Blast disease, caused by hemibiotrophic fungus *Pyricularia oryzae* Sacc. (teleomorph: *Magnaporthe oryzae* (Hebert) Barr.), previously known as *Magnaporthe grisea*, is the most serious disease of rice and causes high yield losses in most rice growing regions every year. Blast is an endemic disease in all Iranian and Uruguayan rice fields, with yield losses up to 90% that has been reported from some rice growing regions. Various types of blast infection can be observed in a field, including symptoms on leaves, collar, neck, panicle, and grain. Although the fungus is only known to reproduce asexually in nature, it is infamous for its diversity. *P. oryzae* is not only pathogenic on rice, but also on other cultivated and wild graminaceous hosts. However, the species is considered to consist of host-limited forms. Knowledge of different rice blast pathogen populations and factors affecting genetic structure of the isolates in some of main rice growing countries, such as Uruguay, is still scarce. However, understanding disease epidemiology and plant-pathogen interactions, and finally sustainable disease management is highly dependent on knowledge of the genetic diversity of the pathogen. Diversity can be studied using a wide array of molecular techniques. AFLP method is based on selective amplification of restricted fragments generated from total genomic DNA. Because of rapidity, replicability, high resolution, and adequate discriminatory power above and below species level in a variety of taxa including bacteria, fungi, plants, and animals, AFLP markers have emerged as a major type of genetic markers with broad spectrum of application, especially in analyzing population structure. Also, the more loci which are screened, the lower the probability of making a mistake by chance factors (ref. 20 of my phytopath. Paper). AFLP is used increasingly to study genetic diversity of several plant pathogenic fungi. The genetic variability of 55 *P. oryzae* isolates from Iran and 32 isolates from Uruguay, was analysed using amplified fragment length polymorphism (AFLP). Cluster analysis using different methods and principal co-ordinate analysis (PCO), based on the AFLP data from 679 monomorphic and polymorphic bands generated with eight primer combinations, was performed. The resulted grouping of the isolates revealed 4 separate AFLP groups among a total of 87 isolates. Within each AFLP group, two or more haplotypes were detected with a genetic similarity of 100%. Overall genetic similarity was greater than 50% between Iranian and Uruguayan populations. Little evidence for gene flow between the two populations of the pathogen. Analysis of Molecular Variance (AMOVA) revealed that rice varietal type and geographic region were the dominant factors determining genetic structure of *P. oryzae* populations; but rice cultivar had not significant effect.