

Crop wild relatives of Cassava as a source of disease and pest resistance

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Cassava (*Manihot esculenta* Crantz) belongs to the Euphorbiaceae family, which includes approximately 6,300 species. The crop is a naturally diploid species ($2n = 36$) with a genome size of 770 Mbp. The crop was originated in tropical America Amazon basin (Olsen and Schaal 1999) and was introduced to Africa around 1958 by Portuguese and Spanish explorers. The crop was domesticated about 5,000-7,000 years BC and was referred to as yuca, cassava, manioc and many other common names. It is an important staple food source for over a billion people in tropical regions around the globe. The crop was widely used as a source of raw material for animal feed, starch industries, ethanol and other processed food products. Although the crop is so important the production of the crop is affected by many pests and diseases. The major pests infesting cassava were cassava green mite (*Mononychellus tanajoa*, *Mononychellus caribbeanae*), whiteflies (*Aleurotrachelus socialis*, *Bemisia tabaci* and *Aleurothrixus aepim*)

and mealybugs (*Phenacoccus manihoti*, *Paracoccus marginatus*). The major diseases affecting cassava were Cassava mosaic disease (CMD) and Cassava brown streak disease (CBSD). With respect to pest and disease resistance the importance of wild relatives of cassava is gaining more importance in the present scenario for identification of novel genes related to host plant resistance. With the advancement of modern biotechnological tools the genome sequence database of cassava was published which can be utilized for developing pest and disease resistant varieties with economically important traits.

Crop wild relatives of cassava as a source of disease and pests

Wild relatives of cassava were always used as a source of useful genetic variation in cassava breeding. All the species which belongs to the genus *Manihot* are reported as native to South America, particularly Brazil. The wild populations of cassava were seen in west central Brazil and eastern Peru. The wild populations of *M. esculenta* were referred as *M. esculenta subsp. flabellifolia* (Pohl) Ciferri (Roa et al., 1997). *M. pruinosa* is one of the closely related species of cassava as proposed to be the secondary gene pool of cassava and is suggested to be sympatry with *M. esculenta*. During early 20th CMD was one of the threats for cassava production in Africa and research for finding resistance source was initiated. Cassava breeding for mosaic disease resistance was initiated at the Amani breeding station in Tanzania in the 1930's. The India rubber tree species or Ceara, *M. glaziovii* was used in the early twentieth century for developing resistance. It is interfertile with cassava and has

been used in African breeding programs to develop the natural resistance in cassava against pathogens. The resistant hybrids were developed from *Manihot glaziovii* with 80% resistance to CMD and moderate resistance to CBSD. CBSD is caused by cassava brown streak virus, and the disease was first reported in Tanzania in the early 1930s in the lowland coastal areas of eastern Africa. The *M. glaziovii* was used as a source of resistance and the hybrids were produced with adequate level of resistance and yield (Jennings 1957) and leads to the end of first CMD epidemics by the 1940s.



Manihot esculenta



Manihot glaziovii

These hybrids were used for current breeding programmes and the Amani-derived lines were identified as important

resistant sources for CMD, CBSD and bacterial blight (Fregene et al., 2000, Lokko et al., 2006, Hahn et al., 1980). The hybrids developed from *Manihot melanobasis* (now recognized as *Manihot ssp. flabellifolia*) expressed strong resistance against viruses with an ability to localize the virus at the base of the stem. A number of wild species which are close taxa of the crop includes *M. aesculifolia*, *M. carthagenensis*, *M. esculenta subsp. flabellifolia* and *M. esculenta subsp. Peruviana* and *M. tristis*. The cassava was domesticated from wild species of *M. esculenta Crantz ssp. flabellifolia* (Pohl) Ciferri and *M. esculenta Crantz ssp. peruviana* (Mueller). Another five Brazilian *Manihot* species (*M. esculenta Crantz ssp. flabellifolia*, *M. triphylla*, *M. pilosa*, *M. brachyloba*, *M. pruinosa*) was also suggested as close relatives of cassava (Allem 1987, 1999). Among these five species *M. esculenta ssp. Flabellifolia* was considered as wild progenitor of modern cultivars with part of primary gene pool of the crop. *M. pruinosa* was also considered as the nearest species to cassava and from wild strain *M. esculenta ssp. Flabellifolia* based on morphological characters (Allem 1999). The interspecific hybrids of cassava with *M. glaziovii*, *M. pseudoglaziovii*, *M. aesculifolia*, *M. pilosa*, *M. corymbifera*, *M. dichotoma*, *M. pohlii*, *M. neusana*, *M. anomala* under controlled crosses. Among all these several wild species *M. glaziovii* is one of the most important species which made significant contributions in developing cassava germplasm resistant to CMD. *M. reptans* lesser-known wild relative of cultivated cassava also shows the resistance against bacterial blight disease caused by *Xanthomonas manihotis*. *M.*

neusana commonly it shows resistance against *X. manihotis* causing disease bacterial blight. *M. neusana* was reported as evergreen, resistant to stem borer and tolerant to low temperature (Nassar 1985). The studies on pest resistance revealed that *M. flabellifolia* showed moderate-to-high levels of resistance for the cassava green mite *Mononychellus tanajoa*, the mealybug *Phenacoccus herreni*, and the whitefly *A. socialis* (Burbano et al., 2003). However the CWR are useful source of potential genes that confer resistance against pest and disease which has not yet fully exploited. Hence the future research should be focused more on CWR for effectively understanding the resistance traits.

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