed filling (DMBSF and %NBSF) and of straw at harvest (DMstraw and %Nstraw), seed number (Seed N), seed yield (Seed Y), one-seed weight (1-seed W), seed protein content (Seed PC), and number and volume of cotyledon cells (NcotCel and VcotCel), and indicators of nitrogen source capacity (quantity of nitrogen in plant at BSF: QNBSF; quantity of nitrogen remobilised from vegetative organs and accumulated during seed filling: QNmob and QNacc).