Proceedings of the Joint Congress SIBV-SIGA
Milano, Italy – 8/11 September, 2015
ISBN **978-88-904570-5-0**

Poster Communication Abstract – B.18

ADDRESSING THE BITTER TRAIT IN CHICORY “PUNTARELLE”: DEVELOPMENT OF TRANSCRIPTIONAL AND SNP MARKERS WITHIN THE SESQUITERPENE PATHWAY

TESTONE G.*, MELE G.*, DI GIACOMO E.*, GONNELLA M.**, RENNA M.**,
TENORE G.C.***, GIANNINO D.*

*) Institute of Agricultural Biology and Biotechnology (IBBA) - CNR, Via Salaria Km 29.300, 00015 Monterotondo Scalo (Italy)
**) Institute of Sciences of Food Production, CNR, Via G. Amendola 122/O, I-70126 Bari (Italy)
***) Department of Pharmacy, University of Naples Federico II, Via D. Montesano 49, 80131 Naples (Italy)

Chicorium intybus, transcriptome, marker development, sesquiterpene lactones

The Catalogna chicory (*Cichorium intybus* L., Catalogna group) is an Italian typical vegetable; *Molfettese* and *Galatina* are Apulian landraces consumed for their tender stems (turions or "puntarelle"). Bitterness is an important organoleptic trait, which directs both consumer and breeding choices and is linked to the content of sesquiterpene lactones (STLs). Major STLs (lactucin, 8-deoxylactucin, lactucopicrin) and respective dihydro- derivatives (1,3-dihydrolactucin, 11(s),13-dihydro-8-deoxylactucin, 11(s),13-dihydrolactucopicrin) were quantified in turions of the two landraces (HPLC). Regardless of the cultivation sites, the content of 1,3-dihydrolactucin and 11(s),13-dihydro-8-deoxylactucin was significantly higher in *Molfettese* than *Galatina*, consistently with the more bitter taste of the former. The *Galatina* reference transcriptome contained 79,716 unigenes and 75 mapped into the sesquiterpenoid and triterpenoid (S&T) biosynthesis pathway (KEGG). In order to survey gene transcriptional variations and polymorphism data, the RNA-seq of *Molfettese* and *Galatina* stem transcriptomes was performed. Over two thousand differentially expressed genes (DEGs) were scored between the two genotypes independently of the cultivation zone. KEGG enrichment analyses revealed that four DEGs were up-regulated in *Molfettese* compared to *Galatina* within the S&T biosynthesis map. Specifically, the expression of the *germacrene A -synthase* and *-oxidase* genes of the Costulonide (a key STL precursor) branch was directly correlated with the contents of 1,3-dihydrolactucin and 11(s),13-dihydro-8-deoxylactucin. The sequences of these genes showed several polymorphic events (SNPs) between the two genotypes and together with the transcriptional divergences represent potential markers for assisted breeding.