Asian soybean rust (ASR) is one of the most serious threats in soybean production in tropical and sub-tropical area. Use of resistant varieties is a practical way to control ASR. A soybean line, No6-12-1, pyramided with three resistance genes (Rpp2+Rpp4+Rpp5) to ASR was compared in disease progress and the number of uredinia per lesion (NoU) with PI 230970 (Rpp2), PI 459025 (Rpp4), PI 200526 (Rpp5) in 2016/2017 season. No6-12-1 was derived from crossing BRS184, PI 230970, PI 459025 and Kinoshita carrying Rpp5. Two other cultivars PI 587880A (Rpp1-b) and BRS 184 (susceptible) were included in the experiment. Each cultivar was sown at the field of Embrapa Soja, Londrina, Paraná on 28 November 2016. Half of the plots was sprayed with fungicides three times. A split-plot design (main plot: fungicide, sub-plot: cultivar) was used with four replications. Analysis of variance for disease severity showed significant difference in factors of fungicide and cultivar in most of evaluations. Disease severity and area under disease progress curve were the highest in BRS 184, slightly less in PI 230970, PI 459025, and PI 200526, then in No6-12-1, and the lowest in PI 587880A. NoU was much less in No6-12-1 than the other cultivars. PI 587880A produced similar NoU to the other cultivars with the single resistant gene. Fungicide sprays did not increase yield significantly on BRS 184, PI 587880A and No6-12-1, although an increase in average yield was observed only in BRS 184. No6-12-1 suppressed disease severity to some extent and reduced NoU significantly comparing to the cultivars carrying single resistance gene each. These results suggest that pyramiding of the three genes has a synergetic effect in the field.

Key words: Phakopsora pachyrhizi, genetic resistance, Glycine max