

THE OILSEED CROP *CAMELINA SATIVA* (CAMELINA): AGRONOMIC AND GENETIC COMPARISON AMONG 11 VARIETIES

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Camelina sativa is a herbaceous annual or winter annual belonging to the tribe Camelinae of the mustard family (Brassicaceae). Plants are erect and typically reach heights between 30 and 90 cm. Rosette leaves are not lobed and are withered at flowering. Stems are single, typically branched above, and become woody as they mature. Flowers are small and pale yellow or greenish-yellow in colour. Inflorescences are racemes with the flowers in terminal clusters and lack bracts (Francis and Warwick 2009). The pear-shaped siliques are smooth and leathery, 7 to 9 mm long and superficially resemble the bolls of flax. Seeds are small, pale yellow-brown, generally 2 to 3 mm long, and are rough, having a deeply ridged surface. Seeds typically contain 38 to 43% oil and 27 to 32% protein. Genetic studies of the genome of *C. sativa* suggest a polyploid structure being more probably a hexaploid species. Chromosome counts have been reported as $n=6$ or 14 or $2n=12$, 26 or 40 , with $2n=40$ being the most common count. In European countries and Russia, *Camelina* was grown as an agricultural crop before the II World War, now the renewed interest on this crop is mainly due to the search for new sources of essential fatty acids, particularly $n-3$ (omega-3) fatty acids to be used in human food and animal feed products.

The seed of *Camelina* can contain more than 40 % oil, 90 % of which is made up of unsaturated fatty acids: about 30–40% fraction of alpha linolenic acid, 15–25% fraction of linoleic acid, 15% fraction of oleic acid and around 15% eicosenoic acid. In this work we compared 11 different commercial varieties of *camelina* coming from a private company and grown in experimental field. We characterized the genetic material by SSRs to assess the genetic diversity to assist future breeding programs. Our results showed a bigger genetic variability among the springer varieties with respect to the winter ones. Further work will be necessary to better understand the genetic structure of the different accessions.