Blast disease caused by *Pyricularia grisea* (Cooke) Sacc. is an important disease of rice causing serious rice yield reduction. The utilization of resistant cultivar is one of the most effective methods to control the disease. Thai traditional rice cultivar is one of the genetic resources for blast resistance. The objective of this research was to identify genetic variation of blast resistance and inheritance of the resistance in the landrace glutinous rice collected from the Northeastern Region Thailand. The disease evaluation was conducted in the greenhouse. Eighty landrace cultivars, eight elite lines and a differential set of ten Near Isogenic Lines (NILs) were tested with a total of 32 blast isolates. The results showed that the percentage of Broad Spectrum Resistance (BSR) index of 53 landrace cultivars were greater than 60%. Among those cultivars, Khao Leuang Kaeo, Daw San Patong, Bak Khuea and Hawm Daeng showed the highest value of BSR (100%). Cluster analysis performed by the Unweighted Pair Group Method with Arithmetic averages (UPGMA), separated the cultivars into two groups (resistance and susceptibility) based on a similarity relationship of 0.60 with the cophenetic correlation of 0.899. All resistant cultivars were clustered in the same group of the NILs carrying resistance genes *Pi2(t)*, *Pi1(t)*, *Pi33*, *Pi1*, *Pi-4a(t)*, *Pi-4a(PKT)*, *Pi-1t(TTP)*, *Pi3(t)*, *Pi-4a(TTP)* and *Pi-4b*. Additional study to identify genetic resistance of 80 landrace cultivars with SSR markers RM 212, RM 224, RM 48, RM 207, RM 277 and RM 313 which located near four blast resistance genes revealed that some landrace cultivars showed monomorphic band with Jao Hom Nin cultivar and P 0489. However, a clear relationship between phenotypic grouping and genetic grouping by the UPGMA was not found. The inheritance of blast resistance was performed in 734 F2 individual plants from a cross between Daw San Patong and Sakhon Nakhon using two blast isolates, THL653 and THL934. The phenotypic distribution of the F2 progenies ratio of resistance:susceptible plants were 3:1 indicated
that the blast resistant gene is a single dominant gene. The genetic resources of blast resistance identified in the present study should be useful for rice breeding programs.