EMERGING PARASITIC WEED BROOMRAPE ISSUES IN CHINA AND ITS POSSIBLE MANAGEMENT SOLUTIONS

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Abstract

Sunflower is one of the most popular crops cultivated from northeast to northwest of China, due to its diverse adaptability to a wide range of soil types and climates. The sunflower cultivation area in China was about 9.23×10^5 ha, with a total yield of approximately 2.42×10^6 t in 2013. From last few years, sunflower broomrape (*Orobanche cumana* Wallr.) infestation has rapidly expanded in China and has become a major threat to sunflower production in Xinjiang, Inner Mongolia, Shanxi, Hebei, Heilongjiang, Liaoning, and Jilin provinces (regions). A large number of reserves of *O. cumana* seeds exist in infected soils, especially in Inner Mongolia. For example, only in Bayan Nur City (Inner Mongolia), 40% of sunflower fields were infested by broomrape, resulting in 25–40% sunflower yield reductions. Similarly, in Dingbian County (Shaanxi province) sunflower plantation covers around 10.000 ha, and 64% of the fields were infested by *O. cumana*, resulting in 40–50% yield losses. In China, confectionary sunflower genotypes/cultivars are considered as a cash crop because of its higher demand and economic value, but its cultivation is severely hampered by *O. cumana,* especially in the Inner Mongolian region. The decrease yield of confectionary types severely affected the outcome of both large and small farmers. Till date, five races (A, D, E, F and G) of *O. cumana* exist in different regions of China, but no consistent comparative studies have been conducted on the race determination and virulence of broomrape populations from different areas in China to clarify and unify the uncertainty. Therefore, the current racial situation of broomrape in the main infested areas remains unclear. To establish strategies to control *O. cumana* growth and restrict its spread in crop fields, it is important to learn more about this pest, studying its life cycle, its development, and its molecular mechanisms of infection. It might be helpful to develop molecular markers associated with geographical origin of *O. cumana*, which could be used as a diagnostic tool for parasite introductions into growing areas where they might represent a threat to sunflower production. Controlling *O. cumana* with trap crops may be a biologically promising and practical method in farming. It may be possible that some plants have potential to be used as a trap crop or can be processed into green herbicide formulations that can be applied in agriculture production to rapidly deplete the seed bank of *O. cumana* in soil. Composition of strigolactone both in quality and quantity is a critical aspect of the sunflower to trigger interactions with *O. cumana,* because differences in the strigolactone composition among Chinese sunflower genotypes/cultivars could also govern compatibility and host preference for *O. cumana* races. Similarly the identification of a set of genes or proteins with key functions in mediating susceptibility or resistance against *O. cumana* infestation via next-generation sequencing platforms will be essential to understand the basis of the *O. cumana*-host interaction and may advance knowledge about plant-weed dialogues.

Keywords: sunflower, broomrape, strigolactone, trap crop, next-generation sequencing