

EDITORIAL

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Harnessing the power of a novel gene to combat Asian soybean rust: a promising breakthrough

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Abstract

Plant diseases have significant implications on agriculture and food security. Recent research published in *Nature Communications* by Hao et al. (*Nat Commun* 15:3310, 2024) has identified a novel disease-resistant gene, *Rpp6907-7*, which shows high potential in enhancing resistance to Asian Soybean Rust (ASR), a major threat to soybean production. This discovery provides valuable insights for developing improved soybean varieties with enhanced disease resistance.

The devastating impact of plant diseases on human societies is well-documented in historical accounts (Fisher et al. 2012). For example, potato late blight caused by *Phytophthora infestans* is responsible for Great Famine in Europe in late 1840s, which led to a million of death and a mass exodus of Irish individuals to the United States. Similarly, Dutch elm blight and chestnut blight decimated urban and forest environments during the 20th century. The fungal rust disease that ravaged coffee crops in Sri Lanka necessitated a shift from coffee cultivation to tea production. *Phakopsora pachyrhizi*, the obligate nutritive fungus causing Asian Soybean Rust (ASR), exhibits a broad host range and is capable of infecting over 150 plants from 53 genera, and poses a major biological threat on food security (Pennisi 2010).

The dissemination of *P. pachyrhizi* through wind-borne urediospore results in the development of the highly

virulent and challenging-to-control Asian soybean rust. Even a minimal incidence of ASR (0.05%) can result in substantial yield reductions up to 90% if not effectively managed. In Asia, soybean rust accounts for approximately 20–80% of soybean yield losses, and represents a significant soybean disease in the southern region of China. As the global center of soybean production has shifted to South America, the continent has emerged as the leading producer of soybean, with a total production of 210 million tons in 2023 and an average output value of 115 billion US dollars per season. However, the tropical and subtropical climate of South America facilitates the proliferation of the soybean rust pathogen, which is prevalent in soybean cultivation regions of the continent. In Brazil, ASR prevention and management expenditures surpass 2 billion US dollars annually, with 60% of fungicides allocated for this purpose. The quantity of fungicides utilized in the last three years significantly exceeds that of the previous decade, approaching saturation levels. The absence of efficacious commercial rust-resistant cultivars necessitates the predominant reliance on chemical control for rust prevention and management. While fungicides ensure abundant agricultural yields, they also pose significant risks on environmental pollution and ecological harmfulness.

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Utilizing disease resistance genes in breeding programs represents a cost-effective and efficient strategy for managing ASR. The current prevalence of ASR can be attributed to the limited availability of soybean germplasm that is resistant to the pathogen. Extensive screening efforts have led to the identification of over 20 resistant resources, including PI200492, PI230970, and Ug5, as well as the characterization of eight rust-resistant loci *Rpp 1* to *Rpp 7*, and *Rpp6907*. Nevertheless, most of the resistant resources, such as *Rpp1–7* and the other loci have been overcome by the current pathogen populations. One exception is SX6907, identified by Shan et al., that exhibits durable resistance to Asian and South American rust populations. The inhibition of rust mycelia growth in the leaf tissue of SX6907 prevents the formation of uredia and the production of new urediospores, thereby conferring resistance to ASR (Fig. 1). Nevertheless, conventional breeding methods are characterized by time consuming and a heavy reliance on known disease resistant resources. These resources can only fish out resistant genes present in their genetic makeup, making it challenging to effectively respond to fast-evolving pathogens. As a result, the full potential of disease-resistant resources remains underutilized. Addressing this issue and achieving stable, long-term utilization of resistant resources has emerged as a scientific challenge in rust resistance breeding. The identification and cloning of essential genes responsible for ASR resistance, along with the subsequent resistant mechanism analyses, are essential for the development of ASR-resistant soybean varieties and the sustainable utilization of resistance genes to combat ASR.

The study conducted by the Southern Soybean Genetics and Breeding team of the Oil Crops Research Institute of the Chinese Academy of Agricultural

Sciences focused on the isolation and characterization of the gene pair *Rpp6907-7* and *Rpp6907-4*, which provide broad-spectrum resistance to ASR. This research, began in 1980s with the screening and identification of rust resistance resources, led to the discovery of the highly resistant germplasm SX6907 from a collection of 1000 samples during the years of 2007–2010, as reported by Shan et al. 2000, 2012. In order to map the resistance genes in SX6907, the genetic analyses and gene mapping were conducted, and *Rpp6907* was successfully mapped on soybean chromosome 18, with SSR24 and SSR40 serving as flanking markers at a distance of 111.9 kb (Chen et al. 2015).

The decision was made to clone the resistance gene in SX6907, leading to the cloning of the broad-spectrum ASR resistance gene pair *Rpp6907-7/Rpp6907-4* from soybean. *Rpp6907-7* induces an AVR-independent hypersensitive response (HR) that is suppressed in the presence of *Rpp6907-4*, which is located at the *Rpp6907* locus. These genes function as an unconventional genomically linked pair, with *Rpp6907-7* and *Rpp6907-4* working synergistically to achieve a balance between yield and plant resistance. A comprehensive investigation was conducted on the gene characteristics, expression pattern, and evolutionary relationship of *Rpp6907*. Additionally, the association between the *Rpp6907* domain and resistance response, subcellular localization, and resistance function were also elucidated. Furthermore, the researchers stepped forward to explore *Rpp6907* interacting proteins to identify the regulatory factors to gain a deeper understanding of *Rpp6907* disease resistance mechanism. This research provided new insights to expand understanding of soybean rust resistance, and established a groundwork for sustainable utilization of resistance genes to develop ASR-resistant soybean varieties.

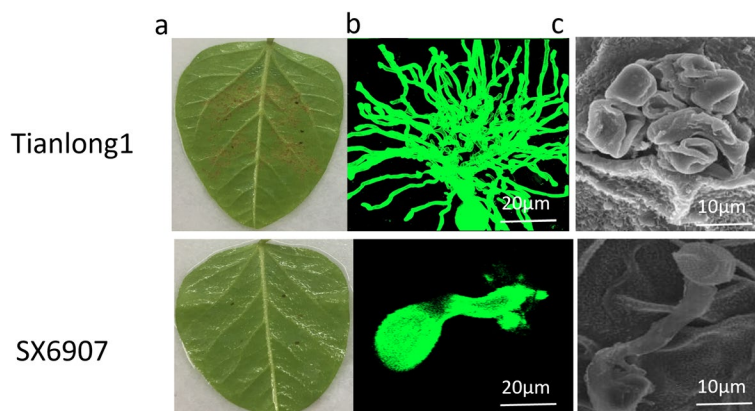


Fig. 1 ASR resistance phenotypes, microscopic observation of SS4 growth in different soybean cultivars. **a** Asian soybean rust resistance phenotypes of SX6907 and Tianlong1. **b** Microscopic observation of pathogen development in SX6907 and susceptible accession Tianlong1 at 5 d after SS4 infection. **c** Scanning electron microscope observation of pathogen development in SX6907 and Tianlong1 at 5 d after SS4 infection

Collectively, the cloning of the soybean Rpp6907-7 resistance gene and the identification of the autoimmune regulatory gene Rpp6907-4 are milestones in ASR resistance breeding. The application of *Rpp6907* will greatly reduce the threat of soybean rust, and at the meantime reduce the huge usage of fungicides, which is of great significance to environment protection. Therefore, the application of this gene will be instrumental for the sustainable control of rust disease in the world. Further studies would be in-depth understanding of NLR activation mechanisms. In previous studies, NLRs with IDs emerged as sources of new recognition specificities (Cesari et al. 2014; Kroj et al. 2016); the mechanism underlying the specific activation of helper NLR without ID (Rpp6907-4) is more worthy of further investigation.

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