

**GENETIC DIVERSITY OF BLAST ISOLATES (*PYRICULARIA GRISEA*)
FROM LAOS AND QUANTITATIVE TRAITS LOCI MAPPING OF
SELECTED ISOLATES IN RICE (*ORYZA SATIVA*)**

INTRODUCTION

Laos is the largest producer and consumer of glutinous rice in the Asian region. Approximately 85% of annual rice production is glutinous rice. Mostly (90%) rice is cultivated in the rainfed lowland and rainfed upland environment. Generally, in the upland environments traditional rice varieties are grown. The rainfed lowland is the most significant production environment, in 2000 accounting for 68% of the area and 74,6% of production. At rainfed lowland, however, almost 70% of the area is planted by improved varieties such as TDK1, TDK2, TDK3, TDK5, TSN1 and PNG1. Areas adjacent to Thailand had been growing some Thai lines, often as a result of farmer-to farmer exchange; among these were RD6, RD8 and RD10 (sometimes known locally as RD16), and the non-glutinous varieties RD23 and KDML105 (Schiller *et al.*, 1998).

Laos has two major rice growing areas, the Central and Southern part, mainly with rainfed lowland in Savanakheth Province and around the Mekong River where some rice growing areas have faced biotic diseases. Savanakheth province in the lower, central agricultural region, with a total of 116,939 ha in the wet-season in 2001 and 22,729 ha in the dry-season 2000-20001. It has area of planted rice in the Lao PDR. In the future, Savanakheth province will be able to further substantially increase national rice production, increasing the annual rice surplus to be available for either export and maintenance of the a national rice reserve.

The economic loss of rice production caused by rice blast disease (*Pyricularia oryzae* Cav; teleomorp *Magnaporth grisea*) was reported worldwide and in Laos. Subsequently, the incidence of the disease has been reported from different parts of

Asia, Northern Australia, Africa and USA. In Laos, the disease has been reported officially from Savanakheth Province since 2000 (DOA, 2001). The yield loss for instance, in some localities of Savanakheth in 2004 just before the harvesting time at dry-crop season ranged from 20 – 30% during survey and collection the blast samples from the field. Many rice scientists consider blast to be the most important disease of rice. The economic loss caused by rice blast (*Pyricularia grisea* Sacc.) was reported to nearly US\$ 5 billion per year. Blast resistance in rice cultivars is generally classified into two types, qualitative (complete) and quantitative (partial). Complete resistance is characterized by prevention of blast fungus reproduction in incompatible combination of the host and pathogenic strains, and a single gene usually controls the resistance. On the other hand, partial resistance reduces the extent of pathogen reproduction in the compatible interaction.

Atkin and Johnson identified two independent genes designated as *Pi-1* and *Pi-6* in US rice cultivars. Hsieh identified four dominant genes *Pi-4*, *Pi-13*, *Pi-22* and *Pi-25*. Kiyosawa and his colleagues identified a total of 14 resistant genes at eight loci: *Pi-a*, *Pi-i*, *Pi-k* (*Pi-k*, *Pi-ks*, *Pi-km*, *Pi-kh* and *Pi-kp*), *Pi-z* (*Pi-z* and *Pi-zt*), *Pi-ta* (*Pi-ta* and *Pi-ta2*), *Pi-b*, *Pi-t* and *Pi-sh*. Since the first RFLP map of rice was constructed, several single-gene characters have been located via linkage to mapped RFLP markers in rice.

Molecular marker technology has been widely used nowadays, It has been applied for the identification and mapping of genes conferring both complete and partial resistance and has provided insight into the genetic basic of durable resistance (Wang *et al.*, 1994). Many major genes for blast resistance have been identified using this method. Resistance rice varieties, especially when resistance is based on single major genes, may be rapidly overcome by compatible races of the pathogen (Kiyosawa, 1982). Gene pyramiding is one way to improve disease resistance in rice. Before this can happen, gene mapping and tagging should be carefully undertaken.

Objectives

1. Survey and Collection blast disease from rice field at Savanakhet, Laos
2. Characterization blast pathogen.
3. Determination the number, genome locations, and genetic effects of leaf blast resistant genes carried by JHN.