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WHOLE GENOME RE-SEQUENCING OF SWEET PEPPER (*CAPSICUM ANNUUM* L.) ECOTYPES GROWN IN PIEDMONT

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In Piedmont (North-West Italy) pepper is cultivated over an area of about 500 ha, and valuable ecotypes (landraces), which are morphologically recognizable and possess a certain genetic identity, are grown. They provide a product with organoleptic and sensorial qualities particularly appreciated by consumers; however, they are giving progressively the way to commercial varieties and hybrids, which guarantee higher and more uniform yields and which often carry resistance to diseases. Now that the reference genome sequences of the *Capsicum annuum* cv. CM334 and Zunla are available, cataloguing sequence variation in valuable ecotypes and understanding its biological consequences has become a major research goal.

Within the project '*Resequencing of sweet pepper ecotypes for enhancing their quality and for their traceability*', funded by the CRC (Cassa di Risparmio di Cuneo) Foundation, we performed the re-sequencing of four breeding lines representative of the main Piedmontese ecotypes: 'Cuneo', 'Quadrato', 'Corno' and 'Tumaticot'.

The Illumina resequencing (paired-end, 2 x 150 bp) was performed at a coverage of ~35X. Reads were aligned to the reference genome using standard pipelines. Following SNP/Indel calling, a set of about 19 M SNP/Indel was detected, of which 16.65M, 18.01 M, 18.07 M and 16.33 M in 'Cuneo', 'Quadrato', 'Corno', and 'Tumaticot' respectively. The heterozygosity ranged from ~0.2% in 'Corno' to ~0.1% in 'Tumaticot'.

The SnpEff variant analysis highlighted that about 250K (0.96%) SNPs in 'Cuneo', 325K (1.15%) in 'Quadrato', 262K (0.95%) in 'Corno' and 251K (0.96%) in 'Tumaticot' were predicted to have an effect at exon level.

The reconstruction of the four genomic sequences at a chromosomal scale, and their structural/functional annotation is ongoing. The identified allelic and structural genetic variants will represent key tools for the development of diagnostic markers and to dissect the path from sequence variation to phenotype.