

GENETIC DIVERSITY FOR THE RESPONSE TO EXTERNAL STIMULI AFFECTING PHYSIOLOGICAL MECHANISMS IN *HELIANTHUS TUBEROSUS* CLONES

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Helianthus tuberosus L. ($2n=6x=102$) (*Ht*), is known for possessing important agronomic and technological traits such as the high nitrogen and water use efficiency, competitive ability against weeds, good resistance to fungal pathogen infection, and fructan-rich biomass. Those features make *Ht* a relevant “non food” bioenergy crop for low-input cropping systems.

Few information are available on the response of *Ht* to external stimuli affecting physiological mechanisms relevant for the biomass yield under different environmental conditions.

Ht clones derived from both the improved primary gene pool (GP-1*i*) and the wild primary gene pool (GP-1*w*) were compared to evaluate differential response to several external stimuli, such as: *i*) fungal infection determining powdery mildew (caused by *Erysiphe cichoracearum* or *Ec*), alternaria leaf spot (caused by *Alternaria alternata* or *Aa*), tuber rot (caused by *Sclerotinia sclerotiorum* or *Ss*), *ii*) drought stress in the field, *iii*) GA₃ treatment for tuber breaking dormancy, *iv*) mechanically-induced injury of the tuber apical bud, and *v*) exposure to intensive thermal units administration in the greenhouse. The GP-1*i* clones were obtained from the “Violet de Rennes” (VR) and the Hungarian (CU-3B) accessions, and from the half-sib progenies produced by the ‘K8’ and ‘D19’ parental accessions (the monostem clones K8-HS142 and D19-HS2). The GP-1*w* clone CSR was sampled from an ecotype growing along a road-side near Ronciglione in the Lazio Italian region.

Tuber and stem biomass yields were evaluated from the treated and control plant materials of each clone. Statistical tests of the differences among clones for biomass yield was performed for each experiment.

The results demonstrate very clearly that: *i*) VR was resistant and the other clones were susceptible to *Ec*, *Aa* and *Ss* infections; *ii*) K8-HS142 displayed a relevant resistance to drought (expressed as biomass yield at the time when foliar senescence extended to the nodes in the lower 50% of the main stem) compared to other clones; under irrigation dry matter was 3.1 kg m⁻² for K8-HS142 and 2.0 kg m⁻² for CU-3B; *iii*) dormant tubers from D19-HS2 and K8-HS142 sprouted faster than tubers from CSR, VR and CU-3B after immersion for 1 hour in a 1 mM GA₃ solution; *iv*) only basal buds on the tubers of the D19-HS2 and K8-HS142 clones sprouted as result of the loss of the apical dominance due to the injury on the tuber terminal bud; *v*) D19-HS2 and K8-HS142 clones displayed 75 days flowering earliness compared to the other clones, when exposed to either regular daily thermal units in the field or to the more intense (+3,5 °C over the external temperature) accumulation of thermal units in the greenhouse; flowering of the earliest clones was anticipated of 60 days when grown in the greenhouse.

Monomorphism observed for the amplicons from the PCR using primers designed from the nucleotide sequence of either the cloned *Ss* resistance gene from *Helianthus annuus* or one of the two key enzymes involved in the fructan biosynthesis (1-FFT), suggested that in some instances, divergent response of the clones to external stimuli may depend on differential modulation of gene expression rather than to polymorphism for the ORF of the involved genes.