Poster D-4

GLUCOSINOLATE PROFILE IN DIFFERENT MEDITERRANEAN BRASSICA SPECIES (N=9)

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Mediterranean basin represent an important centre of origin and diversification of *Brassicaceae* and above all of *Brassica oleracea* because are widespread several Brassica wild species (n=9) which seem support an intense genetic flux among them. In fact, the genetic self-incompatibility system characterize some populations and landraces favors the genetic recombination and the set-up of several forms and types within the same crop, such as in broccoli, cauliflower, kale, etc. That is observed mainly for bio-morphological traits but great variance has ascertained for antioxidant profile.

We compare Glucosinolate (GLS) profile of wild and cultivated *Brassica* species (n=9) analyzed by DISPA (Catania, Italy) and MBG (Pontevedra, Spain) in view to define variation occurs among crops and origin. In particular, DISPA grew and analyzed twelve wild species from Italy, thirty-eight kale grown in four European countries, nine cauliflower landraces and four commercialized cultivars, four broccoli landraces and three commercialized cultivars. MGB grew and analyzed eleven kale, five cauliflower, ten cabbage, three Brussels sprouts, three kohlrabi and three broccoli among landraces and commercialized cultivars.

Leaves were immediately transferred to the laboratory and frozen at -80 °C. All samples from laboratory and field experiments were lyophilized. The dried material was powdered and utilized for GLS analysis. The extraction protocols were similar for both laboratories in Italy and Spain. The data acquired were utilized to prepare the numerical matrix used to analyze any correlation among GLS compounds and for principal component analysis and cluster analysis. Variation of glucosinolate compounds showed several positive and negative correlations between and within the aliphatic, indolic and aromatic type.

The accessions studied were classified in seven groups different for GLS profile characterized by main GLS compounds such as the group were the main are represented by Neo-Glucobrassicin and Gluconasturtiin, or by Gluconapin, or by Progoitrin and other minor GLSs, or by Glucoraphanin, 4-OH Glucobrassicin and Glucobrassicin, or by Glucoiberin and Sinalbin, or by Glucoerucin, or finally by Sinigrin and Glucoibervirin.

The wild Brassica populations showed the highest variability among them and the other Brassica crops, but the major part of the genetic materials analyzed clustered in the same truss. The commercial cultivars seem to be similar to some landraces and clustered in the biggest truss. Of course we registered great variability for GLS profile among and within the crops analyzed according to the recent scientific evidence about the genetic base of metabolic pathways for GLS synthesis.