

**GENETIC AND GENOMIC RESOURCES TO DISSECT THE VARIATION OF ROCKET SALAD: INTEGRATIVE APPROACHES FOR CULTIVAR FINGERPRINTING AND GERMPLASM MANAGEMENT.**

D'ALESSANDRO R.\*, COCOZZA A.\*\*, NICOLIA A.\*, TRIPODI P.\*

\*) Research Centre for Vegetable and Ornamental Crops, Council for Agricultural Research and Economics (CREA), 84098 Pontecagnano Faiano, Italy

\*\*) Department of Agricultural Sciences, University of Naples Federico II, Via Università 100, 80055 Naples, Italy

*Rocket salad, SCOT markers, ddRAD seq, genetic fingerprinting, alien species*

Rocket salad is a leafy vegetable crop member of the Brassicaceae, whose name refers to a set of species part of the *Diplotaxis* and *Eruca* genus characterized by leaves with a typical strong taste and pungent aroma due to the presence of glucosinolates. This crop, which has been originated in the Mediterranean area and is particularly appreciated as a food condiment and in ready-to-use mixed salad packages. In Europe, Italy is the main producer and exporting country thanks to its favourable geographical position and agroclimatic conditions for the cultivation of rocket salad. So far, few genomic resources are available for dissecting the diversity of these crops which are threatened by genetic erosion and weedy competition which may affect the quality of wrapped products for the market with consequences for public health. To that end, a double strategy for precise genetic fingerprinting is here presented. The former relies on the use of start codon targeted (SCoT) markers to discriminate *Diplotaxis tenuifolia* and *Eruca sativa* from alien species with similar leaf morphology. From the identification of polymorphisms, we describe the development of sequence-characterized amplified region (SCAR) markers, through a biotechnological pipeline and Sanger sequencing. Main results with 20 highly polymorphic SCOT markers in 16 leafy vegetable species are discussed. The implementation of next-generation sequencing in large germplasm resources is the second adopted strategy. Double Digest Restriction Associated DNA (ddRAD) sequencing in ~ 300 accessions allowed the detection of over 35 thousand SNP markers to be implemented for genomic diversity and population

ancestry analysis. The big amount of data is used to define specific groups of cultivars and for genome-wide association analysis toward the dissection of the genetic basis of main agricultural traits. The findings and tools produced in this research represent a unique opportunity to revolutionize the breeding strategies in rocket salad.