

Sunflower Broomrape: problems and Solutions for a Global Threat

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Abstract

Sunflower broomrape (*Orobanche cumana* Wallr.) has become a major global threat for sunflower production in the Old World. The capacity of the parasite to evolve to more virulent forms through mutation and recombination, together with the use of resistant sunflower hybrids mainly based on single dominant *Or* genes, has led to an extremely complex racial situation. A detailed characterization of broomrape populations coupled with alternative breeding strategies is required to increase the durability of genetic resistance to broomrape. In this sense, it is important to develop new genetic sources of genetic resistance, to characterize them in detail at the genetic and physiological level, and to characterize avirulence genes in the parasite. The final goal is to develop diagnostic molecular markers for identification of resistance genes in sunflower to support pyramiding strategies as well as for identification of avirulence genes in the parasite. This can be seen nowadays as a kind of science-fiction approach, but the isolation of individual resistance genes in sunflower is becoming already a reality, and will also become a reality soon for avirulence genes, although a lot of research is still required. With such tools available, our capacity to develop sunflower germplasm with a durable resistance to broomrape will go undoubtedly beyond our current expectations.

Key words: broomrape, molecular marker, avirulence genes

向日葵列当：这一全球性的威胁存在的问题及解决方案

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摘要

过去向日葵列当 (*Orobanche cumana* Wallr.) 一直是困扰向日葵生产的一个全球性的威胁。由于突变及重组使病原菌毒力不断增强, 而向日葵抗性杂交种主要仍依赖单一的显性基因 *Or genes*, 这就出现了极度复杂的生理小种情况。所以就迫切需要对列当群体特性进行研究并找到替代的育种策略以增加对列当的持久抗性。鉴于此, 开发新的遗传抗性资源, 阐明遗传及生理特性, 已经病原菌的无毒基因尤为重要。我们的最终目的是找到特征性的抗性分子标记以配合聚合育种的需要以及鉴定病原菌的无毒基因。目前这看起来有点科幻小说的办法, 但分离向日葵单个的抗性基因以及成为现实, 而且对于鉴定无毒基因不久也将成为现实, 当然大量的工作还需要去做。有了这些工具, 鉴定持久性的抗列当的遗传资源就毫无疑问在我们的预期之中。

关键词: 列当、分子标记、无毒基因