

## INCREASING AGRICULTURE PRODUCTION IN MARGINAL LAND: CROP IMPROVEMENT APPROACH

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### Background

History has proved that agricultural sector plays important role in the Indonesian economy. In the 21<sup>st</sup> century, Indonesia is faced with the challenge of fulfilling the food and energy demand of its people. World population in 2025 is predicted to near 8.04 billion people requiring foods supply about 3046.5 million ton, whereas a predicted world food production is only 2977.7 million ton. The world food balance, therefore, will be deficit 68.8 million ton (Mifflin 2000). At that time, Indonesian population will reach about 316-350 million people, thus increasing food demand equal to rice production 65.9 million ton (Research and Development Agency, Department of Agriculture 2005). Since the recent domestic production of rice is only 52.8 million ton, therefore, there will be 13.1 million ton rice deficit, if no increase of production during the remaining period. This indicates that Indonesia is often threatened by food shortage, especially rice. Since the economic crisis until now, Indonesian ability to be self sufficient in food has constantly declining. Indonesia has to import food which has depleted its foreign exchange reserve (US \$ 900 millions). With high dependency on import and the slow rate of productivity increase, Indonesia has to increase its national food production capacity in a sustainable way.

The effort to increase food production is limited by the lack of arable land. Therefore, there is a need to increase the area of arable land to marginal areas which are potential to be developed (30.7 million hectares, Las *et al.* 2008). However, such areas are consisted of acid soils, with low-P soils, rain-fed uplands, tidal swamps, and sulphic acid soils, with low to very low soil fertility (class IV-VI, Table 1). These conditions require crop varieties with specific adaptation and local-specific cultural techniques (Sopandie 2006).

Table 1. Characteristic and constraints of marginal lands

No	Marginal Areas	Characteristic and Constraints
1	Acid Soils (18.2 million ha)	Al toxicity, pH <5.0, P fixation, low P, Ca, Mg, K, N availability
2	Low-P Soils (1.27 million Ha)	Degraded paddy-field, low-P, soil texture, low organic matter
3	Land with low-light intensity under canopies ( $\pm$ 0.5 million ha per year)	Low-light intensity, low pH, low fertility soils, drought stress
4	Rain fed lands (25.3 million ha)	Infertile soils, low organic matter, high soil erosion; drought stress
5	Feat Soils (? ha)	Water flooding, Pyrite, Fe, Al toxicity; low soil fertility especially P

Source: Research and Development Agency, Department of Agriculture 2005

This paper discusses our research in plant physiology, molecular biology and plant breeding conducted in the Faculty of Agriculture, Bogor Agricultural University (IPB) which contributes to improvement of agriculture productivity in marginal areas.

### Improvement of Crop Productivity in Marginal Areas

Production increase in marginal areas could only be achieved by improvement in (1) crop adaptation to abiotic stresses and resistance to biotic stress, (2) yield potential and (3) cultural techniques which are based on knowledge in plant physiology and ecophysiology. The three components should synergized to achieve improvement in productivity under less favorable condition of the marginal areas as shown in Figure 1.

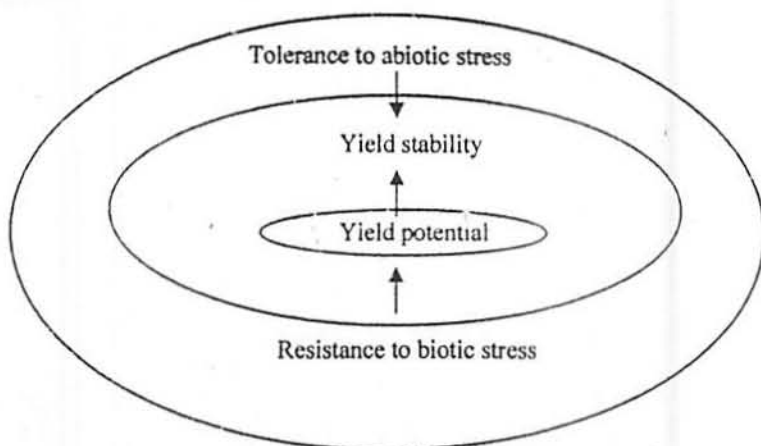


Figure 1. Synergism among components of crop improvement in marginal areas

Improvement in crop productivity in marginal areas requires comprehensive approach which involves basic research in genetic, physiology and molecular biology and applied research of plant breeding and agronomy. The understanding of mechanisms of crop adaptation to various abiotic stresses that limit crop production under marginal areas should be understood to develop adapted crop varieties and agroecosystem specific cultural techniques. Research in plant physiology, genetics and molecular biology in the Department of Agronomy and Horticulture, Bogor Agricultural University (IPB) have played important roles in crop improvement for marginal areas.

Breeding program could improve yield stability in marginal environments through two approaches; (1) improvement in yield potential of widely adapted genotypes, or (2) improvement of crop adaptation to abiotic stresses. Improvement in yield potential in marginal areas is attempted for target environments with moderate stress level (Sopandie 2006).

#### (1). Improvement of Yield Potential for Moderate Stress Areas

Improvement of yield potential in breeding for high yielding varieties could be applied in an effort to improve productivity in marginal areas with low to moderate level of abiotic stress. Under low to moderate level of stress, the yield of *high-yielding varieties* (HYV) decreases, however, the yield is still higher than *local-adapted varieties*. Improvement in yield potential could be achieved through ideotype breeding, a breeding program specific designed based on physiological knowledge of a crop to improve certain combination of characters which enhances productivity.

Ideotype breeding has been applied by breeders in the Department of Agronomy and Horticulture IPB, to improve rice yield potential through selection for characters which support more efficient photosynthesis and respiration, and improve source-and sink partitioning (Sopandie 2006). At present, our program in Faculty Agriculture IPB is focused to create HYV of rice. The ideotype breeding of rice has resulted in several lines of New Plant Type (NPT) rice with higher productivity compared to conventional improved rice varieties. The NPT rice has straighter stature, few tiller all productive tillers, with dark green leaves, deep root system and large number of seed/spikelet. Currently these lines are under evaluation for variety release in multi-location trials. The NPT rice lines, produced 8.2 – 9.8 ton/ha compared to 6.6 – 7.5 ton/ha of the conventional or green revolution rice (Figure 2 and Table 2)



Figure 2. New Plant Type rice line, IPB15-d-13j-1-1-1, developed through ideotype breeding in IPB (Aswidinnoor 2007)

Table 2. Yield potential of New Plant Type Rice developed by IPB

Lines of NPT-rice	Yield potential (ton/ha)
IPB 92-F-5-1-1	8.4
IPB 92-F-49-1-1	8.2
IPB 95-F-10-1-1	8.6
IPB 97-F-13-1-1	9.3
IPB 97-F-13-1-2	9.6
IPB 98-F-5-1-1	9.2
IPB 102-F-2-1	9.7
IPB 102-F-6-1	9.8
IPB 102-F-28-1	8.5
IPB 102-F-46-2	9.1
Compartion (IR64-Ciherang)	6.6 – 7.5

## (2) Improvement of Crop Adaptation to Abiotic Stress

Improvement of crop adaptation to various environmental stress in marginal lands is possible because there are high variability in the level of adaptation to abiotic stress in the germ plasm. The physiological studies conducted in our Department has contributed in the crop improvement programs through the understanding of mechanisms of adaptation and identification of adaptive characters. These adaptive characters have been utilized as selection criteria in the breeding program. Low soil nutrient availability and Aluminium toxicity are the major constraints in crop production in acid soil. Researchers in IPB focused the development of crop for acid soil on rice (Makmur *et al.* 1999, Jagau 2000, Trikoesoemaningtyas 2002), soybean (Jusuf *et al.* 1993, Sopandie *et al.* 1996a, 1999a), and corn (Syafrudin, Trikoesoemaningtyas and Sopandie 2006).

Our studies to evaluate 400 soybean accessions in the acid soils of Gajrug, Bogor followed by nutrient culture studies have identified genotypes tolerant to acid soils, namely Yeliow Riloxi, si Cinang, Genjah Jepang, and Sriyono (Sopandie 1999). Our evaluation on 22 corn genotypes in nutrient culture has identified four genotypes, namely AMTL-(HS) C2, SATP-(S2)-C6-S0, MRSS-1 (S1)C1-29-1 and MRSS-1(S1)C1-57-1 which showed higher tolerance to acid soils compared to the acid tolerant variety Antasena (Syafrudin *et al.* 2006). For adaptation to low-light intensity, our studies have identified a number of shade-tolerant upland rice lines, including Jatiluhur, Dodokan, CS22, and TB177E-TB30-B-2 (Chozin *et al.* 1999); and shade-tolerant soybean lines, namely a local cultivar Ceneng, in addition to Pangrango and B613 (Sopandie, Trikoesoemaningtyas and Khumaida 2005). These tolerant genotypes have been utilized in the breeding program conducted in the Department of Agronomy. For soybean, ten advanced lines are currently under evaluation in multi-location trials in the Province of Jambi to be released as shade-tolerant soybean lines for intercropping with young rubber trees (Figure 3 and Table 3)



Figure 3. Shade-tolerant soybean lines for intercropping with young rubber trees under trials in Sembawa, South Sumatera (Trikoesoemaningtyas, Wirnas and Sopandie 2008)

### Biotechnological Approach

Biotechnology has made important contribution in crop improvement program in IPB. Biotechnology has been used to study the mechanism of crop adaptation to abiotic stress, identification and characterization of genes involved in crop adaptation, characterization of genetic diversity and marker assisted selection.

#### (1). Screening and Identification of Shading-related Genes

Our further research has identified the shading-regulated genes in 2-w-old seedlings of LI-tolerant and LI-sensitive soybean genotypes by differential display. Among 32 differential bands, 9 cDNAs were positive-selected clones which were detected by using reverse northern methods. Using the method of PCR-RACE, the *JJ3* cDNA fragment (261 bp) was extended 485 bp toward 5' and 73 bp toward 3' ends into 841 bp full length sequence of *JJ3* cDNA, comprised of 232 adenin (a), 234 sitosin (c), 192 guanin (g) dan 183 timin (t) as shown in Figure 4 (Khumaida, Sopandie and Takano 2001).

A.						
BASE COUNT	70 a	58 c	58 g	75 t		
1	acggttctac	agggtcttcc	ctaattggga	gggtcagtat	ttgcacccta	aggatgggtg
61	ttaccctgag	aaggccaacg	ccggacgcca	aggggtgggt	caaaacttca	ggtctattgg
121	taagaatggt	agtcctattg	aggtcaagtt	cactggcaag	cagccctatg	atttgtgagc
181	acacaactct	atcttcatca	tcatcatccc	ccgtgcttcc	tttatatgct	atatattctc
241	atgtgaaaaa	aaaaaagctt	a			
B.						
BASE COUNT	232 a	234 c	192 g	183 t		
1	<i>gcaagcagtg</i>	<i>gtatcaacgc</i>	<i>agagtggcca</i>	<i>ttacggccgg</i>	<i>ggaacacttg</i>	<i>tattatctca</i>
61	<i>agcaaccatg</i>	<i>gcaatggcaa</i>	<i>ccaagcctc</i>	<i>tctcttaacc</i>	<i>ccaccctct</i>	<i>ccggtctcaa</i>
121	<i>agccagcgac</i>	<i>cgcgctccg</i>	<i>tgccatgaa</i>	<i>gcaaaactcc</i>	<i>agcctctct</i>	<i>tctccagccc</i>
181	<i>gaagcccctc</i>	<i>aagttctcca</i>	<i>gaacaatcag</i>	<i>agcagcagcc</i>	<i>gccgacgaga</i>	<i>ccacagagcc</i>
241	<i>accagcaaaa</i>	<i>gtagaggctg</i>	<i>caccggctcg</i>	<i>gttcacccca</i>	<i>ccagaacttg</i>	<i>acccaaacac</i>
301	<i>cccttccccg</i>	<i>atcttcgggg</i>	<i>gcagcaccgg</i>	<i>cgggctcctg</i>	<i>cgcaaggcac</i>	<i>aggtggagga</i>
361	<i>gttttatgtc</i>	<i>attacgtggg</i>	<i>actcacccaa</i>	<i>agaacagatc</i>	<i>tttgaaatgc</i>	<i>ccactggcgg</i>
421	<i>cgccgctatc</i>	<i>atgagggagg</i>	<i>gtcctaacct</i>	<i>tctcaagttg</i>	<i>gccaggaagg</i>	<i>agcagtgctt</i>
481	<i>ggctcttggg</i>	<i>actaggctca</i>	<i>ggtccaagta</i>	<i>caagatcaag</i>	<i>taccagttct</i>	<i>acagggctct</i>
541	<i>ccctaattggg</i>	<i>gaggttcagt</i>	<i>atttgacccc</i>	<i>taaggatggt</i>	<i>gtttaccctg</i>	<i>agaaggtcaa</i>
601	<i>cgccggacgc</i>	<i>caaggggtgg</i>	<i>gtcaaaaact</i>	<i>caggtotatt</i>	<i>ggtaagaatg</i>	<i>ttagtctcat</i>
661	<i>tgaggtcaag</i>	<i>ttcaactggca</i>	<i>agcagcccta</i>	<i>tgatttgtga</i>	<i>gcacacaact</i>	<i>ctatcttcat</i>
721	<i>catcatcacc</i>	<i>ccccgtgctt</i>	<i>cctttatatg</i>	<i>ctatatattc</i>	<i>tcatgtgata</i>	<i>tcatgtacct</i>
781	<i>attgtcaatt</i>	<i>ttattatgcc</i>	<i>acaaatattg</i>	<i>ctaaaaaaaa</i>	<i>aaaaaaaaaa</i>	<i>aaaaaaaaaa</i>
841	a					

Figure 4. Nucleotide sequence of *JJ3* cDNA fragment before RACE (A), and full length sequence of *JJ3* cDNA after RACE (B). The italic sequence was the *JJ3* cDNA fragment before RACE. (Khumaida, Sopand'e and Takano 2001)

To determine the protein encoded by *JJ3* gene, the coding sequence (CDS) of *JJ3* full length was analyzed using the program of ORF Finder ([www.ncbi.nlm.nih.gov/gorf/gorf.html](http://www.ncbi.nlm.nih.gov/gorf/gorf.html)) as shown in Figure 5. The coding sequence transcribed 210 amino acids initiated by start codon *atg* (Met) and ended with stop codon *tga*. The homology of *JJ3* cDNA full length sequence has been determined. The homology sequence of *JJ3* cDNA was very high in both nucleotide sequence (79 - 83%) and amino acid sequence (85-96%).

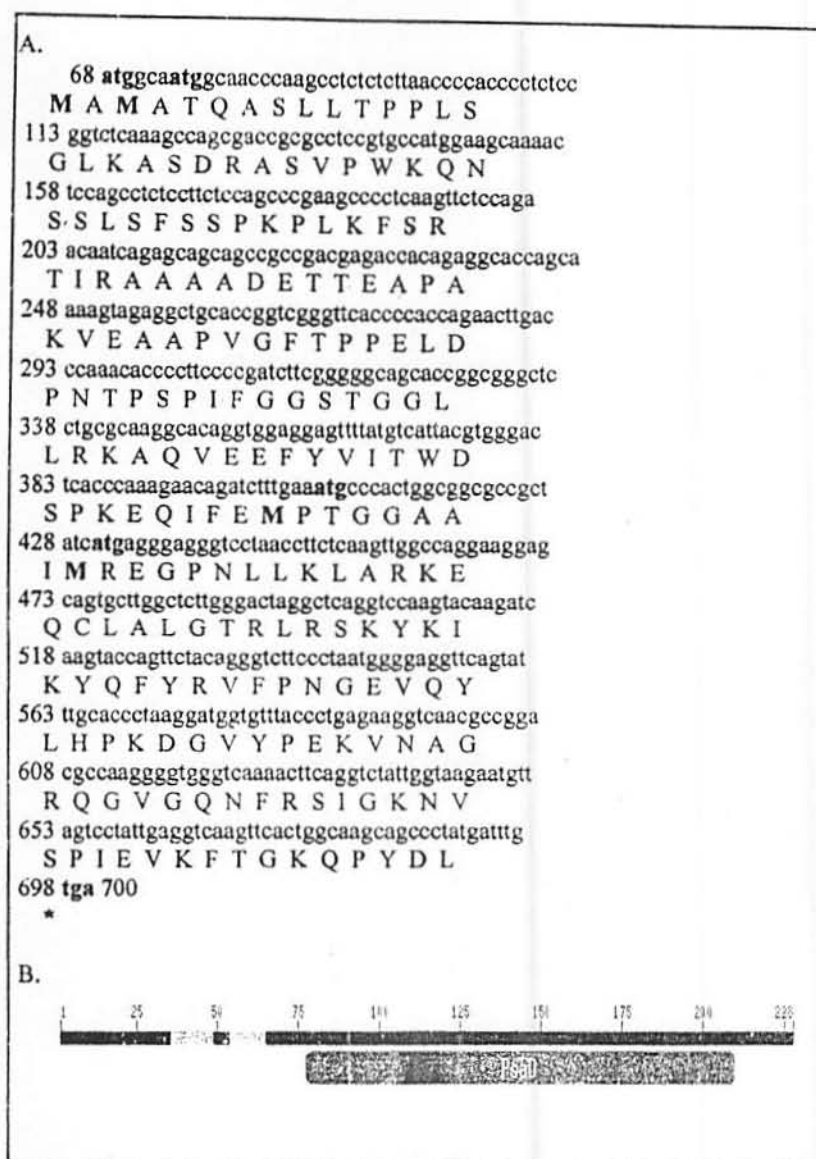


Figure 5. (A). Complete open reading frame (ORF) or CDS of cDNA *JJ3* full length sequence. Small letters are nukleotide sequence of *JJ3* CDS and capital letters are predicted amino acid sequence. (B). Complete putative conserved domain of the cDNA *JJ3* full length sequence. The *JJ3* CDS encodes Psal photosystem I (PSI) subunit (Khumaida et al. 2005)

Expression of other photosynthetic genes: *JJ3*, *phyB*, *ATHB*, *CAB* and *CHS* genes were studied on soybean shade tolerant genotype (Ceneng) and sensitive genotype (Godek) under low light intensity. *β-Actin*, one of the house keeping genes, was used in this study as an internal standard. As shown in Figure 6, the expression pattern of *JJ3*, *phyB*, *ATHB*, and *CHS* genes on soybean shade tolerant genotype (Ceneng) under low light intensity were down-regulated since their expression were increased along with the decreased of light intensity (fully sun light – 50% shade – totally dark conditions). The expression of *JJ3* and *ATHB* genes was high at 50% shading condition, lower expression at dark, and no expression at full sun light.

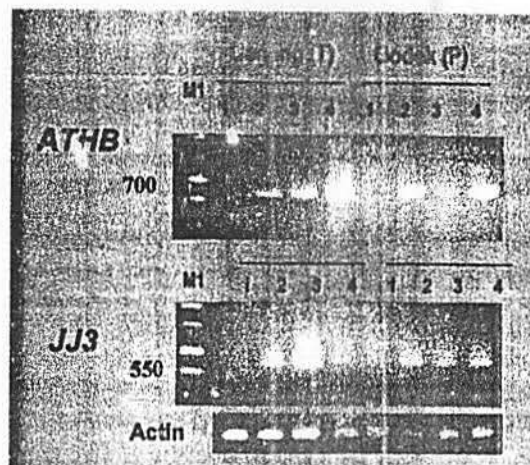


Figure 6. Expression of JJ3 and ATHB-2 genes related to shade tolerance in soybean. (Khumaida *et al.* 2005)

**(2) Marker Assisted Selection**

Other biotechnology approach was used in crop improvement to develop soybean tolerant lines using *marker assisted selection*. We conducted selection of 85 random primer and found 9 markers to linked with soybean tolerance to low light intensity. Further verification resulted in 2 markers, P01-350 and OPM-19-350 which were used to select 150 F8 soybean lines. From this marker assisted selection, 20 advanced soybean lines have been identified as tolerant to lowlight intensity (Figure 7) and were evaluated for yield performance under intercropping condition in the Province of Jambi. Ten tolerant lines were later selected for multilocation trials (Trikoesoemaningtyas, Wirmas and Sopandie 2008).

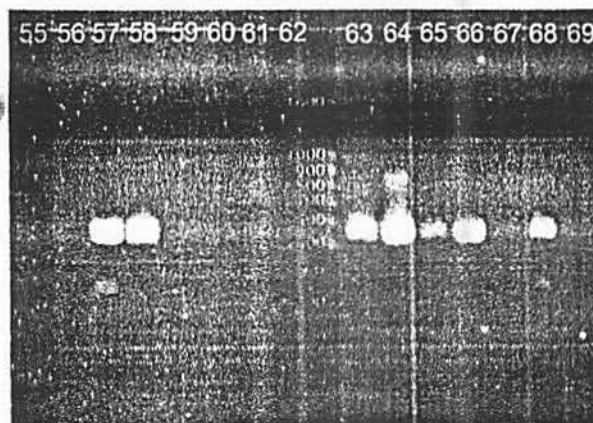


Figure 7. Marker assisted selection of advanced soybean lines for tolerance to low light intensity using P01-350 marker (Trikoesoemaningtyas *et al.*, 2008)

Table 3. Productivity of Shade Tolerant Soybean Lines under Intercropping Condition

Lines	Selection	Yield potential Under shade (ton/ha)*
CP-10-5	Marker P01-350	1.9
PG-57-1	Marker P01-350	1.7
SC-56-3	Tolerance index	1.4
PG-36-8	Tolerance index	1.3

PS-57-6	Marker P01-350	1.3
GC-13-7	Marker P01-350	1.3
GC-70-6	Tolerance index	1.2
SP-16-2	Tolerance index	1.2
SC-68-2	Tolerance index	1.2
SC-21-5	Marker P01-350	1.1

#### Optimising Cultural Techniques in Marginal Areas

Optimising cultural techniques in marginal areas through a combination of the use of adapted varieties, soil amelioration with organic matter, utilization of traditional cropping system (mixed farming, intercropping, agro forestry) maintaining continuous supply of N and P through the use of microbial agents are proven as effective cultural techniques for marginal areas.

**Management of Peatland.** Indonesia has coastal peatland over 20 million hectares or about 10% of its total land areas. Most of them are still growing peatland forest and the others have been converted into agricultural land. Peatland forests have multiple functions such as hydrology, biogeochemistry, biodiversity protection, and forest products functions. In the wise management of tropical peatland, maintaining diversity of plant species and improvement of degraded peatland should be done simultaneously. At present, some Indonesian peat swamp forests have been converted for non forestry uses such as oil palm, forest plantation, rice field, etc.

Some technologies have been used to improve degraded peatland. Application of rock phosphate, macro and micro nutrients, application of adapted rice varieties, and water management could improve rice production in degraded peatland. In forest plantation and oilpalm plantation, water management play an important role besides fertilizers. The other technology appropriate for utilization is selecting suitable plants for acidic and low nutrient soil. *Aqualaria sp* is one of high economical value and suitable for degraded acid sulfate soil (Suwardi 2009).

#### Strategies for future research.

Future research should be focused on upland areas (acid soils, rain fed lands and lands under canopies) through collaborative, interdisciplinary research, primarily plant physiology, genetics, molecular biology, ecology, plant breeding and agronomy. Research on crop improvement including selection and evaluation should be conducted in *participatory research* involving farmers, to allow for the release of commercial varieties which will be adopted by farmers. Availability of adequate funding in long term is needed to achieve the improvement in crop yield. Several policy should be implemented immediately to improve productivity of food crops in marginal areas, primarily (a) utilization of marginal areas left by logging practices, (b) establishment of research, development and application of local-specific cultural techniques, and (c) facilitating the formation of institution at the farmers' level.

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