

## PRELIMINARY CHARACTERIZATION OF EMS TOMATO MUTANTS SELECTED FOR CHANGES IN FRUIT COLOUR

F. CARRIERO\*, C. D'AMBROSIO\*, G. GIOVINAZZO\*\*, A. D'INTRONO\*\*,  
A. PETROZZA\*, G. SOZIO\*, F. CELLINI\*

\*) Metapontum Agrobios, S.S. Jonica 106, km 448.2, 75010 Metaponto (MT), Italy -  
fcarriero@agrobios.it

\*\*\*) ISPA-CNR, Sez. Lecce Via Monteroni, 73100 Lecce, Italy

*tomato, fruit, flavonoids, carotenoids, mutant*

To create tomato mutant collections for reverse genetic studies (TILLING), we treated *Red Setter* tomato seeds with two different Ethylmethanesulfonate (EMS) concentration (0.7% and 1%). A total of 13000 M2 plants, grown in open field, were phenotypically scored for their mutant traits.

Two tomato M2 families showed altered colour fruits. Precisely the mutant lines produced fruits that were orange, externally, while their flesh was yellow instead than red.

In order to characterize the colour mutant lines, molecular and biochemical studies were undertaken to check the pigment biosynthesis pathways. Total RNA was extracted from mutant and control tomato fruits, reverse transcribed and analyzed by RT-PCR with primers complementary to regions of some genes of the carotenoid (Psy-1, ZDS, PDS, Lyc) and flavonoid (PAL, CHS, CHI) pathways. The qualitative molecular analysis showed differences in gene expression levels not only between colour mutant and control lines (*Red Setter*) but also between the two EMS mutant tomato genotypes.

Interestingly, the molecular results were confirmed and supported by the biochemical ones that showed quantitative differences in secondary metabolites, such as lycopene, beta-carotene (carotenoid pathway), rutin, naringenin and kaemferol (flavonoid pathway), between mutant and control fruits.

Our preliminary molecular and biochemical results demonstrated that the two M2 tomato lines, even if phenotypically identical, differed in their carotenoid and flavonoid contents.

Further investigations will be undertaken to better characterize the mutant lines not only molecularly (quantitative RT-PCR) and biochemically but also for their protein contents by means of proteomic studies.