GENETIC STUDIES OF LOWLAND RICE (*Oryza sativa* L.) FOR SUBMERGENCE TOLERANCE IN NIGERIA

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A THESIS SUBMITTED TO THE POSTGRADUATE SCHOOL, FEDERAL UNIVERSITY OF TECHNOLOGY MINNA, NIGERIA IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF DOCTOR OF PHILOSOPHY (PhD) IN CROP GENETICS AND BREEDING

June, 2023

DECLARATION

I hereby declare that this thesis titled **"Genetic Studies of Lowland Rice (*Oryza sativa* L.) for Submergence tolerance in Nigeria"** is a collection of my original research work and it has not been presented elsewhere for award of a degree or certificate. All sources and information (published or unpublished) therein have been duly acknowledged.

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CERTIFICATION

The thesis titled **“Genetic Studies of Lowland Rice (*Oryza sativa* L.) for Submergence tolerance in Nigeria”** by: EHIRIM, Bernard Odirachukwunma (PhD/SAAT/2018/7966) meets the regulations governing the award of the Degree of Doctor of Philosophy (PhD) of the Federal University of Technology, Minna and it is approved for its contribution to scientific knowledge and literary presentation.

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DEDICATION

This Thesis is dedicated to my father for his continued unwavering love and support and to my mother who could not see this thesis completed.

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ABSTRACT

Submergence tolerance has long been regarded as an important breeding objective for rain-fed lowland and deep-water rice areas. Despite this recognition, there has been limited success in developing improved submergence tolerant rice varieties in Africa particularly Nigeria. In this research, study on genetics of *Oryza sativa* lowland rice for submergence tolerance was carried out, using two most farmer-preferred commercial rice varieties in Nigeria. Six generations were developed by crossing a submergence tolerant donor rice line (Swarna Sub-1) with the two commercial varieties (FARO 44 and FARO 57). The six generations of the two crosses were evaluated under submergence stressed and non-stressed conditions. The inheritance of the tolerant gene (*SUB-1 gene*) was determined by *Mendelian Ratio* and the nature of gene actions for some important agronomic traits of the generations was estimated by generation mean analysis. The submergence screening was performed in a controlled condition that allowed flooding with water depth of 1.0 metres for a period of 14 days. The evaluation was done in a complete randomized block design with three replications. Data were collected on Percentage Survival of the test entries, Percentage Survival of the resistant entries, Percentage Comparative Survival, Percentage Elongation, Plant height (cm), Number of tillers per plant, Days to 50% flowering, 100 grain weight (g), Panicle length (cm), Panicle number, Grain width (mm), Grain length (mm), Flag leaf width (cm), Flag leaf length (cm), Straw girth (mm), and Internode length. The result revealed that the Analysis of Variance were significantly different for all the traits at both vegetative and reproductive growths, except for the flag leaf width (FLW) and Stem Girth (SG) in both crosses under normal condition. Survival rate (%) ranged between 0.00% - 100% was observed in the Cross I. In the Cross II, a range between 0.00% and 95.24% survival rate was recorded. High Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were registered for the grain yield among the generations of the two crosses. Moderate to high narrow sense heritability in conjunction with moderate to high expected gain were observed in most of the traits, especially the yield component traits. The results of the generation mean analysis showed significance of at least one out of the four scales (A, B, C and D) for all the traits studied in the two crosses. The six parameters analyzed revealed that besides the additive and dominance gene actions, epistatic interaction mechanisms have also contributed to the expressions of the traits studied. However, the relative magnitudes of these effects varied from character to character and cross to cross. Despite the stressed conditions of submergence, the introgression of the *Sub1A gene* demonstrated considerable improved survival ratio and 54.1% to 66% obtainable grain yield after recovery from complete submergence of the rice field. This can be the next quick crop development area to be considered which would help generate desirable varieties for the Nigerian farmers especially with the consistent flood being experienced in our unpredictable weather faced with climate change.

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List of Abbreviations, Glossaries and Symbols

FAO - Food and Agriculture Organization

SSA - Sub-Saharan Africa

IRRI - International Rice Research Institute

FAOSTAT - Food and Agricultural Organization Statistics

CBN - Central Bank of Nigeria

US - United State

SUB-1A - Swarna Submergence Tolerant Gene *1A*

UNDRR - United National Disaster Risk Reduction

FARO - Federal Agricultural Research *Oryza*

NCRI - National Cereals Research Institute

USDA - United State Department of Agriculture

CO_2 - Carbon Dioxide

IPCC - Intergovernmental Panel on Climate Change

IFAD - International Fund for Agricultural Development

ERF - Ethylene Response Factor

Kb - kilobases

QTL - Quantitative Trait Loci

GCA - General Combining Ability

SCA - Specific Combining Ability

kg/ha - Kilogram Per Hectare

g - Gram

^0C - Degree Centigrade

GCV - Genotypic Coefficient of Variation

PCV - Phenotypic Coefficient of Variation

F_1 - First Filial Generation

AATF - African Agricultural Technology Foundation

F_2 - Second Filial Generation

BC - Backcross

σ^2_g - Genotypic Variance

$\sigma^2 g$e - Genotype G) x Location (L) Variance

σ^2_p - Phenotypic Variance

σ^2 - Residual Variance

H^2 - Broad Sense Heritability

GA - Genetic Advance

σ_p - Phenotypic Standard Deviation

I - Selection Differential

GAM - Genetic Advance as Percentage of Mean (expected genetic gain)

DF - Degree of Freedom

m - F2 Population Mean

a - Additive Gene Effect

d - Dominance Gene Effect

aa - Additive X Additive Type of Epistasis

ad - Additive X Dominance Type of Epistasis

dd - Dominance X Dominance Type of Epistasis

h^2 - Narrow Sense Heritability

σA - Phenotypic Standard Deviation

$\mu P1$ - Population Mean of P1

$\mu P2$ - Population Mean of P2

σ^2 - Variance

$\chi 2$ - Chi-square

V_e - Environmental Variance

V_a - Additive Variance

V_d - Dominant Variance

V_p - Phenotypic Variance

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background to the study

Rice (*Oryza sativa* L.) has become a commodity of strategic importance across most of Africa countries (AfricaRice, 2020). Driven by changing food preferences in both urban and rural areas and compounded by high population growth rates, rice consumption in the Saharan and sub-Saharan Africa (SSA) increased by 5.6 % per annum between 2009 and 2012, a rate more than double the rate of population growth (AfricaRice, 2020). Projections by the Food and Agriculture Organization (FAO) suggested that rice consumption in West Africa will remain high with a continuous increase of about 4.5 % through the year 2014 and beyond (OECD/FAO, 2016). In 2012, world production of rice was 661 million tons from 155.7 million ha (PWC, 2017). Of these total, Asian farmers produced about 600 million tons, which represents more than 90 % of global rice production. India and China together accounted for 341 million tons, with India producing 148 million.

In Africa, rice accounts for 24 % of food intake by households which represents just 6 % (9.4 million ha) of the world rice-growing area (156.7 million ha) (USAID, 2017), and only 3.2 % with respect to world production (22.7 of 710 million metric tonnes). FAO (2016) estimated that, by 2025, sub-Saharan Africa (SSA) rice production (17.2 million metric tonnes annually) would be about 22.23 million metric tonnes while the estimates of future increase in world demand for the same period would be 75 %. This suggests that SSA needs to increase rice production from the current 17.2 to almost 38.2 million metric tonnes in fifteen years (FAO, 2022).

In West Africa, rice consumption keeps increasing at an annual rate of 4.5 % even as more than seventeen (17.2) million tonnes of milled rice is consumed annually (FAO, 2022). This phenomenon has led West African countries to resort to imports to meet 40% of their rice demand and have spent at least US$ 2 billion per year on rice purchase over the last five years, with a record of US$ 3.6 billion in 2008 (Diagne *et al.*, 2010). In 2006, Africa accounted for about 30% of world rice imports for only 14% of the world's population (FAO, 2016). Of all the food items, rice is the most widely consumed in Nigeria (Food Guide, 2022). The crop is commonly consumed even as a food crop for household food security. An average Nigerian consumes 24.8 kg of rice per year, representing 9% of annual calorie intake (Bamidele *et al*., 2010). About 3 billion people eat rice everyday with Nigerians consuming 4.5 million metric tons (CBN, 2016). Though per capita consumption in Nigeria has increased, it still lags behind compared to the rest of West African sub region at 34 kg per capita (Bamidele *et al*., 2010).

Rice is cultivated under diverse ecologies, ranging from irrigated, rain fed upland, rain fed lowland to deep water. Irrigated rice accounts for 55 % of world area and about 75 % of total rice production. Rain fed lowland represents about 25 % of total rice area, accounting for 17 % of world rice production while upland rice covers 13 % of the world rice area and accounts for 4 % of global rice production. Deepwater rice, although it has less area (90,000 km^2), provides food for 100 million people (Bashir *et al.*, 2018).

The rain fed lowland agriculture system which is typical to sub-Saharan Africa and most developing countries depends entirely on rainfall which is sometimes unpredictable. During the rainy season, the high incidence of rainfall can sometimes lead to floods (Goyol and Pathirage, 2018). These flooding incidences have been projected to be on the increase as a result of climate change (Oladosu *et al.*, 2020). Flooding imposes severe pressure on plants, principally because excess water in the plant surroundings can deprive them of certain basic needs, notably oxygen, carbon dioxide and light for photosynthesis (Sakagami *et al.,* 2020). More than 16 million hectares of rice land in the world is lowland and deep-water rice areas and are unfavorably affected by flooding due to complete submergence, causing an annual economic loss of more than US$600 million (World Bank Group, 2017). About 70% of the rain-fed lowland rice farms in Nigeria are prone to seasonal flooding, making submergence a critical breeding objective in Nigeria (Akinwale *et al.*, 2015).

In 2006 the gene *SUB-1A*, derived from an India rice variety grown in Orissa, was isolated and the genetic code controlling submergence tolerance was identified (Oladosu *et al.*, 2020). This has led to significant progress in the breeding of submergence tolerant rice varieties across the globe; however, this progress is limited in Nigeria and Africa (Oladosu *et al.*, 2020). Based on this background, the need to assess the possibility of developing desirable submergence varieties for Nigerian farmers cannot be overstressed.

1.2 Statement of the research problem

Rainfed lowland rice production, occupying more than 70 % of total rice area in Nigeria, is prone to recurrent flooding caused by heavy rainfall or overflow of nearby rivers. This often leads to yield losses which may range from 10 % to total crop loss (Bashir *et al.,* 2018). In 2012, when Nigeria experienced the worst flooding in 40 years, floods reduced rice production by about 22 % (UNDRR, 2017). Flooding is expected to be increasingly problematic under global warming, as studies by AfricaRice on future rice climates projected massive increases in overall precipitation in north and northwest Nigeria (Africa Rice, 2017). Most of the already released rice varieties in Nigeria can get severely damaged or killed within a week of severe flooding except for FARO 66 and 67 whose post release survey revealed that farmers did not like the breeding background.

Depending on the intensity of flooding, it can reduce yield or prolong the growth duration and in extreme cases, it can cause total crop loss and the only possible solution to tackle this problem is the use of flood-tolerant varieties (Africa Rice, 2017). The available flood-tolerant rice varieties (FARO 66 and 67) in Nigeria are less adopted by Nigerian farmers due to low yield, less extent (< 10 days) of tolerance and grain quality (NCRI, 2020). The parental lines (FARO 52 and 60) used to develop the varieties contributed to the adoption rate as they are not major farmers' varieties. The survey conducted in 2020 by NCRI revealed the extent of farmers' request for a submergence variety with characteristic features of the FARO 44 and FARO 57 (Most Preferred commercial Rice Varieties in Nigeria). Improving the ability of the two rice plants to survive under flooding conditions by studying the genetics involved in the mechanism remain a major constraint for sustainable local rice production in unstable environments undergoing climate change (NCRI, 2017). Previous studies have reported successful development of submergence tolerant varieties by introgressing the *Sub1* locus (Bashir *et al.*, 2018; Kuanar *et al.*, 2019; Oladosu *et al.*, 2020). However, in all the studies, background parentages have showed a significant influence on the nature of the progenies and their characteristic features. Thus, it is important to develop more submergence tolerant varieties using major farmers' cultivars as a parent.

1.3 Justification of the study

Attaining self-sufficiency in rice production is an important goal of many African countries, including Nigeria. Studies on flood-tolerant varieties can contribute to achieving this goal by boosting rice production and helping reduce dependence on costly rice imports. Providing farmers with protection against short-term flooding can serve as a type of 'insurance policy' for their rice, making them feel reassured to invest in agriculture, leading to higher rice yields (AfricaRice, 2017). While proffering solution to farmers' problems, the cognizance of adoption of the technology should not be under rated. However, SUB1 gene technology for submergence has revealed significant tolerance to short-term submergence, referred to as flash flooding which lasts for a few days or weeks. However, introgression of the technology into rice varieties has a parental influence due to genetic differences. Therefore, it is important to assess the inheritance of the SUB 1 genes in some of local varieties to ensure possible selection procedures to develop a farmers' acceptable flood-tolerant rice variety. Based on this background, the importance of the present study cannot be overemphasized in the face of the present rice production status in Nigeria and the lingering climate change. The study is expected to generate useful segregating populations and provide genetic information on successful selection programme to develop a flood-tolerant rice variety with characteristic features of the mega rice varieties in Nigeria.

1.4 Aim and objectives of the study

The aim of this research is to evaluate the genetics of *O. sativa* lowland rice for submergence tolerance in Nigeria.

The objectives of the study were to:

(i) Introgress submergence tolerant gene (*SUB-1* gene) into two major commercial rice varieties (FARO 44 and FARO 57) in Nigeria

(ii) Assess the performance of the progenies of the two crosses under normal and submergence conditions.

(iii) Determine the inheritance of the *SUB-1* gene by survival ratio, using *Mendelian* inheritance.

(iv) Determine the nature of gene actions for some important agronomic traits of the crosses, using generation mean analysis.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and domestication of rice

The two cultivated species of rice evolved from a pool of wild *Oryza* species (Hamzelou *et al.*, 2020). Tropical and subtropical Asia is said to be the home for the domestication of rice, but the center of its origination has been a matter of contention. Its sporadic but simultaneous domestication in various center's extends from the plains below the eastern foothills of the Himalayas, through upper Burma, northern Thailand, Laos, and northern Vietnam to southwest and west China (Wang *et al.*, 2022).

The effects of the domestication of rice are better understood when cultivars are compared to their wild relatives (Hamzelou *et al.*, 2020). Wild rice propagates independently of humans, while cultivated rice is much more dependent on human interventions (Izawa, 2008). This dependence has come about through selection against survival traits such as seed shattering, dormancy and ratooning (Wang *et al.*, 2022). However, the changes in the morphology of rice flowers has diminished the effect and rates of outcrossing over time. Wild rice varieties often have longer, exerted (protruding) stigmas that are more exposed to pollen from nearby plants than those of cultivars, which tend to remain at least partially within the hull and are more protected from non-self-pollen. In some species, the anthers are also shorter and overhang the stigma, and pollen is released shortly after the florets open. Pollen of wild plants are released later, from longer anthers (Izawa, 2008). Wild rice is also known to show resistance to common pests and diseases of cultivated rice, making it valuable for use in breeding programmes (Hamzelou *et al.*, 2020).

It is believed that both cultivated species (*O.glaberrima* and *O. sativa*) may have evolved from an unknown common ancestor following a sequence from wild perennial, wild annual to cultivated annual ancestors (Hamzelou *et al.,* 2020). However, research has suggested that the progenitors of *O. sativa* are *O. rufipogon* and *O. nivara,* which are perennial and annual, respectively (Sandamal *et al.,* 2018). Within the cultivars that have been developed, there is a range of forms bearing more or less similarity to the wild progenitors. *O. barthii* and *O. longistaminata* are thought to be the progenitors of the African cultivated rice, *O. glaberrima* (Choi *et al.,* 2019). *O. barthii* is restricted to West Africa but *O. longistaminata* is widely distributed in most parts of Africa, except for the northern part of the continent (Choi *et al.,* 2019). *O. sativa* is the most widely grown of the two cultivated species. It is grown worldwide; in Asian, North and South American, European Union, Middle Eastern and African countries. *O. glaberrima* however, is grown solely in West African countries. *O. sativa* and *glaberrima-sativa* hybrids are replacing *O. glaberrima* in many parts of Africa due to higher yields (Sikirou *et al.*, 2018).

2.2 Taxonomy of rice

Oryza sativa is of the division Angiospermae, class Monocotyledon, order Glumiflorae, family Poaceae and genus *Oryza*. While the genus *Oryza* has 20 species or more, only the two of these are cultivated species. All species within the *Oryza sativa* complex have 2n=24 chromosomes and AA genome with 12 chromosomes (Reuscher *et al.*, 2018; Ma *et al.*, 2019).

Garris *et al*., (2004) established that *Oryza officinalis* is the largest complex in the genus and includes 10 species out of which five species are diploid (2n=24), four tetraploid (2n=48) and one (*O. punctata*) which has both diploid and autotetraploid ecotypes. The species of this complex they reported, are found in Asia, Africa and Latin America. The rest are wild species, which grow naturally in marshes, swamps and semi-shady land in thin woods in Southeast Asia, Australia, Africa, South and Central America (Sandamal *et al.*, 2018)

2.3 Morphology and development of the rice plant

Singh *et al*. (2009) and Page *et al.* (2023) described cultivated rice to be semi-aquatic annual grass, forming a fibrous root system bearing erect culms and developing long flat leaves, although in the tropics it can survive as perennial, producing new tillers from nodes after harvest (Ratooning). It requires water particularly during the reproductive growth phase. It forms multiple tillers, consisting of culms and leaves with or without a panicle. The panicle usually emerges on the uppermost node of a culm, from within a flag-leaf sheath and bears the flowers and spikelets. In trying to describe the tillers, Singh *et al.* (2009) said that primary tillers emerge from nodes near the base of the main culm, and secondary and tertiary tillers emerge sequentially from these. Single leaves develop alternately on the culm, consisting of a sheath, which encloses the culm and a flat blade. The leaf forms a collar juncture between the sheath and blade and a ligule and two auricles develop on the inside of the junctura and the base of the leaf blade respectively.

Cultivars have been found to vary widely in length, width, colour and pubescence of the leaf. The panicle consists of a central rachis with up to four primary branches at each node (Adriani *et al.*, 2016). Primary and secondary branches bear the flower spikelets. Each spikelet has a single floret and two glumes. It is enclosed by a rigid keeled lemma, which is sometimes extended to form an awn and partially envelopes the smaller palea. The floret contains six stamens and a single plumose ovary with two branches. At anthesis, the two lodicules at the base of the floret swells and force the lemma and palea apart as the stamens elongate and emerge. The stigma is sometimes exposed as well. The fertilized ovary is a single seeded dry fruit with the pericarp and seed coat and fused. It is commonly referred to as grain. The grain consists of embryo, endosperm, pericarp and testa, surrounded by the husk or hull. Grain length varies with cultivars, often between 5 and 7 mm, and the grains can be bold or slender. At maturity the rice plant has a main stem and a number of tillers. Each productive tiller bears a terminal flowering head or panicle. Plant height varies by variety and environmental conditions, ranging from approximately 0.4 m to over 5 m in some floating rice (Paul, 2018). The morphology of rice is divided into the vegetative phase which includes germination, seedling, and tillering stages and the reproductive phases which include panicle initiation and heading stages (Paul, 2018).

2.3.1 Seed of the rice plant

The grain, commonly called a seed, consists of the true fruit or brown rice (caryopsis) and the hull, which encloses the brown rice (Juliano and Tuano, 2019). Brown rice consists mainly of the embryo and endosperm. The surface contains several thin layers of differentiated tissues that enclose the embryo and endosperm. The palea, lemmas, and rachilla constitute the hull of indica rice (Juliano and Tuano, 2019). It has also been reported that in *japonica* rice, the hull usually includes rudimentary glumes and a portion of the pedicel. A single grain weighs about 10-45 mg at 0% moisture content. Grain length, width, and thickness vary widely among varieties. Hull weight averages about 20% of total grain weight (Juliano and Tuano, 2019).

2.3.2 Germination of rice seed and development of the seedling

Germination and seedling development start when seed dormancy has been broken. The seed absorbs adequate water and is exposed to a temperature ranging from about 10 to 40^{o}C (Abubakar and Attanda, 2022). Bareke (2018) reported that the physiological definition of germination is usually the time when the radicle or coleoptile (embryonic shoot) emerges from the ruptured seed coat. Under aerated conditions the seminal root is the first to emerge through the coleorhiza from the embryo, and this is followed by the coleoptile. Under anaerobic rice conditions, the coleoptile is the first to emerge, with the roots developing when the coleoptile has reached the aerated regions of the environment (Shiono *et al*., 2022). If the seed develops in the dark as when seeds are sown beneath the soil surface, a short stem (Mesocotyl) develops, which lifts the crown of the plant to just below the soil surface. After the coleoptile emerges it splits and the primary leaf develops (Shiono *et al*., 2022).

2.3.3 Pollination and fertilization in rice

Oryza sativa is basically a self-pollinated crop, with limited degree of outcrossing (< 5%) (Fentie *et al*., 2021). The factors limiting the receptivity of rice flowers to outcrossing include a short style and stigma (1.5 to 4 mm in combined length), short anthers, limited pollen viability and brief period between opening of florets and release of pollen (between 30 seconds and 9 minutes) (Nadir *et al.,* 2018). Nadir *et al.* (2018) reported that when spikelet opens at flowering, pollen that shed on the protruded stigma of the same spikelet or neighboring spikelets of the same plant, results in self-pollination. The maturation of pollen in an anther is synchronized with the maturation of the ovule within the same spikelet. All wild and cultivated rice can also be wind-pollinated, with a few varieties having scented flowers that attract bees (Dafni *et al.,* 2000). The wind-assisted pollen dispersal distance has been estimated at up to 110 metres (Song *et. al.,* 2004). Greater outcrossing has been observed when honeybees are present (Gealy *et. al.,* 2003). Rice pollen is short-lived, with most pollen grains losing viability after approximately five minutes under typical environmental conditions (Nadir *et al.,* 2018).

Hu *et al.* (2021) reported that the morphology of rice pollen grain also changes dramatically after it has been shed from the anther. Initially, grains are spherical but within minutes they begin to collapse and this collapse of the pollen grains coincide with a measured loss of viability. Viability of the pollen grains which was found to be 90% up to four minutes after shedding decreased to about 33% by five and eight minutes after shedding. However, ovules are viable for several days after maturation. Fertilization is completed within six hours of the pollination. Only one pollen tube reaches an ovule to initiate double fertilization. During fertilization rice is most sensitive to cold temperatures (Juliano and Tuano, 2019).

2.3.4 Asexual reproduction

Although *O. sativa* is cultivated annually, the rice plants can grow vegetative and continuously under favorable water and temperature conditions, even after they have borne seeds (Alam *et al*., 2020). This perennial character in *O. sativa* is considered to have been inherited from the *O. rufipogon*. Under natural conditions, tiller buds on the basal nodes of rice plants start to re-grow after rice grains have been harvested. These new tillers, called ratoons, grow best under long day conditions and are used in some countries to obtain second harvest (Page *et al*., 2023). Cell/tissue culture techniques can be used to propagate calli and reproduce tissues or plants asexually under the appropriate cultural conditions (Ferreres *et al*., 2019). Haploid plants can be easily obtained through anther culture and they become diploid spontaneously or when artificially treated with colchicine (Ferreres *et al*., 2019; Seeja and Sreekumar, 2020).

2.3.5 Methods of reproductive isolation

The commonly used method of reproductive isolation for rice is spatial isolation (Nadir *et al.*, 2018). Isolation distance of about 3 meters has been recommended for seed production by many national agencies. However, for conducting the trials of genetically modified rice, a wider isolation distance recommended for reproductive isolation (Abbas, 2018). A buffering isolation zone wider than 110 metres is required to prevent gene flow (Giraldo *et al*., 2019; Mi *et al.,* 2020).

2.3.6 Tillering in rice

Each stem of rice is made up of a series of nodes and internodes. The internodes vary in length depending on variety and environmental conditions, but generally increase from the lower to upper part of the stem. Each upper node bears a leaf and a bud, which can grow into a tiller (Pawar *et al*., 2016). The number of nodes varies from 13 to 16 with only the upper 4 or 5 separated by long internodes. The International Rice Research Institute described the tillering behavior of rice under rapid increases in water level by revealing that some deep-water rice varieties can also increase the lower internode lengths by over 30 cm each.

The leaf blade is attached at the node by the leaf sheath, which encircles the stem. Where the leaf blade and the leaf sheath meet is a pair of claws like appendage, known as auricle, which encircles the stem. Coarse hairs cover the surface of the auricle. Immediately above the auricle is a thin, upright membrane called the ligule (IRRI, 2013). Paul (2018) opined that tillering usually begins with the emergence of the first tiller when seedlings have five leaves. This first tiller develops between the main stem and the second leaf from the base of the plant. Subsequently when the 6th leaf emerges the second tiller develops between the main stem and the 3rd leaf from the base. Tillers growing from the main stem are called primary tillers. These may generate secondary tillers, which may in turn generate tertiary tillers (Paul, 2018). Varieties and races of rice differ in tillering ability. Numerous environmental factors also affect tillering including spacing, light, nutrient supply, and cultural practices (IRRI, 2013; Paul, 2018).

2.3.7 Panicle and spikelets of the rice plant

The major structures of the rice panicle are the base, axis, primary and secondary branches, pedicel, rudimentary glumes, and the spikelets (Li *et al*., 2021). The panicle axis extends from the panicle base to the apex; it has 8 - 10 nodes at 2 to 4-cm intervals from which primary branches develop.

Secondary branches develop from the primary branches. Pedicels develop from the nodes of the primary and secondary branches; the spikelets are positioned above them. Since rice has only one fully developed floret (flower) per spikelet, these terms are often used interchangeably. The flower is enclosed in the lemma and palea, which may be either awned or awnless. The flower consists of the pistil and stamens, and the components of the pistil are the stigma, style, and ovary (IRRI, 2013; Li *et al*., 2021).

2.3.8 Roots growth in rice

Roots that develop from nodes above the soil surface usually are referred to as nodal roots. Nodal roots are often found in rice cultivars growing at water depths of about 80 cm from the nodal points to the soil (IRRI, 2013). Qu *et al.* (2008) reported a maximum depth of 1 m or deeper in soft upland soils and flooded soils, however, rice roots seldom exceed a depth of 40 cm. This is largely a consequence of limited O_2 diffusion through the gas spaces of roots (aerenchyma) to supply the growing root tips (Qu *et al.*, 2008).

2.3.9 Life cycle of the rice plant

The life cycle of the rice plant is 3-5 months, depending on the variety and the environment under which it is grown. During this time, rice completes two distinct growth phases: vegetative and reproductive. The vegetative phase is subdivided into germination, early seedling growth, and tillering; the reproductive phase is subdivided into the time before and after heading, i.e. panicle exertion. The time after heading is better known as the ripening period. Potential grain yield is primarily determined before heading. Ultimate yield, which is based on the amount of starch that fills the spikelets, is largely determined after heading. Hence, agronomically it is convenient to regard the life history of rice in terms of three growth phases: vegetative, reproductive, and ripening. A 120-day variety, when planted in a tropical environment, has about 60 days vegetative phase, 30 days reproductive phase, and 30 days ripening phase (NCRI, 2019).

2.3.10 Vegetative phase in rice

The vegetative phase is characterized by active tillering, gradual increase in plant height, and leaf emergence at regular intervals. Tillers that do not bear panicles are referred to as ineffective tillers. The number of ineffective tillers is a closely examined trait in plant breeding since it is undesirable in irrigated varieties (NCRI, 2019).

2.3.11 Reproductive phase in ice

The reproductive growth phase is characterized by culm elongation (which increases plant height), decline in tiller number, emergence of the flag leaf (the last leaf), booting, heading, and flowering of the spikelets. Panicle initiation is about 25 days before heading when the panicle has grown to about 1 mm long and can be recognized visually or under magnification following stem dissection (Siddiq and Viraktamath, 2001; Li *et al.,* 2021).

Spikelet anthesis (or flowering) begins with panicle exsertion (heading), or on the following day. Consequently, heading is considered a synonym for anthesis in rice. It takes 10-14 days for a rice crop to complete heading because there is variation in panicle exsertion among tillers of the same plant and among plants in the same field. Agronomically, heading is usually defined as the time when 50% of the panicles have exerted (Siddiq and Viraktamath, 2001; Li *et al.*, 2021).

Anthesis normally occurs between 1000 and 1300 hours in tropical environments and fertilization is completed within 6 hours. Only very few spikelets show anthesis in the afternoon, usually when the temperature is conducive for anthesis. Within the same panicle it takes 7-10 days for all the spikelets to complete anthesis. Ripening follows fertilization, and may be subdivided into milky, dough, yellow-ripe, and maturity stages. These terms are primarily based on the texture and color of the growing grains. The length of ripening varies among varieties from about 15 to 40 days after transplanting (IRRI, 2013; Hu *et al.*, 2021; Li *et al.*, 2021).

2.4 Rice production ecosystems in Africa

The potential arable land in Africa is 637 million hectares, and about 68 percent of the total area is in reserves (Bjornlunda *et al*., 2020). Africa has great potential for expanding its agricultural production in general, and rice production in particular (Bjornlunda *et al*., 2020). He also reported that plasticity allows rice to grow in almost any biophysical environment. Thus, making rice to be grown in a whole range of agro-ecological zones, from the humid forest to the Sahel. Within these agro-ecological zones, five main rice-based systems can be distinguished with respect to water supply and topography in West Africa (Oosterbaan *et al.*, 2017; Mi *et al.*, 2020; Duvallet *et al.*, 2021).

West African rice ecosystems are conventionally classified as rainfed-upland, rainfed-lowland, irrigated, mangrove swamp and deep-water systems. The total area under rice cultivation in west Africa is about 4.4 million hectares (ha), with the rainfed upland and rainfed lowland ecosystems each accounting for about 1.7 m ha and irrigated rice for another 0.5 m ha (Duvallet *et al.,* 2021). In Nigeria, rice production is classically classified the same way it exists within the west African region. In 2021, total area cultivated to rice was about 3.7 million hectares representing 47% of total west African production and 10.6% of total arable land area of 70 million hectares in Nigeria. Out of the 3.7 million hectares under rice cultivation, 77% is rain-fed. (NCRI, 2021)

2.5 Principal constraints to lowland rice cultivation in Africa

Rice yields in Africa are affected by a large number of abiotic and biotic stresses (Mogga *et al.*, 2019). The area of lowland is limited in comparison to the upland, but the yield potential is much higher in the lowland, due to water availability and an opportunity to grow more than one crop cycle per year (NCRI, 2019). However, land use intensification can result in pest and disease build-up, degradation of the resource base and sometimes abandonment of sites. The research strategy to increase and sustain future rice productivity will have to do with rising yield potential of irrigated rice, incorporation of durable resistance to disease and insects and tolerance to abiotic stresses and finally increase of productivity in less favourable production environments (Fahad *et al.*, 2019). The principal constraints to rice cultivation in Africa can be categorized into biotic and abiotic constraints.

2.5.1 Flooding and submergence

Complete submergence is a common natural disaster that damages rice production in many rice growing areas throughout the world. Africa is prone to flooding and this problem is becoming progressively more serious with climate change (Futakuchi, 2005; Fahad *et al.*, 2019; United Nations, 2020). Flooding of agricultural fields results in crop submergence. This can occur at any stage of crop development and in all rice production systems, including the irrigated lowlands at the seedling stage because of poor water management. In the flood plains, sudden floods can submerge the rice crop and waterlogging can persist during the life cycle of the crop. In savanna and forest zones in West and Central Africa, inland valleys prevail and rice in valley bottoms may experience waterlogging for several days after excessive rainfall. Water has slower rates of gas exchange, less capacity to hold gases such as oxygen and CO_2, and a higher extinction coefficient for light than air. In addition, flood water is usually turbid, severely limiting the penetration of light required for photosynthesis. Under complete submergence, therefore, photosynthesis and respiration of rice plants are suppressed (Futakuchi, 2005; Hattori, *et al.*, 2009; Sakagami *et al.*, 2020) leading to low concentrations of carbohydrates, reduced growth and finally death of tissues (Sakagami *et al.*, 2020).

One of the most serious long-term challenges to achieve sustainable growth in rice production is climate change (Fahad *et al.*, 2019; Sakagami *et al.*, 2020). By 2100, the mean surface temperature of the Earth is expected to rise by 1.4 to 5.8ºC and extreme events, such as floods, droughts, and cyclones, are likely to become more frequent (IPCC, 2007; Ighedosa, 2022). In delta/coastal regions, climate change is expected to raise sea levels, and this will increase the risk of flooding and salinity problems in major rice-growing areas (Wassmann *et al.,* 2004; Ighedosa, 2022). Droughts and floods already cause widespread rice yield losses across the globe (Mishra *et al*, 2019; Mukamuhirwa *et al*., 2020; Mohapatra *et al.*, 2021). The research strategy to increase and sustain future rice productivity will have to be to raise yield potential of irrigated rice, incorporate durable resistance to disease and insects, tolerance to abiotic stress and increased productivity in less favourable production environments (Kuanar *et al.*, 2017; Dar *et al.*, 2021). Flooding is a serious constraint to rice plant growth and survival in rainfed lowland and deepwater areas (Kuanar *et al.*, 2017; Panda and Barik, 2021). Recently, the extent of submergence stress has increased due to extreme weather events including unpredicted heavy rains that have flooded wider areas across many states of the country. Among the most frequently and severely affected states in Nigeria are Kebbi, Niger, Kogi and Taraba states which together accounts for over 80 % of lowland rice ecology in Nigeria (Erenstein *et al.,* 2003; Omoare and Oyediran, 2020).

2.6 Physiology of submergence tolerance in rice

Submergence of plants inhibits aerobic respiration and photosynthesis and stimulates a variety of responses that can enhance survival, such as a switch from aerobic to anaerobic respiration (Fukao and Bailey-Serres, 2004; Yuan *et al*., 2020). Plant submergence restricts the diffusion of oxygen by 104-folds and this has a dramatic impact on biochemical activities such as aerobic respiration and photosynthesis (Nakamura and Noguchi, 2020; Sun *et al*., 2020). Environmental characterization of flood water causing complete submergence in South and Southeast Asia shows that this is a complex environment which may need different strategies for optimizing different plant types. One very important factor in all locations is gas diffusion (Sun *et al*., 2020).

In all locations where complete submergence occurs, gas diffusion is 10,000-folds less in the water than in air (Colmer *et al.*, 2011). In most environments, flood water oxygen concentrations during flash floods are usually below saturation. In some, oxygen is completely absent (anoxia) particularly during the night but may even become supersaturated during the day (Setter *et al*., 1997; Joehnk *et al*., 2020). Anoxia for 24hours can result in death of many plants including intolerant rice cultivars like IR8 (Leonardo *et al.*, 2009), probably because the absence of oxygen stops respiration and reduces energy production for survival or elongation growth processes (Nakamura and Noguchi, 2020). Deep-water rice avoids submergence stress by growing above the water surface thereby restoring gas exchange. Submergence-tolerant rice however can survive 10-14 days of complete submergence and renew growth when water level subsides (Hattori, 2011; Panda and Barik, 2021).

The duration of survival however depends on the character of flood water such as water turbidity, temperature, O_2 diffusion, CO_2 concentration and light penetration (Panda and Barik, 2021). Limited CO_2 supply is a common characteristic of flood-prone environment. During turbulent flash floods the flood water tends to be at equilibrium with the CO_2 partial pressure in air due to rapid mixing. However, once the water level stabilizes, the flood water may become stagnant resulting in low CO_2 supply due to large boundary layer effects (Kuanar *et al.*, 2017; Sakagami *et al.*, 2020). Rice has adapted to flood-prone environments by either submergence tolerance or elongation ability (Nakamura and Noguchi, 2020). These two responses are usually associated with different water regimes. Submergence tolerance is required in rainfed areas where flash flooding results in rapid rise in water level and submergence occurs for up to about 14 days. Elongation under such condition is a disadvantage because it results to lodging once water level recedes. In contrast leaf and internode elongation is appropriate for deepwater and floating rice areas (>100cm water) where water remains at these depths for several months. Submergence tolerance is aimed at reducing yield lose in rain fed lowland and deepwater rice areas, but this has enjoyed limited success in Africa (Oteyami *et al.,* 2018). Systematic screening of rice germplasm in Asia has shown that there are excellent flood-tolerant rice genotypes locally available. Among these are FR13A and FR43B of India, Kurkaruppan of Sri Lanka and Goda-Heenati of Indonesia. It is from these local genotypes that flood-tolerant rice types were developed. Some of the newly developed lines include Swarna-Sub1, Swarna Mahsuri-Sub1, TDK1-Sub1 and BR11-Sub1 (Singh *et al.*, 2009; Weerasinghe *et al*., 2022).

2.7 Genetics of submergence tolerance in rice

Submergence tolerance is controlled by a single major quantitative trait locus (QTL) on chromosome 9, along with a number of minor QTLs (Toojinda *et al.*, 2003; Oladosu *et al*., 2020). Most studies used the landrace FR13A, which is one of the most submergence-tolerant donor varieties. The major QTL, named *Sub1*, with a LOD score of 36 and an R_2 value of 69%, provide tolerance to complete submergence for up to 2 weeks (Solis *et al.*, 2017). The Sub1 locus was mapped to an interval of 0.06 centimorgans on chromosome 9 using a mapping population of 4022 plants developed from the hybridization of a tolerant Indica derivative of FR13A and an intolerant japonica cultivar M-202. (Kumar *et al*., 2020; and Ma *et al*., 2019)

The region physically spans over 182 kilobases (kb) and encodes three genes containing ethylene-response-factor (ERF) and is designated Sub1a, Sub1B and Sub1C, ten non- ERF genes, including four transcribed and six hypothetical protein-coding genes, and >50% retrotransposon related sequences (Trijatmiko and Pereira, 2013). The fine mapping of *Sub1* employing 2950 F_2 segregating individuals indicated that it occupies a genomic region of approximately 0.06 centimorgans (cM). Sequencing the Sub1 region in an FR13A-derived line revealed the presence of three genes encoding putative ethylene responsive factors (ERF); *Sub1A*, *Sub1B* and *Sub1C* were subsequently identified (Xu and Mackill, 2006; Solis *et al.*, 2017).

It was also observed that *Sub1C* alleles were associated with tolerance; however, it was not known if the tolerant *Sub1C* allele had any effect on the level of tolerance. The ethylene response factors genes *snorkel 1* (*SK1*) and *snorkel 2* (*SK2*) allow rice to adapt to deep water whereas *submergence 1A-1* (*sub1A-1*) allows rice to acclimatize under flash flooding (Nagai *et al.*, 2022). Both SKs genes and *Sub1A-1* are connected with gibberellins biosynthesis or signal transduction, yet deepwater and submergence-tolerant rice seem to have opposite flooding response; namely, escape by elongation or remain stunted under water until flood recedes (Xu and Mackill, 2006; Bailey-Serres and Voesenek, 2010; Xiang *et al*., 2017; Wang and Komatsu, 2022).

Genetics research has demonstrated that for 15 to 50 days-old seedlings there is one major dominant gene involved in inheritance of submergence tolerance from FR13A and Kurkaruppan, this was shown by analysis of segregating populations and backcrossing populations produced by crossing submergence tolerant with intolerant cultivars were tested along with the parents for submergence tolerance in greenhouse concrete tanks and field ponds (Emerick and Pamela, 2019). The results obtained were consistent with the hypothesis that submergence tolerance is governed by one dominant gene which has a high probability of 3:1 in segregating F_2 (Akinwale *et al*., 2015; Oladosu *et al*., 2020). Previous studies have reported the development of submergence tolerant varieties by introgressing the *Sub1* locus (Kuanar *et al.,* 2019; Oladosu *et al*., 2020). More recently this gene has been successfully introgressed through marker-assisted backcrossing (MAB) into a popular high-yielding variety from India, Swarna, within a 2-years' time frame (Hasan *et al.,* 2015; Kumar *et al*., 2020). Swarna-Sub1 has been evaluated in submergence-prone areas of India and Bangladesh (Das *et al.*, 2022). Under non-submerged control conditions, no significant differences in agronomic performance, grain yield and grain quality between Swarna and Swarna-Sub1 were observed indicating complete restoration of the Swarna background in Swarna-Sub1 (Dar *et al.*, 2018; Mohapatra *et al.,* 2021), but Swarna-Sub1 showed a 2-fold or higher yield advantage over Swarna after submergence for 10 days or more during the vegetative stage (Das *et al.,* 2022). These results highlighted the opportunity to develop additional high-yielding varieties that are adapted to other regions or environments (Dar *et al.,* 2018). In addition, hybrid rice has been viewed as a promising approach that can be used as a vehicle to boost rice production. In recent years, there has been increasing interest to grow hybrid rice in several countries, and the potential use of Sub1 in hybrid rice has great promise for flood-prone areas.

Introgression of *Sub1* QTL into 'Swarna' greatly enhanced its survival under submergence, and plant productivity under flash flood conditions (Kuanar *et al.,* 2019; Kumar *et al.,* 2021). A wide-ranging on farm and on station trials showed that under normal conditions both cultivars have similar grain yield potential whereas under complete submergence (submergence period varied between 3 and 14 days in different locations), a yield of 1.65 t / ha (an average of 0.81 t / ha over five locations) were obtained from Swarna-Sub1 compared to Swarna (Sarkar and Bhattacharjee, 2011; Sarkar *et al.*, 2014; Dar *et al.*, 2018).

Subsequently several submergence tolerant mega varieties namely IR64-Sub1, SambaMahsuri-Sub1, Thadokkam1-Sub1 and BR11 Sub1 were developed (Iftekharuddaula *et al.*, 2011; Haider *et al.*, 2018). Swarna-Sub1 was released in India, Indonesia and Bangladesh; BR11-Sub1 was released in Bangladesh; and IR64-Sub1 was released in the Philippines and Indonesia. Breeders are now using the Sub1 locus to develop tolerant rice varieties for submergence-prone areas in Asia and Africa (Haider *et al.,* 2018; Oladosu *et al.*, 2020).

2.8 Gene effects for some important traits of rice

To establish a sound basis for any breeding programme aimed at achieving higher yield, breeders must have genetic information on the nature of combining ability of the parents, their behaviour and performance in the hybrid combination (Liu *et al.*, 2021). The knowledge of combining ability is essential for selection of suitable parents for hybridization and identification of promising hybrids for future exploitation in a breeding programme (Fasahat *et al.*, 2016). The concepts of general and specific combining ability were introduced by Sprague and Tatum (1942). General combining ability (GCA) is the average performance of a line in hybrid combination and specific combining ability (SCA) is the deviation of crosses on the basis of average performance of the lines involved. General combining ability is associated with additive genetic effects while specific combining ability is associated with non-additive genetic effects (Begna, 2021; Gunasekaran *et al.*, 2023).

Several studies on combining ability indicated that GCA is more important than SCA, although specific effects are of sufficient importance to merit attention in breeding programmes (Guo *et al*., 2018; Nyaga *et al.*, 2020). Combining ability for quantitative characters in rice, include days to heading, plant height, panicle length, number of panicles per plant, number of productive tillers, number of spikelets per panicle, 1000- grain weight and grain yield were reported by Xie *et al*. (2019); Zhong *et al.* (2021) and Gunasekaran *et al.* (2023). The values of variance of GCA, SCA, and their ratio (GCA: SCA) indicated the preponderance of non-additive type of gene actions for most of all the traits. Zewdu (2020) and Suvi *et al*. (2021) investigated the nature of gene action for rice grain and yield components through line × tester analysis and non-additive gene action was implicated for plant height, tillers per hill, filled grains per panicle, 100-grain weight, and grain yield but additive gene action for days to 50% flowering and panicle length. Ganapati *et al*. (2020) estimated the gene effects for yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh and reported vital role of additive and non-additive gene actions in the expression of the traits studied. Kargbo *et al*. (2019) Variances of Specific Combining Ability (SCA) higher magnitude than the corresponding General Combining Ability (GCA) for all 15 rice traits studied with the except panicle length and a number of effective tillers per plant which showed higher effects of General Combining Ability (GCA).

The additive genetic variance was greater than non-additive genetic variance for days to heading, plant height, panicle length, number of panicles per plant, spikelet sterility, number of spikelets per panicle, harvest index and 1000-grain weight except for grain yield in F_1 and F_2 generations (Tomitaa *et al*., 2021; Awad-Allah *et al*., 2022; Denis *et al*., 2022). In a combining ability study for yield and yield components of rice, Rahman *et al.* (2022) estimated predominance GCA effects than SCA effects for all traits assessed. Significant role of additive gene action was observed for days to 50% flowering, plant height, panicle length, grains per panicle, yield per plant, spikelet fertility, 1000-grain weight, and harvest index (Tripathi *et al*., 2019; Faysal *et al*., 2022). General and specific combining ability variances were significant for yield per plant, harvest index, days to 50% flowering, plant height and number of productive tillers, indicating significance of both additive and non-additive gene action in the expression of these traits.

Shobhana *et al*. (2018) conducted line × tester analysis for economic traits in rice and reported predominant non-additive gene action for the traits studied, except days to 50 per cent flowering and harvest index. The GCA: SCA variance showed equal importance of both additive and non-additive gene actions for the control of ear length and 100-grain weight. Similarly, SCA variance was higher than GCA variance signifying the non-additive gene action for grain yield. Hijam *et al.* (2019) reported importance of additive and non-additive gene effects in yield and most of the yield components in F1 generation of diallel crosses in rice. Additive gene action was important for 1000-grain weight and plant height. Sharma and Mani (2005) hypothesized that the crosses involving at least one parent with good GCA effects could be attributed to additive × additive and / or additive × dominant gene interaction in sizable amount while the crosses involving average × average, poor × average and poor × poor GCA effects could be attributed to complementary type of gene interaction that might be explored in succeeding generations. In such crosses where non-additive gene effects played a dominant role in association with additive components, the recurrent and reciprocal recurrent selection could be used to exploit both components at the same time.

2.9 Heritability of important traits rice

Heritability estimates the amount of genetic variation existing in a set of genetic materials and can be used to predict the magnitude of genetic improvement that can be achieved when selection is practiced (Salihu *et al.*, 2019). Heritability estimates for agro-morphological traits in rice are sparse and contradictory, depending on the genetic materials used (Rafii *et al*., 2014). Adhikari *et al*. (2018) reported significant genetic variability for days to flowering, maturity, thousand grain weight and plant height in a study on 26 advanced genotypes of lowland irrigated rice. Heritability estimates were maximum for days to flowering, 1000-seed weight, plant height. Tripathi *et al*. (2019), in a study on genetic variability parameters in rice, indicated significant genetic differences and high to moderate heritability for 5 out of the 10 traits studied. Broad sense heritability for days to flowering, 1000-grain weight, panicle length and plant height was from 0.39 to 0.88. Similarly, high to medium level heritability for the traits were also reported by Gyawali *et al*. (2018) and Bandi *et al*. (2018). Appreciable amount of genetic variability, heritability and genetic advance was observed for panicle number, spikelet fertility and grain yield per plant (Okoye *et al*., 2021).

In a study on forty-six genotypes of rice, Rachana *et al*. (2018) observed moderate PCV and GCV for days to 50% flowering, panicle length and harvest index and also reported moderate heritability and genetic advance for panicle length and high for all the other traits viz., days to 50% flowering, plant height, number of tillers per plant, number of panicles, panicle length, panicle weight, grain number, test weight, single plant yield, plot yield, biomass and harvest index. In another investigation by Sadhana *et al.* (2022), total grain number per panicle, filled grain number per panicle, weight of 1000 grains, grain yield per plant, weight of panicle, head rice recovery, length of kernel after cooking, linear elongation ratio, length of kernel and kernel length/breadth ratio exhibited high heritability along with high genetic advance as percentage of mean. High heritability coupled with high genetic advance as per cent of mean was observed for flag leaf area, grains per panicle, panicle bearing tillers per plant, spikelet per panicle, and plant height which indicated that these traits were controlled by additive type of gene action (Singh and Verma, 2018). Tripathi *et al.* (2018) also reported high genetic advance in percent mean for flag leaf area, panicle bearing tillers per plant, spikelets per panicle, biological yield per plant in a Studies on Genetic Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.) for Yield and Its Components under Salt Affected Soil.

However, panicle length and number of primary branches per panicle recorded low heritability. Shanthi and Singh (2002) conducted an experiment on 16 F_6 generations of induced mutants along with the non-mutant Mahsuri rice. The analysis of variance indicated that genotypes considerably varied for plant height, number of tillers per plant, panicle length, number of grains per panicle, 1000-grain weight and yield per plant. Heritability in broad sense was high (more than 80%) for all the characters except for grain yield per plant (78.99%) and number of tillers per plant (63.04%). The maximum genetic advance was recorded for number of grains per panicle (107.13%). High heritability coupled with high genetic advance was observed in plant height, number of grains per panicle and 1000-grain weight.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Study Location

The experiments were carried out at the Crossing Block (Longitude N 09^o 04.921′ and Latitude E 006^o 07.206′) and the Rice Production and Research Field (N09^o 04.238′ and Latitude E 006^o 06.638′) of the National Cereals Research Institute (NCRI), Badeggi. NCRI averagely receives an annual rainfall of about 1184 mm, with temperature ranging from 25.9 to 31.1 ^{0}C and relative humidity of about 77 %.

3.2 Sources of Experimental Materials

The seeds used for the research were obtained from the National Cereals Research Institute and the rice breeding unit of Africa Rice Center, Ibadan, Nigeria. The parent materials used for the study were three *Oryza sativa* lines, of which one is a donor parent line (Swarna Sub-1) already developed as being tolerant to submergence and the two others are susceptible parents to submergence (FARO 44 and 57). These two susceptible parents are commercially released and highly adopted and cultivated across wide agroecological spread in Nigeria.

3.3 Establishment of Crossing Block and Hybridization

Two sets of crossing blocks were established at two weeks intervals to synchronize the flowering of the parents. Each of the crossing blocks was cleared and puddled with the dried weed incorporated into the soil. The blocks were levelled with help of a hand rake and then marked out. Each block consists of a 5m x 2 row plots for the donor parent and 5m x 3 row plot each for the susceptible parents. All the seeds were sown directly at a spacing of 20 cm x 20 cm. Fertilizer was applied as 15-15-15, N P K at the rate of 40 kg each of P_2O_5 and K_2O/ha at planting, plus 40 kg N/ha as urea, three weeks after planting. Hand weeding was carried at 21 and 42 days after planting. The donor parent (Swarna Sub-1) was crossed to as many susceptible plants (FARO 44 and 57) plants as possible. Matured spikelets from a selected panicle (from the susceptible parents) were incised with a pair of scissors at ¼ lengths from the top of the spikelets to expose the anthers. Forceps was used to carefully remove the anthers without destroying the stigma. Magnified glass was used to confirm that no anther was left in the spikelet. The emasculated panicle was then covered with a seed envelope. Crossing was initiated between 0630 and 0800h. Anthesis commenced between 1030h and 1200h during which time a panicle shedding pollen was gently cut and the pollen dusted on the emasculated spikelet of the female parent to effect pollination; it was then covered with 8 cm x 13 cm white seed envelopes and appropriately labelled.

3.4 Validation of the F_1 and Development of F_2 Seeds

True crosses (F_1 seeds) were pre-germinated in Petri dishes of 90 mm diameter and 15 mm depth under optimum germination condition or *in vitro*. Three-week old seedlings were transplanted and flanked with both parents to facilitate identification of selfers for discard and advance the actual F_1 plants to generate F_2 seeds. All the self-fertilized F_1 plants were uprooted from the field and the true crosses of F_1 plants were harvested as F_2 seeds, dried and kept for further studies.

The field where these activities were carried out was cleared and heaped to allow for decomposition of weeds. Two weeks old heaps were scattered and levelled with the use of rake and the F_1 with both parents, planted at the rate of one seedling per hole and in single rows of 20 cm spacing for the F_1's and double rows for the parents. Fertilizer was applied as 15-15-15 N P K at the rate of 40 kg each of N, P_2O_5 and K_2/ ha at transplanting, plus 40 kg N/ ha as urea, three weeks after transplanting Bashir *et al.* (2018). Hand weeding was carried out at 20 and 40 days after transplanting (DAT). The freshly harvested F_1 seeds were kept in the oven for five days at 52

^{o}C. The F_1 seeds were divided into two equal sizes, one sample was kept as back-up and the second sample was used to generate the F_2 seeds.

3.5 Development of Backcrosses (BC1 and BC2 Generations)

The backcross generations were developed by crossing validated (true cross) F_1 individuals to both of their parents (Swarna sub 1 and, FARO 44 or FARO 57). The field preparation and management were done as stated in 3.4.

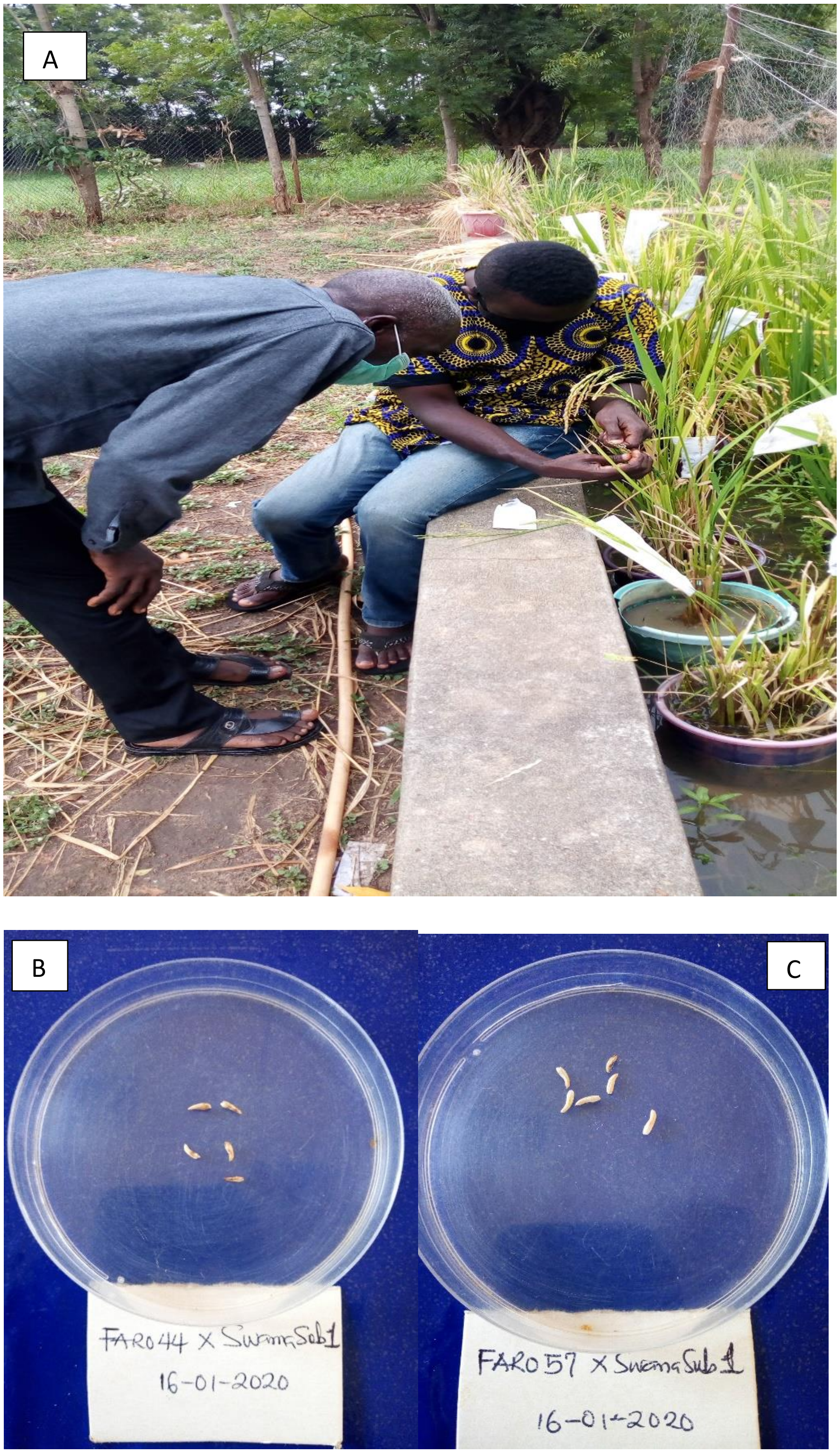

Plate I: (A): Hybridization block established at NCRI in 2019 (B): progeny of crosses FARO44 x Swarna sub1 (C): progeny of crosses FARO57 x Swarna sub1.

3.6 Screening of the Parents and their Crosses under Normal and Submergence Conditions

Six generations, namely, Parent one (P1), Parent two (P2), filial generations (F_1, F_2) and the two backcrosses (BC1, BC2) were raised in a complete randomized block design in normal and submerged condition, with three replications. Twenty-one days old seedlings were evaluated in both conditions. Recommended packages of practices were followed to raise healthy crops. Submergence screening was performed in controlled conditions that allowed flooding with water depth of 1.0 meters for a period of 14 days. The plants were de-submerged and the survival of plants was scored after 20 days of recovery according to Pamplona *et al.*, (2007). For each set of the crosses, a minimum of twenty (21) seedlings of both parents (P1 and P2), twenty-one (21) seedlings for F_1, four hundred and two (402) seedlings of F_2 and fifteen (15) seedlings each of BC1 and BC2 were evaluated.

3.7 Data Collection

i. Percentage Survival of the Test Entries = $\frac{Number\ of\ Seedling\ Survived}{Number\ of\ Seedling\ Transplanted} \times 100$

ii. Percentage Survival of the Resistant Entries = $\frac{Number\ of\ Seedling\ Survived}{Number\ of\ Seedling\ Transplanted} \times 100$

iii. Percentage Comparative Survival = $\frac{\text{\% Survival of the Test Entries}}{\text{\% Survival of the Resistant Entries}} \times 100$

{Scaling of Comparative Survival: 1 = 100%, 3 = 95-99%, 5 = 75-94%, 7 = 50-74%, 9 = 0-49% (IRRI, 2013)}

iv. Percentage Elongation = $\frac{\text{Height before submerged – height after submerged}}{\text{height before submerged}} \times 100$

v. Plant height (cm): The length from ground level to the tip of the longest panicle was measured at maturity.

vi. Number of tillers per plant: The number of tillers per plant will be counted for each genotype at maturity.

vii. Days to 50% flowering: The number of days from sowing to when half plant population in each plot are at anthesis.

viii. 100 grain weight (g): The actual measurement in grams of 100 well developed whole grains, dried to 14% moisture content was weighed on a precision balance.

ix. Panicle length (cm): The length from the base to the tip of the topmost grain of the panicle was measured at maturity.

x. Panicle number: The number of panicles per plant stand was counted.

xi. Grain width (mm): The actual measurement of width in millimeters from across the fertile lemma and the palea at the widest point was taken.

xii. Grain length (mm): The mean length in millimeters from the base of the lowermost sterile lemma to the tip (apiculus) of the fertile lemma or palea was taken.

xiii. Flag leaf width (cm): The actual measurement, in centimeters of the widest portion of the flag leaf blade was taken.

xiv. Flag leaf length (cm): The actual measurement; in centimeters of the flag leaf from the leaf base to the flag leaf tip was taken.

xv. Straw girth (mm): The actual measurement in millimeters from the outer diameter of the straw at the basal portion of the main culm was taken.

xvi. Internode length: The outer surface of the internodes on the straw is recorded.

xvii. Grain yield: The actual weight of the threshed and winnowed paddy after harvest

All data were collected as stipulated by the Standard Evaluations System - SES of the International Rice Research Institute (IRRI, 2013).

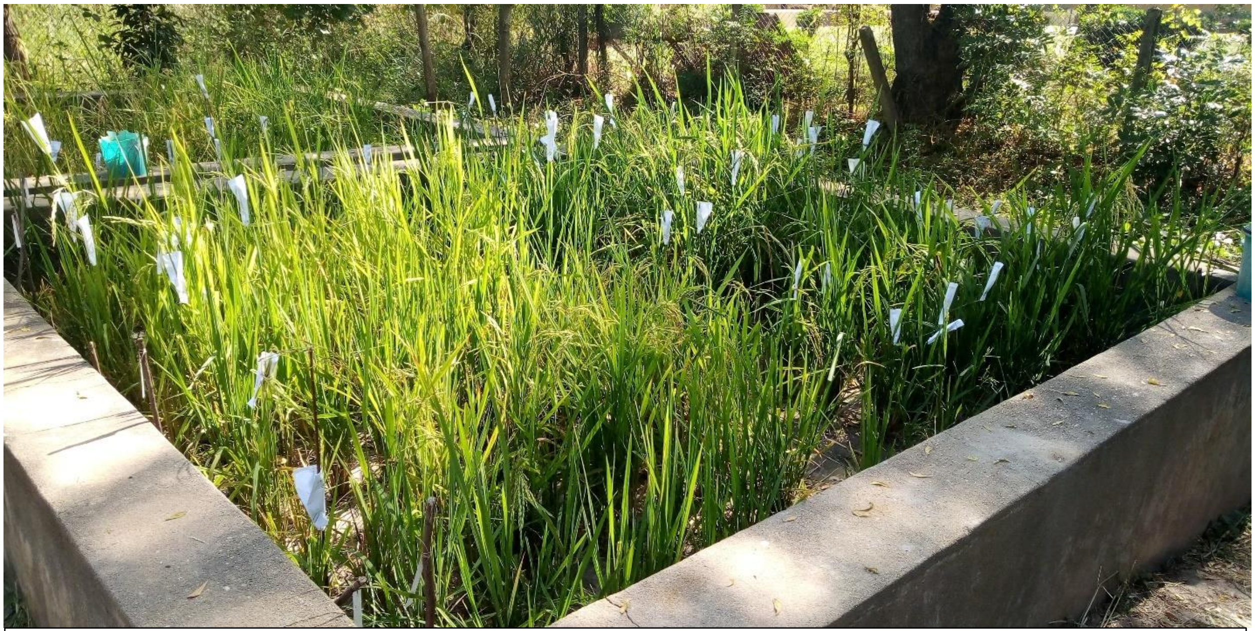

Plate II: Crossing block showing F2 and Backcrosses in 2020 wet season.

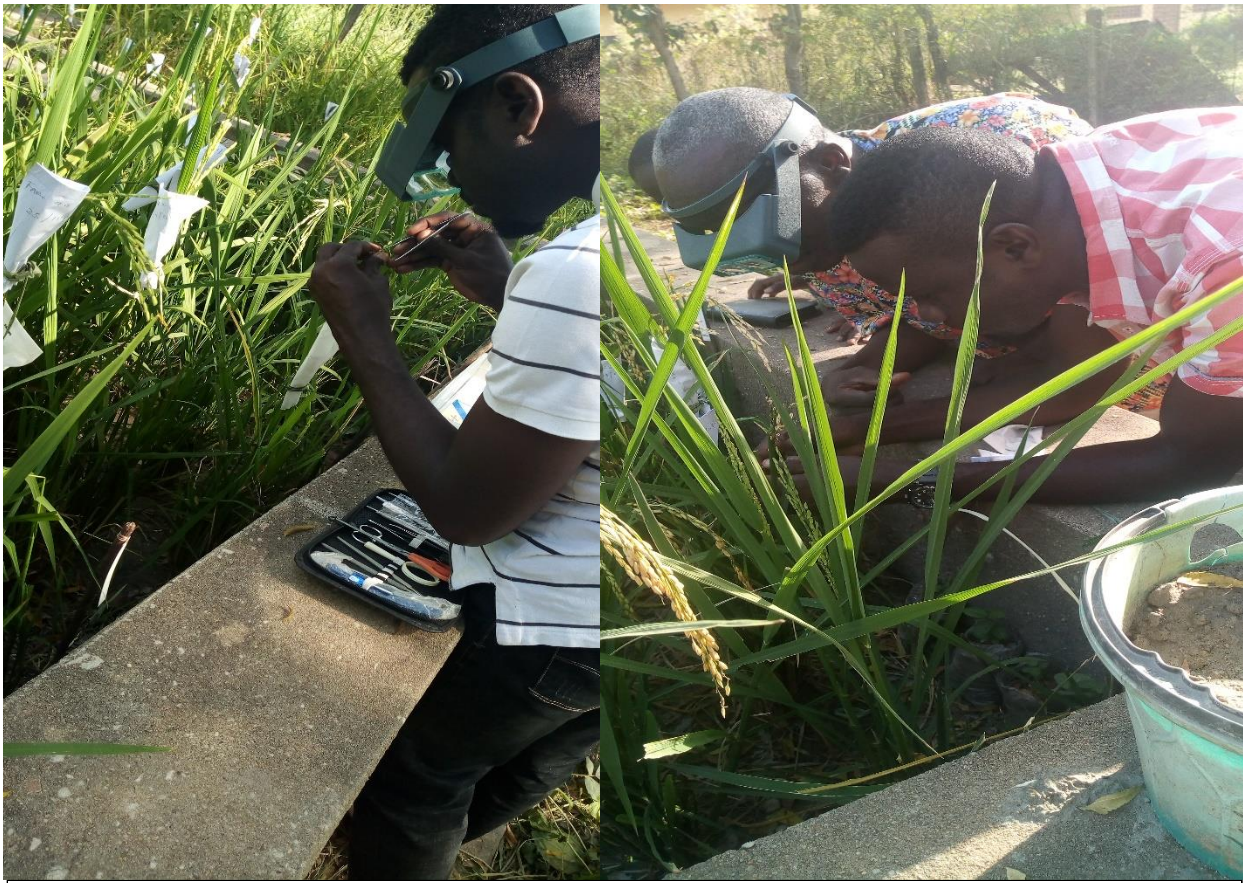

Plate III: Showing emasculation of one of the crosses and Prof. S.A. Gana Visit to Site

Source: field Photograph

3.8 Data Analysis

3.8.1 Analysis of variance

Analysis of variance (ANOVA) was performed to assess the significance among the entries across the environments (conditions). Scaled values were transformed according to Wening *et al.,* (2019).

3.8.2 Phenotypic and Genotypic Co-efficient of Variation

The formula suggested by Singh and Chaudhary (1985) was followed for the computation of Phenotypic and Genotypic Co-efficient of Variation among the generations.

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma_g{}^2}}{\overline{X}} \times 100$

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma_{ph}{}^2}}{\overline{X}} \times 100$

Where:

$\sigma_g{}^2$ = Genotypic variance

$\sigma_{ph}{}^2$ = Phenotypic variance

$\overline{X}$ = Mean

3.8.3 Mendelian Inheritance of *Sub 1 Gene*

Chi-Square for the Mendelian inheritance of submergence tolerant plants was determined as indicated below:

Chi-Square (Cal.) = $\frac{(Number\ of\ Observed\ Survived\ Plants - Number\ of\ Expected\ Survived\ Plants)^2}{Number\ of\ Expected\ Survived\ Plants} \times 100$

Chi-Square Tabulated was considered at 0.05 p-value

3.8.4 Generation Mean Analysis

A package called "TNAUSTAT General breeding procedure" was used for the generation mean analysis. The three parameters model was estimated according to Jinks and Jones (1958), the six generation parameters was according to Hayman (1958), while the perfect fit model was calculated as described by Mather and Jinks (1982).

3.8.5 Estimation of Heritability

Heritability in broad sense ($h^2{}_b$) was calculated as the ratio of genotypic variance to the phenotypic variance (Salihu *et al*., 2018).

$$h_b{}^2 = \sigma_g{}^2 \Big/ \sigma_{p_h}{}^2$$

Where;

$h_b{}^2$ = broad sense heritability estimate

$\sigma^2{}_g$ = genotypic variance

$\sigma^2{}_{p_h}$ = phenotypic variance

Narrow-sense heritability ($h^2{}_n$) estimates was calculated as the ratio of additive genetic variance to total phenotypic variance (Acquaah, 2007).

$$h^2{}_n = \sigma_a{}^2 \Big/ \sigma_{p_h}{}^2$$

Where:

$\sigma_a{}^2$ = Additive variance

$\sigma_{p_h}^{2}$ = Phenotypic variance

3.8.6 Genetic Advance

Genetic advance in next generation in response to selection was determined as described by Salihu *et al.*, (2018) as under:

$$GA = K \times \sigma p_h \times h^2$$

Where;

K = Selection intensity at 0.05 = 2.06

σp_h = Standard deviation of the phenotypic variance under selection

h^2 = Heritability in broad sense

GA = Genetic Advance

Genetic advance in term of percentage of mean = $GA/GM*100$

Where;

GM = Grand Mean (parents and hybrids)

The range of genetic advance in percentage of mean was classified as suggested by Johnson *et al.*, (1995). Low = less than 10%, moderate = 10-20% and high = more than 20%

CHAPTER FOUR

4.0 RESULTS AND DISCUSSION

4.1 Results

4.1.1 Analysis of variance

Table 4.1 presents the mean square values from the Analysis of Variance (ANOVA) for the 14 agronomic traits assessed among the six generations of the two crosses (Cross I and Cross II) across two cropping seasons. The ANOVA showed significant differences for all the traits at vegetative growth, except for the Flag Leaf width (FLW) and Stem Girth in both crosses under normal condition and G × E for the two traits in the Cross I (Table 4.1). The mean squares for all the sources of variation revealed significant differences for all the reproductive parameters (50%F, TN, PN, PL and SY) in both crosses (Table 4.1). There were significant differences for the grain physical parameters among the generations of the crosses (Table 4.1). The 100 seed weight (SW) revealed statistical difference among the generations of the two crosses under normal and submerged conditions in both evaluation years. The combined mean square revealed significant difference at 1% probability level for the SW under normal and submerged conditions in the Cross I and Cross II. No significance G×E interaction was shown for the trait in Cross I; however, this was significant in Cross II. The pooled mean square and G×E showed significant differences. The grain width (GW) among the generations of the two crosses showed significant mean squares for all sources of variation, except in the Year II and G×E for the Cross I. All sources of variations revealed significant differences for the Grain Length in the generations of the two crosses. The Comparative Survival Scores (CSS) were significant among the genotypes in both crosses for the two evaluation years.

Table 4.1: Mean Square for 14 agronomic traits of two rice crosses evaluated under normal and submergence condition over two years

	Cross I (Swarna sub1 × FARO 44)						**Cross II (Swarna sub1 × FARO 57)**							
	Normal		Submerged		Combined		Normal		Submerged		Combined		Pooled	
Traits	Year I	Year II	Year I	Year II	Genotype	G x E	Year I	Year II	Year I	Year II	Genotype	G x E	Entries	G x E
FLW	0.09^{ns}	0.13 ^{ns}	2.03**	1.66**	2.75**	0.38^{ns}	0.07^{ns}	0.09^{ns}	1.34**	1.08**	1.81**	0.26*	4.48**	0.29*
FLL	21.43*	24.50*	953.70**	787.23**	891.52**	298.44*	16.07*	17.93*	599.19**	485.28**	538.96**	193.17**	1397.34**	215.43**
SG	0.13**	0.13**	3.60**	2.98**	2.56**	1.42^{ns}	0.10**	0.10**	2.71**	2.31**	2.15**	1.02**	4.57**	1.07*
50%F	285.02**	327.57**	6944.92**	5762.07**	8471.23**	1616.11**	284.56**	329.38**	4110.21**	3342.17**	5502.37**	854.65**	13778.94**	1086.71**
TN	40.37**	42.68**	516.50**	424.85**	632.27**	130.70**	24.96**	31.12**	428.64**	345.56**	527.71**	100.86**	1147.86**	100.98**
PH	148.63*	252.97*	5814.89**	4744.96**	3873.56**	2362.62**	92.89*	173.73*	5144.30**	4148.75**	3517.93**	2013.91**	7382.91**	1876.89**
PN	50.72**	57.80**	153.38**	135.33**	301.19**	32.01**	34.43**	37.78**	130.51**	111.38**	240.89**	24.40**	538.74**	24.65**
PL	23.90*	26.12*	472.74**	392.87**	352.92**	187.56**	18.68*	19.55*	362.87**	293.06**	270.70**	141.15**	612.31**	142.50**
IL	43.52**	46.20**	181.43**	146.28**	282.31**	45.03**	33.19**	33.00**	137.43**	113.37**	221.29**	31.90**	501.00**	33.35**
GY	393.08**	527.48**	433.71**	375.69**	1276.61**	151.11**	275.10**	339.01**	303.96**	260.79**	868.53**	103.44**	2124.74**	112.01**
GW	0.64**	0.59**	4.01**	4.51**	4.17**	1.86^{ns}	0.52**	0.47**	3.84**	3.14**	3.63**	1.44**	7.78**	1.42*
GWt	0.03**	0.04^{ns}	4.02**	3.24**	3.85**	1.16^{ns}	0.01**	0.03**	3.21**	2.69**	3.00**	0.98**	6.73**	0.93*
GL	2.10**	2.18**	75.83**	63.34**	72.01**	23.81*	1.23**	1.78**	48.02**	40.74**	44.82**	15.65**	113.48**	17.39*
CSS			0.92**	1.04**	1.96**	0.00^{ns}			0.64**	1.43**	1.83**	0.23**		

Note: FLW – Flag leaf width (cm), FLL – Flag leaf length (cm), SG – steam girth (cm), 50%F- Days to 50% flowering, TN – Number of tiller, PH – Plant height (cm), PN – Number of panicles, PL – Panicle Length (cm), IL – Internode Length (cm), GY – Grain yield (g/plant), GW – Grain weight (g), GWt – Grain width (mm), GL – Grain length (mm), CSS – Comparative Survival Score, ns= not significant *,**,***= significantly different at $P \leq 0.05$, $P \leq 0.01$, $P \leq 0.001$.

4.1.2 Mean performance of six generations of two rice crosses under normal and submergence conditions

Table 4.2 presents the mean values and coefficients of variation for flag leaf width (FLW), flag leaf length (FLL) and straw girth (SG) among the six generations of the two rice crosses (Cross I and Cross II) evaluated under normal and submerged conditions.

Minimum and maximum values of 1.43cm (P1) and 1.94cm (BC2) respectively were observed for flag leaf width among the generation of Cross I under normal condition. Under Cross I submerged condition, mean values ranged between 1.53 (P2) and 2.24 (BC2). For the Cross II, ranges from 1.26cm to 1.70cm and 1.24cm to 1.70cm were recorded under normal and submerged conditions respectively. In both crosses under the two conditions, the F1 recorded higher means than the two parents. High phenotypic coefficients (PCV > 20%) of variation were registered under the two conditions in both crosses; however, low (PCV < 10%) and moderate (PCV: 10 – 20%) coefficients were observed in Cross I under normal and Cross II under submerged conditions respectively (Table 4.2).

The F1s recorded longer flag leaf length in the two crosses, except under normal condition in Cross II. A range of 33.6cm to 40.37 with low phenotypic and genotypic coefficients of variation was recorded for Cross I under normal condition. The PCV and GCV were high for the trait under submerged condition in Cross I and normal condition in Cross II. Cross II under submerged conditions showed low coefficients of variation (Table 4.2).

None of the crossed generations (F_1, F_2, BC1 & BC2) registered wider straw girth than the parental lines under normal conditions in the two crosses (Table 4.2). Only F_1 and F_2 in Cross I and BC1 in Cross II recorded higher mean values than the better parents under submerged condition. Low to high genotypic and phenotypic coefficients of variation were observed for the straw girth under the two conditions.

Mean values for internode length, days to 50% flowering and plant height assessed among six generations of the two rice crosses are presented in Table 4.3. High phenotypic and genotypic coefficients of variation were observed for the internode length in both crosses and under the two conditions. In the two crosses, the F_1 values were higher than that of the mid parents; however, the population means in Cross I under both conditions were higher than that of Cross II (Table 4.3). Moderate to high coefficients of variation (PCV and GCV) were observed for days to 50% flowering in the two crosses (Table 4.3). The F_1 generations recorded high days to 50% flowering than their mid parents in both crosses under the two conditions. In both crosses, F_1 generations had taller plants under submerged conditions than those under normal conditions. PCV and GCV were moderate to high for plant height in the two crosses (Table 4.3).

Low number of panicles, number of tillers and panicle length were observed in the F_1 generations under submerged condition when compared to the F_1 generations under normal conditions (Table 4.4). The population means for the number of panicles, number of tiller and panicle length were all higher under normal condition than submerged condition in the two crosses. High PCV and GCV were observed for the number of panicles in both crosses under the two conditions (Table 4.4). Number of tillers among the generations registered high PCV in both crosses except for Cross II under submerged condition. Moderate to high GCV were observed for the number of tillers in the two crosses. High PCV and moderate to high GCV were observed for the panicle length among the generations of the two crosses (Table 4.4).

Table 4.5 shows mean values and coefficients of variation for grain yield, grain weight, grain width and grain length of the six generations of the two rice crosses evaluated under normal and submerged conditions. Grain yield per plant of the two F_1s, under normal and submerged conditions, ranged between 16.13g and 30.55g, with reduced grain yield under submerged condition observed in both crosses. The F_1 and F_2 generations of the crosses recorded higher yield than the mid parents under the two conditions. Average yield reduction of 33.4% was observed in Cross I and 45.9% in Cross II after the submergence stress (Table 4.5). High PCV and GCV were registered for the grain yield among the generations of the two crosses. The F_1 as well as F_2 generations of both crosses recorded high 100 grain weight than the mid parents (Table 4.5). The population means for grain weight under normal condition were higher than that under submerged condition. The coefficients of variation (PCV and GCV) for 100 grain weight were moderate to high under the two conditions (Table 4.5). Low to moderate PCV and GCV coefficients of variation were observed for the grain width and grain length under both conditions in the two crosses (Table 4.5).

Table 4.2: Mean values and coefficients of variation for flag leaf width, flag leaf length and straw girth assessed among six generations of the two rice crosses

	Flag Leaf Width (cm)				**Flag Leaf Length (cm)**				**Straw Girth (cm)**			
	Cross I		Cross II		Cross I		Cross II		Cross I		Cross II	
Generations	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged
P1	1.43	0.00	1.26	0.00	39.64	0.00	35.04	0.00	2.87	0.00	2.52	0.00
P2	1.58	1.53	1.35	1.24	33.60	31.75	29.64	28.73	2.81	2.52	2.42	2.36
F1	1.82	1.96	1.53	1.52	36.16	40.12	32.01	31.09	2.51	2.71	2.19	1.96
F2	1.80	1.64	1.55	1.51	39.68	36.60	34.60	33.10	2.28	2.68	2.00	2.07
BC1	1.80	1.70	1.59	1.58	40.37	44.69	35.24	33.58	2.70	2.40	2.36	2.48
BC2	1.94	2.24	1.70	1.70	40.25	45.46	35.00	35.45	2.64	2.34	2.30	2.07
Mean	1.79	1.81	1.50	1.26	38.01	39.72	33.59	26.99	2.59	2.53	2.30	1.82
Minimum	1.43	1.53	1.26	1.24	33.60	31.75	29.64	28.73	2.28	2.34	2.00	2.07
Maximum	1.94	2.24	1.70	1.70	40.37	45.46	35.24	35.45	2.87	2.71	2.52	2.48
LSD	NS	0.87	NS	0.61	4.06	6.04	3.49	5.81	0.14	0.22	0.12	0.46
PCV (%)	20.39	41.44	39.36	24.49	7.65	35.72	33.65	9.26	6.99	34.07	33.76	8.67
GCV (%)	8.60	35.16	34.59	10.36	5.93	34.91	32.57	7.19	6.57	30.70	31.44	8.20

P1- (FARO44 and 57), P2- Swarna Sub1, F1- First filial generation, F2- progenies from F1, BC1- backcross from Parent 1, BC2- Backcross to parent 2, LSD – Least significance Difference, PCV – phenotypic coefficient of variation, GCV - genotypic coefficient of variation

Table 4.3: Mean values and coefficients of variation for internode length, days to 50 % flowering and plant height assessed among six generations of the two rice crosses

	Internode Length (cm)				Days to 50% Flowering				Plant Height (cm)			
	Cross I		Cross II		Cross I		Cross II		Cross I		Cross II	
Generations	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged
P1	15.52	0.00	13.40	0.00	67.95	0.00	67.95	0.00	97.19	0.00	113.38	0.00
P2	12.32	11.56	10.91	11.11	87.73	117.59	88.50	94.96	79.21	96.08	94.66	92.89
F1	13.99	15.37	12.18	12.74	68.36	98.36	69.09	73.01	80.76	98.72	94.33	96.96
F2	22.77	21.32	19.88	19.28	81.83	118.64	82.44	84.52	87.61	103.78	105.05	99.56
BC1	12.45	12.34	11.07	10.61	70.13	90.39	70.13	71.10	86.65	110.26	98.80	102.95
BC2	15.30	18.14	13.59	15.13	89.50	117.99	89.50	91.22	82.41	102.04	94.02	91.11
Mean	15.37	15.75	13.51	11.48	79.51	108.59	77.94	69.14	83.33	101.78	100.04	79.58
Minimum	12.45	11.56	10.91	10.61	67.95	90.39	67.95	71.10	79.21	96.08	94.02	90.96
Maximum	15.52	21.32	19.88	19.28	89.50	118.64	89.50	94.96	97.19	110.26	113.38	102.95
LSD	3.01	3.13	2.64	2.54	5.23	7.16	3.48	4.16	12.23	14.65	10.32	12.14
PCV (%)	22.37	39.42	40.04	25.81	10.69	34.78	37.02	12.24	13.54	34.33	32.63	19.09
GCV (%)	20.53	38.19	38.98	23.60	10.16	34.50	36.80	11.78	10.60	31.55	30.01	16.58

P1- (FARO44 and 57), P2- Swarna Sub1, F1- First filial generation, F2- progenies from F1, BC1- backcross from Parent 1, BC2- Backcross to parent 2, LSD – Least significance Difference, PCV – phenotypic coefficient of variation, GCV - genotypic coefficient of variation

Table 4.4: Mean values and coefficients of variation for number of panicle, number of tiller and panicle length assessed among six generations of the two rice crosses

	Number of Panicle				Number of Tiller				Panicle Length (cm)			
	Cross I		Cross II		Cross I		Cross II		Cross I		Cross II	
Generations	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged	Normal	Submerged
P1	14.40	0.00	12.10	0.00	28.55	0.00	24.15	0.00	32.51	0.00	28.17	0.00
P2	14.66	14.34	12.38	12.29	37.01	33.50	30.97	31.48	26.68	24.18	23.03	24.29
F1	24.00	21.17	19.91	19.64	26.87	25.65	23.32	22.84	27.92	22.19	24.11	21.80
F2	12.40	11.12	10.35	9.82	31.68	28.86	26.88	25.89	29.87	30.00	25.84	26.48
BC1	13.55	14.41	11.45	10.84	27.47	30.05	22.85	21.74	32.28	28.80	28.05	27.11
BC2	13.91	12.81	11.69	12.58	32.25	31.02	26.76	29.30	25.72	28.16	22.27	24.37
Mean	15.70	14.77	12.98	10.86	31.06	29.82	25.82	21.88	28.49	26.67	25.25	24.18
Minimum	12.40	11.12	10.35	9.82	26.87	25.65	22.85	21.74	25.72	22.19	22.27	21.29
Maximum	14.66	14.41	19.91	19.64	32.25	33.50	30.97	31.48	32.51	32.19	28.17	27.11
LSD	1.26	2.14	1.05	1.80	4.60	6.64	3.89	3.89	4.61	3.22	3.93	5.62
PCV (%)	22.43	38.92	40.46	26.45	21.88	35.78	36.61	13.98	21.03	34.63	35.32	22.83
GCV (%)	22.05	38.30	29.87	21.05	19.68	34.21	25.79	11.32	18.24	24.12	23.71	19.73

P1- (FARO44 and 57), P2- Swarna Sub1, F1- First filial generation, F2- progenies from F1, BC1- backcross from Parent 1, BC2- Backcross to parent 2, LSD – Least significance Difference, PCV – phenotypic coefficient of variation, GCV - genotypic coefficient of variation

Table 4.5: Mean values and coefficients of variation for grain yield, grain weight, grain width and grain length assessed among six generations of the two rice crosses

	Grain Yield (g/plant)				**100 Grain Weight (g)**				**Grain Width (mm)**				**Grain Length (mm)**			
	Cross I		Cross II		Cross I		Cross II		Cross I		Cross II		Cross I		Cross II	
Generations	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S
P1	38.26	0.00	31.68	0.00	3.01	0.00	2.88	0.00	2.70	0.00	2.36	0.00	11.36	0.00	9.71	0.00
P2	26.40	18.90	21.07	16.07	2.32	2.33	2.01	2.06	2.63	2.65	2.26	2.40	9.66	8.05	8.07	7.49
F1	57.66	36.44	47.28	30.60	3.02	2.27	2.77	2.87	2.89	2.65	2.44	2.48	11.43	13.52	9.94	9.37
F2	30.55	19.88	24.80	16.13	3.00	2.93	2.81	2.72	2.79	2.59	2.41	2.35	11.02	11.48	9.59	8.87
BC1	32.63	21.13	27.61	15.69	3.09	2.85	2.80	2.71	2.76	2.92	2.35	2.18	11.77	10.12	9.78	9.64
BC2	23.66	17.26	19.78	14.67	2.36	2.56	2.15	2.28	2.87	2.55	2.40	2.60	10.78	11.46	9.21	10.27
Mean	34.18	22.72	28.70	15.53	2.76	2.59	2.57	2.11	2.79	2.67	2.37	2.00	10.93	10.93	9.38	7.61
Minimum	23.66	17.26	21.07	14.67	2.32	2.27	2.01	2.06	2.63	2.55	2.26	2.18	9.66	8.05	8.07	7.49
Maximum	57.66	36.44	47.28	30.07	3.09	2.93	2.88	2.87	2.89	2.92	2.44	2.60	11.77	13.52	9.94	10.27
LSD	5.75	3.93	2.68	3.33	0.13	0.23	0.07	0.22	0.17	0.29	0.09	0.28	0.78	1.00	0.30	1.49
PCV (%)	30.67	42.49	28.11	53.95	13.54	38.15	34.43	15.81	4.31	14.01	13.62	3.65	7.26	16.28	14.26	7.89
GCV (%)	29.32	41.67	27.55	52.83	13.33	37.02	34.16	15.67	3.00	13.48	11.08	2.04	5.88	15.89	13.09	7.18
% Yield Reduction	33.4		45.9													

P1- (FARO 44 and 57), P2- Swarna Sub1, F1- First filial generation, F2- progenies from F1, BC1- backcross from Parent 1, BC2- Backcross to parent 2, LSD – Least significance Difference, PCV – phenotypic coefficient of variation, GCV - genotypic coefficient of variation

4.1.3 Inheritance of SUB 1 gene by seedlings survival ratio, using *Mendelian* method

Table 4.6 presents the results of seedling survival ratios for the generations of the two rice crosses evaluated in two years.

Out of the 21 seedlings of the parental lines evaluated, none of the seedlings survived from the parental lines P1 (Susceptible lines) throughout the experiments. Two extremely weak seedlings of the P1 which eventually died were observed in the Cross I during the Year II experiment (Table 4.6). The percentage survival of 0.00%, 95.20%, 100.00%, 77.11%, 53.33% and 83.33% were recorded for the P1, P2, F_1, F_2, BC1 and BC2 respectively in Cross I of the Year I trial. In Year II, percentage survival of 9.52%, 95.24%, 100.00%, 75.37%, 53.33% and 86.67% were recorded respectively for the P1, P2, F_1, F_2, BC1 and BC2 of the Cross I (Table 4.6).

For Cross II, the percentage survival of generations was 4.76% for P1, 90.48% for P2, 90.48% for F_1, 74.12% for F_2, 46.67% for BCI and 86.67% for BC2 in the Year I (Table 4.6). In Year II, 0.00% of P1 seedlings, 100.00% of P2, 95.24% of F1, 73.38% of F2, 53.33% of BC1 and 80.00% of BC2 survived the submergence (Table 4.6).

The Calculated Chi-Square values for fitting the ratios into Mendelian Model were less than the Tabulated Chi-Square values for the generations of the two crosses in the two years of evaluation (Table 4.6).

Comparative survival scales between 1 and 3 were observed among the donor parents (P2) and F_1 generations of the two crosses in the two years of evaluations (Table 4.6). The F_2 populations of the two crosses recorded comparative scales of 5 in the two years of the trial. The susceptible parental lines (P1) and their backcrosses (BC1) recorded 7 to 9 scales in Cross I and 5 to 9 in Cross II during the two years evaluation.

Percentage elongation of the shoots observed in the Cross I ranged from 0.00% to 12.87% with the BC2 recorded the highest elongation percentages among the generations within the two years (Table 4.6). Similar patterns of the shoot elongations were observed in the Cross II but with less elongation observations of 9.37% to 11.22% in BC2 (Table 4.6).

Table 4.6: Inheritance of SUB 1 gene by survival ratio, using *Mendelian* method

Year	Crosses	Generations	Number of individuals planted	Number of plants survived	Observed % survival	Expected (Plant survival)	Chi-square (X^2) Cal.	Chi-square (X^2) Tab.	Degree of Freedom (DF)	Mendelian Ratio	Scaling by comparative survival %	% Shoot elongation (cm)
YEAR I	Cross I	P1	21.00	0.00	0.00	0.00	--	--	--	--	9	0.00
		P2	21.00	20.00	95.24	21.00	0.048	3.841	--	--	1	5.54
		F1	21.00	21.00	100.00	21.00	--	--	--	--	1	6.41
		F2	402.00	310.00	77.11	302.00	0.212	3.841	1	3:1	5	5.47
		BC1	15.00	8.00	53.33	7.50	0.033	3.841	1	1:1	7	5.18
		BC2	15.00	14.00	83.33	15.00	0.067	3.841	1	0:1	5	10.82
	Cross II	P1	21.00	1.00	4.76	0.00	0.000	--	--	--	9	1.00
		P2	21.00	19.00	90.48	21.00	0.190	3.841	--	--	1	6.75
		F1	21.00	19.00	90.48	21.00	0.190	--	--	--	1	6.24
		F2	402.00	298.00	74.12	302.00	0.053	3.841	1	3:1	5	4.53
		BC1	15.00	7.00	46.67	7.50	0.033	3.841	1	1:1	7	1.56
		BC2	15.00	13.00	86.67	15.00	0.267	3.841	1	0:1	3	11.22
YEAR II	Cross I	P1	21.00	2.00	9.52	0.00	0.000	--	--	--	9	1.29
		P2	21.00	20.00	95.24	21.00	0.048	3.841	--	--	1	5.81
		F1	21.00	21.00	100.00	21.00	0.000	--	--	--	1	6.89
		F2	402.00	303.00	75.37	302.00	0.003	3.841	1	3:1	5	7.45
		BC1	15.00	8.00	53.33	7.50	0.033	3.841	1	1:1	7	8.79
		BC2	15.00	13.00	86.67	15.00	0.267	3.841	1	0:1	5	12.87
	Cross II	P1	21.00	0.00	0.00	0.00	0.000	--	--	--	9	0.00
		P2	21.00	21.00	100.00	21.00	0.000	3.841	--	--	1	7.08
		F1	21.00	20.00	95.24	21.00	0.048	--	--	--	3	7.33
		F2	402.00	295.00	73.38	302.00	0.162	3.841	1	3:1	5	6.62
		BC1	15.00	8.00	53.33	7.50	0.033	3.841	1	1:1	5	1.72
		BC2	15.00	12.00	80.00	15.00	0.600	3.841	1	0:1	5	9.37

Cross I = Swarna sub1 × FARO 44; Cross II = Swarna sub1 × FARO 57; P1 = Commercial varieties (FARO 44, FARO 57), P2 = Swarna sub {Scaling of Comparative Survival: 1 = 100%, 3 = 95-99%, 5 = 75-94%, 7 = 50-74%, 9 = 0-49% (IRRI, 2013)}

4.1.4 Gene effects for the inheritance of 13 traits studied among six generations of two rice crosses

Table 4.7 to Table 4.10 shows the results of generation mean analysis for the studied traits in the two rice crosses.

Simple additive-dominance model was observed to be inadequate to explain the inheritance of flag leaf length, flag leaf width, straw girth and internode length in the two crosses according to the scaling test; however, the joint scaling test only supported the inadequacy of the model for the flag leaf width and internode length in the two crosses (Table 4.7). The Perfect Fit Model showed significant main effect (*m*), additive (*a*) and dominant gene effects (*d*) for the flag leaf length in the two crosses (Table 4.7). Significant gene effects of additive, dominant, additive-dominance and dominance-dominance with duplicate epistasis were observed for the flag leaf width in the two crosses. All the six parameters were significant for the internode length in the crosses (Table 4.7). A duplicate epistasis with high magnitude of dominant gene effect was observed for the internode length.

At least two out of the four scales (A, B, C and D) in the scaling test and the Chi-square of the joint scaling test were significant for the plant height, days to 50% flowering, number of tillers and number of panicles (Table 4.8). The perfect fit model revealed significant effects for all the six parameters for the plant height in the two crosses, except for the additive-additive interaction effect which was not significant in the Cross I. However, the results showed duplicate epistasis with high magnitude of dominant gene effects for the plant height in the two crosses. The perfect fit model for days to 50% flowering showed significant gene effects for all the six parameters in both crosses (Table 4.8). The gene effect with highest magnitude was dominant gene effects in both crosses and the type of epistasis revealed for the trait was duplicate epistasis in the two crosses. Significant positive main effect (*m*) and significant negative dominant effect and additive dominant interaction effects were revealed for number of tillers in Cross I, while in Cross II only dominant gene effect that was negative and significant out of the two aforementioned two gene effects (Table 4.8). The results revealed duplicate type of epistasis with high positive magnitude of dominant gene effect for the inheritance of the number of panicles in the two crosses evaluated (Table 4.8).

Inadequacy of simple additive-dominance model to depict the gene action for the inheritance of panicle length and 100 grain weight was revealed by both scaling and joint scaling tests carried out in the two crosses (Table 4.9). Only scaling test showed inadequacy of the simple three parameters model for the inheritance of the grain length and grain width in the two crosses (Table 4.9). The six parameters model revealed positive and significant additive gene effects for the panicle length, 100 grain weight and grain length (Table 4.9). The perfect fit model showed significant effects of all the six parameters with high magnitude of dominant gene effects and duplicate epistasis for the panicle length and 100 grain weight in the crosses. Only the main effect (*m*) and additive gene effect were significant for grain length in Cross I, while main effect, additive gene effect and dominant effect were significant for the trait in Cross II (Table 4.9).

The three parameters model was not adequate to explain the gene effects for the grain yield and comparative survival of the seedlings under submerged condition (Table 4.10). All the scales (A, B, C and D) and the Chi-square of the joint scaling test revealed statistical differences for the two traits in the two crosses. The perfect fit model revealed significant differences for all the six parameters for the grain yield and comparative survival scores (CSS), except for the dominance-dominance interaction for CSS in the Cross II. High magnitude of dominant main effects and dominance-dominance interactive effects with duplicate type of epistasis were observed for the grain yield in the two crosses (Table 4.10). Dominant main effect (*d*) and dominance-dominance epistasis interaction were shown to be more important for the CSS in Cross I; however, in Cross II, dominant effects and additive-additive gene effect showed higher magnitude for the CSS (Table 4.10).

Table 4.7: Gene effects for flag leaf length, flag leaf width, straw girth and internode length of the two rice crosses evaluated

Models	Gene Effect	Flag Leaf Length (cm)		Flag Leaf Width (cm)		Straw Girth (cm)		Internode Length (cm)	
		Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Scaling test	A	-3.80*±1.25	2.72±1.44	-0.44±0.21	-0.24*±0.07	-0.08±0.29	-0.09*±0.01	-0.62±1.00	0.58±1.17
	B	5.58*±1.36	-4.84*±1.47	0.55*±0.16	0.90*±0.11	-0.01±0.33	-0.01±0.08	6.04**±0.70	17.09**±0.93
	C	2.57±1.82	-6.55*±2.16	-1.37**±0.16	0.47*±0.13	-1.46*±0.35	-0.02±0.13	20.19**±1.81	38.94**±1.83
	D	0.39±0.94	-2.21±1.08	-0.74*±0.13	-0.10±0.06	-0.69*±0.16	0.04±0.06	7.38**±0.86	10.64**±0.82
Joint Scaling Test	X^2	0.44	1.40	21.63**	42.81**	3.77	0.03	52.39**	17.56**
3 parameters	*M*	31.35**±1.94	36.89**±2.23	-0.27±0.27	1.43**±0.13	1.16*±0.35	2.07**±0.13	26.32**±1.75	32.67**±1.68
	A	2.17*±0.48	-1.81*±0.59	-0.15*±0.05	0.45**±0.05	0.03±0.13	0.05±0.03	0.54±0.29	0.53±0.37
	D	-0.46±5.16	5.53±5.79	3.77*±0.77	1.40*±0.33	2.30±1.03	-0.24±0.35	-23.81*±4.09	-23.50*±4.20
6 parameters	*M*	30.87**±0.31	39.08**±0.38	1.22**±0.03	1.92**±0.02	1.99**±0.02	2.00**±0.02	16.75**±0.37	21.83**±0.32
	A	-2.52*±0.71	1.97±0.76	-0.64*±0.12	-0.13*±0.04	-0.01±0.15	0.01±0.05	-2.79**±0.44	-7.73**±0.52
	D	-1.45±2.00	3.22±2.29	2.18**±0.27	0.55*±0.13	1.02*±0.36	-0.06±0.14	-14.47**±1.80	-19.88**±1.77
	Aa	-0.79±1.88	4.43±2.15	1.48*±0.26	0.19±0.12	1.37*±0.32	-0.08±0.13	-14.77**±1.72	-21.28**±1.64
	Ad	-4.69**±0.86	3.78*±0.96	-0.50*±0.13	-0.57**±0.06	-0.04±0.20	-0.04±0.06	-3.33**±0.53	-8.26**±0.64
	Dd	-0.99±3.39	-2.31±3.74	-1.59*±0.51	-0.85*±0.22	-1.28±0.71	0.18*±0.03	9.35*±2.53	3.62*±0.77
Perfect fit	*M*	31.35**±1.94	36.89**±2.23	-0.27±0.27	1.43**±0.13	1.16*±0.35	2.07**±0.13	26.32**±1.75	32.67**±1.68
	A	2.17*±0.48	-1.81*±0.59	-0.15*±0.05	0.45**±0.05	0.03±0.13	0.05±0.03	0.54±0.29	0.53±0.37
	D	-0.46±5.16	5.53±5.79	3.77*±0.77	1.40*±0.33	2.30±1.03	-0.24±0.35	-23.81**±4.09	-23.50*±4.20
	Aa	-0.79±1.88	4.43±2.15	1.48*±0.26	0.19±0.12	1.37*±0.32	-0.08±0.13	-14.77**±1.72	-21.28**±1.64
	Ad	-4.69**±0.86	3.78*±0.95	-0.50*±0.13	-0.57**±0.06	-0.04±0.20	-0.04±0.06	-3.33**±0.53	-8.26**±0.64
	Dd	-0.99±3.39	-2.31±3.74	-1.59*±0.51	-0.85*±0.22	-1.28±0.71	0.18*±0.03	9.35*±2.53	3.62*±0.77
Type of epistasis		NS	NS	Duplicate	Duplicate	NS	NS	Duplicate	Duplicate

[m] = main effect; [a] =additive effect; [d] =dominance effect; [aa] = additive x additive gene interaction; [ad] = additive x dominance gene interaction; [dd] = dominance x dominance gene interaction, $\chi 2$ = Chi-square, A, B, C & D are scales, ns= not significant *,**,***= significantly different at P≤0.05, P≤0.01, P≤0.001.

Table 4.8: Gene effects for plant height, days to 50% flowering, number of tiller and number of panicle of the two rice crosses evaluated

		Plant Height (cm)		Days 50% Flowering		Number of Tiller		Number of Panicle	
Models	**Gene Effect**	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Scaling test	A	-12.81*±2.78	-59.58**±4.06	1.40±2.30	-1.80±1.94	-1.15±2.67	0.70±1.72	-0.70±1.06	-8.80**±0.68
	B	4.13±2.91	-4.05±3.03	10.50*±2.53	4.80*±1.64	10.85**±1.39	-18.70*±5.11	0.30±0.80	5.10*±0.99
	C	-4.19*±1.07	42.49**±6.48	26.06**±4.24	28.08**±2.54	16.18*±4.15	-29.38*±5.24	-6.38*±1.18	-15.32**±0.96
	D	2.25±2.04	53.06**±3.32	7.08*±1.99	12.54**±1.26	3.24±2.76	-5.69±3.12	-2.99*±0.55	-5.81**±0.52
Joint Scaling Test	X^2	13.78*	186.59**	14.95*	19.30**	14.30*	32.66**	48.31**	15.16**
3 parameters	*m*	89.77**±4.22	211.06**±6.74	90.66**±4.03	111.38**±2.59	30.83*±5.73	28.32*±6.59	5.52*±1.16	0.43±1.07
	a	4.75*±1.11	28.81**±1.15	-10.80**±0.63	-4.60**±0.55	-2.05±1.51	-7.80*±2.14	-0.10±0.38	-0.05±0.28
	d	-22.96**±1.15	-295.32**±16.46	-22.92**±1.06	-46.96**±6.95	-6.26±6.46	-12.34*±4.56	9.36*±3.30	26.39**±3.10
6 parameters	*m*	81.58**±0.68	105.83**±1.32	79.77**±0.76	93.42**±0.40	26.90*±0.56	23.81**±0.35	8.81**±0.13	11.65**±0.10
	a	-3.73±1.51	1.04±2.00	-15.35**±1.29	-7.90**±0.99	-8.05*±2.53	1.90±1.04	-0.60±0.48	-7.00**±0.48
	d	-9.79±4.35	-125.59**±6.90	-20.66*±4.24	-24.88**±2.72	-9.48±5.80	-5.72±3.72	3.78*±1.22	18.47**±1.12
	aa	-4.49±4.08	-106.11**±6.64	-14.16*±3.98	-25.08**±2.53	-6.48±5.53	11.38±6.23	5.98*±1.10	11.62**±1.03
	ad	-8.47*±1.88	-27.77**±2.31	-4.55*±1.43	-3.30*±1.13	-6.00±2.94	9.70*±3.71	-0.50±0.61	-6.95**±0.55
	dd	13.17**±1.30	169.73**±10.31	2.26*±0.64	22.08*±4.69	-3.22±2.92	6.62±3.23	-5.58±2.26	-7.92*±2.13
Perfect fit	*m*	89.77**±4.22	211.06**±6.74	90.66**±4.03	111.38**±2.59	30.83*±5.73	28.32*±6.59	5.52*±1.16	0.43±1.07
	a	4.75*±1.11	28.81**±1.15	-10.80**±0.63	-4.60**±0.55	-2.05±1.51	-7.80*±2.14	-0.10±0.38	-0.05±0.28
	d	-22.96**±1.15	-295.32**±16.46	-22.92**±1.06	-46.96**±6.95	-6.26*±1.46	-12.34*±4.56	9.36*±3.30	26.39**±3.10
	aa	-4.49±4.08	-106.11**±6.64	-14.16*±3.98	-25.08**±2.53	-6.48±5.53	11.38±6.23	5.98*±1.10	11.62**±1.03
	ad	-8.47*±1.88	-27.77**±2.31	-4.55*±1.43	-3.30*±1.13	-6.00*±1.94	9.70*±3.71	-0.50±0.61	-6.95**±0.55
	dd	13.17**±1.30	169.73**±10.31	2.26*±0.64	22.08*±4.69	-3.22±3.92	6.62±3.23	-5.58*±2.26	-7.92*±2.13
Type of epistasis		Duplicate	Duplicate	Duplicate	Duplicate	NS	NS	Duplicate	Duplicate

[m] = main effect; [a] =additive effect; [d] =dominance effect; [aa] = additive x additive gene interaction; [ad] = additive x dominance gene interaction; [dd] = dominance x dominance gene interaction, $\chi 2$ = Chi-square, A, B, C & D are scales, ns= not significant *,**,***= significantly different at P≤0.05, P≤0.01, P≤0.001.

Table 4.9: Gene effects for panicle length, 100 grain weight, grain length and grain width of the two rice crosses evaluated

Models	Gene Effect	Panicle Length (cm)		100 Grain Weight (g)		Grain Length (mm)		Grain Width (mm)	
		Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Scaling test	A	3.53±1.39	5.51*±1.35	0.04±0.06	-0.02±0.04	0.68±0.27	0.17±0.21	-0.27*±0.06	-0.13±0.06
	B	-0.61±1.08	-5.34*±0.92	-0.65*±0.20	-1.08**±0.13	0.71*±.22	0.66*±0.21	0.04±0.05	-0.06±0.08
	C	-11.43**±1.53	6.76*±1.30	0.89**±0.09	0.79**±0.06	1.87*±0.34	1.13*±0.29	-0.10±0.08	0.28**±0.04
	D	-7.18**±0.75	3.29*±0.71	0.75**±0.08	0.94**±0.17	0.25±0.11	0.16±0.11	0.07±0.04	0.24±0.22
Joint Scaling Test	X^2	15.26**	641.15**	18.67**	30.22**	0.16	0.06	0.09	0.43
3 parameters	*m*	11.47**±1.56	34.90**±1.47	3.91**±0.19	4.29**±0.13	9.18**±0.25	9.25**±0.24	2.43**±0.07	2.76**±0.44
	a	3.64**±0.43	-1.39*±0.38	0.46**±0.04	0.41**±0.02	0.59*±0.13	0.84**±0.09	0.05±0.03	-0.08*±0.03
	d	28.26**±4.45	-14.78*±4.24	-3.31*±0.58	-4.56**±0.38	1.01±0.72	0.51±0.68	-0.39±0.21	-1.02±0.91
6 parameters	*m*	21.28**±0.17	29.11**±0.14	2.78**±0.01	2.75**±0.12	9.46**±0.67	9.38**±1.03	2.32**±0.01	2.41**±0.11
	a	5.70**±0.67	4.03**±0.65	0.80**±0.09	0.94**±0.06	0.57**±0.09	0.59**±0.09	-0.11*±0.03	-0.11*±0.04
	d	10.98**±1.65	-8.36*±1.54	-1.20**±0.19	-1.58**±0.13	0.12±0.27	0.01±0.26	-0.03±0.08	-0.36±0.44
	aa	14.35**±1.50	-6.59*±1.42	-1.50**±0.17	-1.89**±0.12	-0.49±0.22	-0.31±0.22	-0.13±0.07	-0.47±0.42
	ad	2.07*±0.79	5.42**±0.75	0.35*±0.10	0.53**±0.06	-0.02±0.16	-0.25±0.13	-0.16*±0.04	-0.04±0.05
	dd	-17.27*±3.07	6.42**±0.91	2.11*±0.39	2.99**±0.25	-0.89±0.51	-0.51±0.48	0.36±0.14	0.66±0.47
Perfect fit	*m*	11.47**±1.56	34.90**±1.47	3.91**±0.19	4.29**±0.13	9.18**±0.25	9.25**±0.24	2.43**±0.07	2.76**±0.44
	a	3.64**±0.43	-1.39*±0.38	0.46**±0.04	0.41**±0.02	0.59*±0.13	0.84**±0.09	0.05±0.03	-0.08*±0.03
	d	28.26**±4.45	-14.78*±4.24	-3.31*±0.58	-4.56**±0.38	1.01±0.72	0.51**±0.07	-0.39±0.21	-1.02±0.91
	aa	14.35**±1.50	-6.59*±1.42	-1.50**±0.20	-1.89**±0.12	-0.49±0.22	-0.31±0.22	-0.13±0.07	-0.47±0.44
	ad	2.07*±0.79	5.42**±0.75	0.35*±0.10	0.53**±0.05	-0.02±0.16	-0.25±0.13	-0.16*±0.04	-0.04±0.05
	dd	-17.27*±3.07	6.42**±0.91	2.11*±0.39	2.99**±0.22	-0.89±0.51	-0.51±0.48	0.36±0.14	0.66±0.47
Type of epistasis		Duplicate	Duplicate	Duplicate	Duplicate	NS	NS	NS	NS

[m] = main effect; [a] =additive effect; [d] =dominance effect; [aa] = additive x additive gene interaction; [ad] = additive x dominance gene interaction; [dd] = dominance x dominance gene interaction, $\chi 2$ = Chi-square, A, B, C & D are scales, ns= not significant *,**,***= significantly different at P≤0.05, P≤0.01, P≤0.001.

Table 4.10: Gene effects for seed yield and comparative survival scores of the two rice crosses evaluated

		Seed Yield (g/plant)		**Comparative Survival Scores**	
Models	**Gene Effect**	Cross I	Cross II	Cross I	Cross II
Scaling test	A	-13.15**±1.41	-12.47**±0.99	-2.32**±0.02	-0.76**±0.04
	B	-19.75**±0.88	-15.54**±1.18	-2.08**±0.01	-1.20**±0.03
	C	20.08*±4.64	-14.50*±2.63	-4.42**±0.02	-3.79**±0.05
	D	26.49**±2.24	6.75**±1.14	-0.01*±0.00	-0.91**±0.02
Joint Scaling Test	X^2	24.47**	143.30**	12.64*	11.55*
3 parameters	*M*	72.03**±4.51	29.30**±2.30	1.24**±0.01	-0.56**±0.04
	A	-0.58**±0.02	-1.23*±0.25	0.12**±0.01	0.21**±0.01
	D	-120.23**±9.37	-39.03**±5.17	-4.47**±0.03	1.46**±0.11
6 parameters	*M*	33.39**±1.09	20.16**±0.52	0.11**±0.00	0.21**±0.01
	A	2.72*±0.49	0.30±0.48	0.00±0.00	0.43**±0.02
	D	-34.35**±4.54	2.48±2.42	-0.08**±0.01	1.61**±0.05
	Aa	-52.98**±4.48	-13.51**±2.28	0.01*±0.00	1.82**±0.04
	Ad	3.29*±0.71	1.53**±0.05	-0.12**±0.01	0.22**±0.02
	Dd	85.88**±5.04	41.51**±3.27	4.39**±0.02	0.14±0.08
Perfect fit	*M*	72.03**±4.51	29.30**±2.30	1.24**±0.01	-0.56**±0.04
	A	-0.58**±0.02	-1.23*±0.25	0.12**±0.01	0.21**±0.01
	D	-120.23**±9.37	-39.03**±5.17	-4.47**±0.03	1.46**±0.11
	Aa	-52.98**±4.48	-13.51**±2.28	0.01*±0.00	1.82**±0.04
	Ad	3.29*±0.71	1.53**±0.05	-0.12**±0.01	0.22**±0.092
	Dd	85.88**±5.04	41.51**±3.27	4.39**±0.02	0.14±0.08
Type of epistasis		Duplicate	Duplicate	Duplicate	NS

[m] = main effect; [a] =additive effect; [d] =dominance effect; [aa] = additive x additive gene interaction; [ad] = additive x dominance gene interaction; [dd] = dominance x dominance gene interaction, $\chi 2$ = Chi-square, A, B, C & D are scales, ns= not significant *,**,***= significantly different at $P \leq 0.05$, $P \leq 0.01$, $P \leq 0.001$.

4.1.5 Genetic variance components for 13 traits studied in two rice crosses

Partitioning of the genetic variance components into non-heritable variance due to environment (V_e), fixable variance component due to additive genes (V_a), non-fixable component due to dominance (V_d) alongside with degree of dominance ratio for traits studied are presented in Table 4.11 to Table 4.13.

The environmental variance component (V_e) was lower than the additive genes (V_a) and dominance (V_d) components for flag leaf width in the two crosses (Table 4.11). Additive genes variance component (V_a) was negative in the Cross I, whereas this was positive in Cross II for the trait. The dominance variance component (V_d) was greater than the additive genes variance (V_a) for the flag leaf width in both crosses (Table 4.11). Low narrow sense heritability ($h^2 < 30\%$) and moderate genetic advance as percentage of mean (GAM) were recorded for the flag leaf width in Cross I. Low heritability ($h^2 < 30\%$) coupled with low GAM was observed for the trait in Cross II.

In the two crosses, the environmental component of variance (V_e) for the flag leaf width was lower than the additive component. The additive was positive and greater than the dominance variance, which were negative in the crosses. The narrow sense heritability in the two crosses was moderate with high genetic advance of 32.24% in Cross I and 21.96% in Cross II (Table 4.11).

For Internode Length, the environmental variance was lower compared to both additive and dominance-variances in the two crosses (Table 4.11). While the dominance variance (Va) was higher than additive in Cross I and Cross II, the dominance variance was negative in Cross I but positive in Cross II. Moderate narrow sense heritability ranging from 49% to 33% was observed in the crosses. However, these were coupled with high genetic advance (69.14% to 71.38%) in the crosses.

From the two crosses evaluated, low environmental variance was recorded for Straw Girth (cm) (Table 4.11). Positive additive variance in Cross II and positive dominance variance in Cross I were observed. Moderate heritability and high genetic advance were observed for the trait in the Cross I. Moderate heritability coupled with moderate genetic advance was observed in Cross II.

Positive but lower additive variances compared to dominance components, moderate heritability and low to high genetic advance as percentage of mean were observed for days to 50% flowering in the two crosses (Table 4.12). Number of Tiller showed lower and negative additive variance, low heritability and genetic advance in the Cross I. However, in Cross II, higher and positive variance due to additive, moderate heritability and moderate genetic advance were recorded for the trait (Table 4.12). Low environmental variance compared to additive and dominance variances with moderate heritability were observed for the plant height in the two crosses (Table 4.12). Number of Panicle recorded positive additive variance components coupled with moderate heritability in the two crosses (Table 4.12). Higher variance due to additive, moderate heritability and genetic advantage were observed for Panicle Length in Cross I. In the Cross II, the trait showed moderate heritability however with high genetic advance as percentage of the mean (Table 4.12).

Table 4.13 presents the genetic components for grain yield, seed weight, grain width and grain length of the two rice crosses evaluated. The variance due to additive observed for the grain yield in the crosses ranged between 0.60 and 4.28 while the dominance variance recorded a range between -1.40 and -0.40. The heritability and genetic advance for the grain yield were 70% and 13.26% respectively in Cross I, and there were 44% and 4.81% respectively in Cross II. The two crosses showed lower environmental variance than both additive and dominance variances for the seed weight (Table 4.13). Negative additive variances, positive and higher variances due to dominance, and moderate heritability were observed for the seed weight in the two crosses. Low to moderate genetic advance was observed in the crosses for the trait. For the grain width and grain length, positive but low variances due to additive effect and negative dominance variances were observed in the two crosses (Table 4.13). Moderate heritability was observed for the grain width in the two crosses; however, this was coupled with moderate genetic advance in Cross I while high genetic advance in the Cross II. Grain length showed low genetic advantage as percentage of mean in the two crosses (Table 4.13).

Table 4.11: Genetic components for flag leaf width, flag leaf length, internode length and straw girth of the two rice crosses evaluated

Traits	Genetic Variance	Cross I	Cross II
Flag Leaf Width	Environmental Variance (V_e)	0.04	0.02
	Additive Variance (V_a)	-0.06	0.01
	Dominant Variance (V_d)	0.46	0.03
	Phenotypic Variance (V_p)	0.56	0.06
	Narrow Sense Heritability (h^2)	0.10	0.18
	Genetic Adv. as % of Mean *GAM*	10.72	5.88
	Degree of Dominance	-2.84	1.68
Flag Leaf Length (cm)	Environmental Variance (V_e)	4.59	2.73
	Additive Variance (V_a)	54.40	33.81
	Dominant Variance (V_d)	-52.34	-32.90
	Phenotypic Variance (V_p)	111.33	69.44
	Narrow Sense Heritability (h^2)	0.48	0.49
	Genetic Adv. as % of Mean *GAM*	32.24	21.96
	Degree of Dominance	-0.98	-0.99
Internode Length (cm)	Environmental Variance (V_e)	2.36	21.31
	Additive Variance (V_a)	101.37	-75.46
	Dominant Variance (V_d)	-102.99	128.93
	Phenotypic Variance (V_p)	206.72	225.70
	Narrow Sense Heritability (h^2)	0.49	0.33
	Genetic Adv. as % of Mean *GAM*	71.38	69.14
	Degree of Dominance	-1.01	-1.31
Straw Girth (cm)	Environmental Variance (V_e)	0.32	0.01
	Additive Variance (V_a)	-0.63	0.07
	Dominant Variance (V_d)	0.34	-0.07
	Phenotypic Variance (V_p)	1.26	0.15
	Narrow Sense Heritability (h^2)	0.50	0.49
	Genetic Adv. as % of Mean *GAM*	50.58	19.68
	Degree of Dominance	-0.71	-0.96

Table 4.12: Genetic components for days to 50% flowering, number of tiller, plant height, number of panicle and panicle length of the two rice crosses evaluated

Traits	Genetic Variance	Cross I	Cross II
Days to 50% Flowering	Environmental Variance (V_e)	17.20	4.47
	Additive Variance (V_a)	398.13	30.14
	Dominant Variance (V_d)	-401.59	-35.80
	Phenotypic Variance (V_p)	816.93	70.41
	Narrow Sense Heritability (h^2)	0.49	0.43
	Genetic Adv. as % of Mean *GAM*	37.59	8.33
	Degree of Dominance	-1.00	-1.09
Number of Tiller	Environmental Variance (V_e)	35.41	11.51
	Additive Variance (V_a)	-2.43	1406.74
	Dominant Variance (V_d)	115.95	-1405.57
	Phenotypic Variance (V_p)	153.79	2823.82
	Narrow Sense Heritability (h^2)	0.02	0.50
	Genetic Adv. as % of Mean *GAM*	1.61	18.21
	Degree of Dominance	-6.90	-1.00
Plant Height	Environmental Variance (V_e)	23.40	0.65
	Additive Variance (V_a)	280.39	1.80
	Dominant Variance (V_d)	-282.33	-1.73
	Phenotypic Variance (V_p)	586.13	4.18
	Narrow Sense Heritability (h^2)	0.48	0.43
	Genetic Adv. as % of Mean *GAM*	28.54	2.00
	Degree of Dominance	-1.00	-0.98
Number of Panicle	Environmental Variance (V_e)	2.80	1.00
	Additive Variance (V_a)	4.15	6.70
	Dominant Variance (V_d)	-5.99	-5.78
	Phenotypic Variance (V_p)	12.94	13.47
	Narrow Sense Heritability (h^2)	0.32	0.50
	Genetic Adv. as % of Mean *GAM*	19.18	27.72
	Degree of Dominance	-1.20	-0.93
Panicle Length (cm)	Environmental Variance (V_e)	4.35	1.89
	Additive Variance (V_a)	5.49	20.52
	Dominant Variance (V_d)	-5.12	-21.43
	Phenotypic Variance (V_p)	14.96	43.84
	Narrow Sense Heritability (h^2)	0.37	0.47
	Genetic Adv. as % of Mean *GAM*	11.79	23.72
	Degree of Dominance	-0.97	-1.02

Table 4.13: Genetic components for grain yield, seed weight, grain width and grain length of the two rice crosses evaluated

Traits	Genetic Variance	Cross I	Cross II
Grain Yield (g/plant)	Environmental Variance (V_e)	0.45	0.36
	Additive Variance (V_a)	4.28	0.60
	Dominant Variance (V_d)	-1.40	-0.40
	Phenotypic Variance (V_p)	6.12	1.36
	Narrow Sense Heritability (h^2)	0.70	0.44
	Genetic Adv. as % of Mean *GAM*	13.26	4.81
	Degree of Dominance	0.57	0.81
Seed Weight (g)	Environmental Variance (V_e)	0.02	0.01
	Additive Variance (V_a)	-0.32	-0.03
	Dominant Variance (V_d)	0.59	0.04
	Phenotypic Variance (V_p)	0.93	0.07
	Narrow Sense Heritability (h^2)	0.35	0.37
	Genetic Adv. as % of Mean *GAM*	27.20	8.10
	Degree of Dominance	-1.35	-1.22
Grain Width (mm)	Environmental Variance (V_e Ve	0.01	0.01
	Additive Variance (V_a)	0.04	1.05
	Dominant Variance (V_d)	-0.05	-1.06
	Phenotypic Variance (V_p)	0.10	2.11
	Narrow Sense Heritability (h^2)	0.37	0.50
	Genetic Adv. as % of Mean *GAM*	10.34	64.34
	Degree of Dominance	-1.18	-1.00
Grain Length (mm)	Environmental Variance (V_e)	0.28	0.04
	Additive Variance (V_a)	0.28	0.10
	Dominant Variance (V_d)	-1.07	-0.13
	Phenotypic Variance (V_p)	1.63	0.27
	Narrow Sense Heritability (h^2)	0.17	0.38
	Genetic Adv. as % of Mean *GAM*	4.93	4.44
	Degree of Dominance	-1.95	-1.10

4.2 Discussion of Results

Mitigating the effects of recurrent rice field submergence caused by heavy rainfalls is a critical breeding objective in the recent rice breeding activities in Nigeria. Among all the mitigating measures, developing tolerant rice varieties has been prioritized as a sustainable strategy that can reduce the impact of the submergence problem in the major rice production areas of the country. Farmers' preference for the grain quality has reduced the adoption of the few available resistant varieties in the country. Therefore, the present genetic study was aimed at introgressing the submergence tolerant gene *SUB-1A* into two most farmer-preferred commercial rice varieties in Nigeria. The study assessed the performance of six generations of two rice crosses, determined the survival ratios of the generation and estimated the gene effects for some important traits of the two crosses. The findings of the study are discussed as follows:

4.2.1 Analysis of variance

Mean performance of any crop is influenced by joint contributions of the genes (genotype), environments (locations) as well as the interaction between the major sources of the variation. Precise estimate of the contributions of these sources of variation is of high importance in ensuring reliability of any genetic study; as no valid or meaningful genetic analysis can be done on any genetic materials which revealed no significant genetic variation in the traits of study (Salihu *et al.*, 2019).

The Analysis of Variance revealed significant differences for all the traits at vegetative growth, except for the Flag Leaf width (FLW) and Stem Girth in both crosses under normal condition and G×E for the two traits in the Cross I. The mean squares for all the sources of variation revealed significant differences for all the reproductive parameters in both crosses. The significant difference observed in some of the sources of variation is an indication to take cognizance of the sources. The effect of the genotypes indicated optimum variation among the generations, and this could be exploited for breeding purposes. The significance of G x E revealed the need for evaluation of the lines in more environment or over many years for optimum and reliable results as the source could influence the breeding decision. Similar patterns of significant differences have been earlier documented in the reports of Bekele *et al*. (2013), Rashid *et al*. (2017), Bandi *et al*. (2018) and Gyawali *et al*. (2018). Rao *et al*. (2017) reported significant difference for majority of the traits reported here except flowering time and maturity. Wening *et al.* (2019) reported significant effect of genotype and G x E for days to flowering among 17 rice genotypes evaluated under optimum and submerged conditions. Oladosu *et al.* (2018) reported similar significant differences in number of panicles and grain yield among 11 rice lines evaluated under normal and stressed conditions in Pakistan.

4.2.2 Mean performance of six generations of two rice crosses under normal and submergence conditions

Variations in traits studied have been assessed based on mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). Variation based on mean and range only gives insight on the variables while the actual variability independent of units is estimated through phenotypic and genotypic coefficient of variations. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (GCV) could be described as high (>20%), moderate (10-20%) or low when it is less than 10% (Salihu *et al.*, 2018). According to Salihu *et al.* (2018) moderate to high GCV and PCV were observed for most of the traits studied. Moderate to high PCV and GCV were observed among the traits studied, revealing adequate phenotypic variation among the generations of the two crosses. The magnitude of differences between PCV and GCV was low for most of the traits, revealing low influence of environmental factors on the phenotypic expression for the traits. This finding reported here is in consonant with the report of

Barik *et al.* (2020). The effect of submergence on phenotypic variation of rice plants has been widely assessed by several researchers (Solis *et al.*, 2017; Xiang *et al*., 2017; Wang and Komatsu, 2022; Nagai *et al.*, 2022; Iftekharuddaula *et al*., 2004). Similar mean performance of rice genotypes under submergence condition was documented by Wening *et al.* (2019). Rao *et al*. (2017) reported high phenotypic variation among six generations of a rice cross evaluated under submerged and non-submerged conditions. A panicle range between 7 and 15 was reported among 11 rice genotypes evaluated under optimum condition by Oladosu *et al.* (2018). This is in contrary to the present study where panicle range of 10 to 24 was recorded among generations of the two crosses. The average yield reduction of 33.4% to 45.9% observed under submerged conditions of the crosses is similar to that reported by Sarkar *et al.* (2009) who also reported an average range of 34.31% to 46.8% for six generations of rice under submerged condition. Despite the stressed conditions of submergence, the introgression of the *Sub1A gene* demonstrated considerable improved survival ratio and 54.1% to 66% obtainable grain yield after complete submergence of rice field.

4.2.3 Seedlings percentage survival and *Mendelian ratio* of the two rice crosses evaluated in two years

High percentage survivals were observed in the donor parent (P2), F1 and BC2 generations of the two crosses. This is an indication of successful introgression of the submergence tolerance genes in the crosses. Previous studies have also reported the development of submergence tolerant varieties by introgressing the *Sub1* locus (Toojinda *et al.*, 2005; Xiang *et al*., 2017; Wang and Komatsu, 2022; Nagai *et al.*, 2022). The high percentage survival observed among the tolerant generations is similar to the range of survival rate reported by Wening *et al.* (2019), while screening some rice genotypes under artificial condition. Also, the trial reported by Rao *et al.* (2017) revealed survival range 20% and 98% in a cross between a submergence tolerant and susceptible genotype. Survival percentage of 5.0% to 98.0% among indigenous rice landraces from Koraput, India was also reported by Barik *et al.* (2020). Yullianida *et al.* (2014) reported significant correlation between the survival rate and the grain yield. The low Calculated Chi-Square compared to the Tabulated values observed for the generations of the crosses revealed that the survival percentage recorded in the study is fitted into the Mendelian Ratio. The results obtained were consistent with the hypothesis that submergence tolerance is governed by one major dominant gene which has a high probability of 3:1 in segregating F_2 (Akinwale *et al*., 2015; Oladosu *et al*., 2020). Rao *et al.* (2017) also reported similar findings in rice, while evaluating six generations of a cross between HUR-105 and Swarna Sub1 in India. The percentage shoot elongation observed among the generations was between 5.8% and 12.87% in the two years. This is contrary to the report of Barik *et al.* (2020) who documented 10.5% to 97.4% shoot elongation among 88 rice landraces in India. The disparity in the findings may be as a result of the difference in genetic bases of the materials evaluated as the landraces often adopt extensive shoot elongation to escape submergence condition.

2.2.4 Gene effects for the inheritance of the traits studied among six generations of two rice crosses

Success of any breeding programme is fundamentally dependent on adequate knowledge of gene actions for the expression of the breeding characters. Generation mean analysis provides information on the gene actions through the estimation of mean effect (*m*), additive effect (*a*), dominance effect (*d*) and their interactive effects (*aa, ad & dd*). The magnitudes of the six parameters and signs (- or +) of dominance effect (*d*) and dominance × dominance epistasis (*dd*) determine the traits inheritance (Salihu *et al.,* 2018). Association and dispersion of alleles in parents is shown by positive and negative form of additive x additive (*aa*) interaction respectively. Negative sign of dominance (*d*) gene effect reflects reduced allelic involvement in dominant phenotype while when positive reflect increasing alleles involved in dominant phenotype. Negative sign of dominance x dominance (*dd*) interaction is an indication of ambi-directional dominance. The gene relation is measured to be complementary in nature when the (*d*) and (*dd*) estimations have similar signs and considered to be duplicating in interaction when the signs are not similar (Mather and Jinks, 1982). Understanding these gene actions and their relations among the whole operating genes is a prerequisite to depict good parental lines and appropriate selection programme for the breeding traits.

The results of the scaling test showed significant difference for at least one out of the four scales (A, B, C & D) in the two crosses for all the traits studied. In addition to the scaling test, the joint scaling tests were also significant for most of the traits studied. This showed that the simple additive-dominance model is inadequate to elucidate the mode of gene actions for the characters studied, indicating the need for analysis of digenic interaction model involving the six genetic parameters (*m, a, d, aa, ad & dd*). Had the simple additive-dominance model with three parameters (*m, a* & *d*) was adequate to explain the genetic system of any of the traits, none of the scales (A, B, C and D) as well as the chi-square values would have been significant (Mather and Jinks, 1977). The findings reported here are related to those described by Zewdu (2020) and Suvi *et al*., (2021) who also found the three parameters model inadequate for the explanation of the inheritance of the traits.

The results of the six parameters analysis revealed that besides the additive and dominance gene actions, epistatic interaction mechanisms have also contributed to the expressions of the characters studied. However, the relative magnitudes of these effects varied from character to character and cross to cross.

The six parameters model revealed significant effects of additive gene in the presence of significant additive × dominance interaction for the inheritance of flag leaf length in the two crosses. Although the magnitudes of the dominance and additive × additive effects were higher in the Cross II, this might be due to mere chance because of the high errors of the estimates. Therefore, selection for superior genotypes with high flag leaf length may be more effective if the selection is delay to later generation when optimum exploitation of the additive genes could be achieved. The significance and high magnitudes of the dominance gene effects coupled with the duplicate epistasis observed for the flag leaf width and internode length showed that the simple selection procedure may not be adequate to isolate the superior genotype for the traits because the effects always result to reduction in the expression of phenotypic dominance necessary for the selection (Kargbo *et al*., 2019; Ganapati *et al*., 2020). The selections hindrance may be averted by delaying selection to later generations with increased homozygosity, when the magnitude of the additive gene effect could be predominant.

The results revealed duplicate form of epistasis for the plant height, days to 50% flowering and number of panicles in the two crosses evaluated. There was dispersion of alleles in the parents for plant height and days to 50% flowering as indicated by negative form of additive x additive (*aa*) interaction. The positive form of additive × additive (*aa*) interaction indicated allele association for the number of panicles. All these findings coupled with the high magnitude and significant effects of the dominance genes suggest hybrid breeding and/or delay selections for the improvement of the traits. The result is in conformity with the report of Xie *et al*. (2019). Rao *et al.* (2017), in a study on six generations of a cross between HUR-105 × Swarna Sub1, also reported duplicate epistasis effect for plant height and panicle characters.

The inheritance of the panicle length and seed weight was predominantly determined by the dominance gene effect with substantial dominance × dominance (*dd*) interaction in the two crosses. However, the contributions of the additive genes and additive × additive (*aa*) interaction were also significant indicating the possibility of exploiting the significant fixable genes in the selection programme. To exploit the fixable genes, the selection may be exerted on nearly homozygous generations to isolate superior individuals for the traits. In some earlier studies, non-additive gene actions have been implicated for the inheritance of the panicle characters (Saleem *et al.,* 2010; Kamara *et al*., 2017a and Kamara *et al*., 2017b). Grain weight inheritance was also reported to have been majorly governed by non-additive gene actions (Rao *et al.,* 2017).

All the main gene effects (*m, a & d*) and the interaction effects were significant for the grain yield in the two crosses. The perfect-fit six parameter model revealed predominance of the dominance gene effects compared to others in the crosses. Evidence of dispersion of alleles in the parents, reduced dominant alleles in the hybrids and directional dominance were recorded for the yield in the crosses. All these revealed the effects of non-additive gene actions on the inheritance of the trait. However, the available and significant fixable genes observed could also be exploited if the selection is delayed to the later generations when the manifestation of homozygous populations could be easily identified. Similar findings have been reported from earlier studies (Saleem *et al.,* 2010; Rao *et al.,* 2017; Xie *et al*., 2019).

The simple additive-dominance model being not fitted for the survival scores after the submergence, the perfect fit model revealed significant effects of all the six parameters, except dominance × dominance (*dd*) interaction in Cross II. The positive values of the additive x additive interaction in the three crosses indicated that there were associations between the alleles of the two parents in each of the crosses for the trait. The predominance effect due to the dominant genes among the three main effects and the significance of the interactive effects of the genes proposed the adoption of hybrid breeding for development of superior submergence tolerant variety. Nevertheless, the significant effects of the additive genes also revealed the possibility of exploiting the fixable genes in the selection programme for traits. This showed that both additive and non-additive are important for the expression of submergence ability of the crosses. Previous studies on understanding the genetic mechanism of submergence tolerance in rice revealed that the trait is controlled by both additive and non-additive gene effects (Oladosu *et al*., 2020). Ganapati *et al*. (2020) reported dominant genes as major gene effects for submergence tolerance in rice. Involvement of one major gene for the inheritance of submergence tolerant in rice was reported by Akinwale *et al*. (2015). The findings reported here is in conformity with earlier reports by Suvi *et al*. (2021) and Kargbo *et al*. (2019). Dominant effects of Sub1 provided a substantial enhancement in the level of tolerance of all the sensitive mega varieties in Philippines (Kargbo *et al*. (2019).

4.2.5 Genetic variance components for 13 traits studied in two rice crosses

Prediction of outcome of selection of a trait in a population requires adequate knowledge of the magnitude of genetic variance compared to environmental variance within the total phenotypic variance. In the present research, environmental variance (V_e) estimated for each of the traits considered was lower than additive and dominant variance for most traits in the crosses, establishing less influence of the environment on the expression of the traits. The positive and considerable additive variances observed in one or both crosses for Flag Leaf Length, Internode Length, Days to 50% Flowering, Plant Height, Number of Panicle, Panicle Length, Grain Yield, Grain Width and Grain Length in the crosses revealed the vital role of the additive gene actions in the expression of the traits. Related findings to the aforementioned were observed by Ganapati *et* *al*. (2020). Genetic variances due to additive and dominance gene actions were reported as important for morphological and agronomic traits such as plant height, days to flowering, panicle number per hill, panicle length, and grain yield per plant (Nikita *et al*., 2019).

The moderate to high narrow sense heritability in conjunction with moderate to high expected gain recorded in most of the traits especially the yield component traits are a pointer to a predictable success in the selection for the traits. However, the low genetic advance as percentage of mean observed for Flag Leaf Width, Number of Tiller, Plant Height, Grain Yield, Seed Weight and Grain Length in one or both of the crosses evaluated showed that simple selection procedure may be relatively difficult for the traits, rather complex selection such as backcross and/or recurrent selections to optimize the major genes may be more rewarding. Similar narrow sense heritability range of 0.17 to 0.55 was also observed for the traits in a genetic study reported by Ganapati *et al*. (2020). High heritability ranges of 0.55 – 0.74 and genetic advance as percentage of mean between 7.89% and 36.91% for similar traits in rice were reported by Shrestha *et al.* (2021). This is contrary to the genetic advance range of 1.61% to 64.34% obtained in the present study. The difference could be due to materials evaluated and/or number of samples considered in the two studies. Ogunbayo *et al.* (2014) reported genetic advance of 5.14% to 69.93% for the traits in an assessment of genetic variability in yield and its components in 48 rice lines.

CHAPTER FIVE

5.0 CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

The present research was conducted with a view to assess the possibility of improving the submergence tolerance of most preferred commercial rice varieties in Nigeria. The result has revealed adequate genetic variability inherent in the progenies generated from the study. The performance evaluation revealed an obtainable yield percentage of 54.1% to 66% from the tolerant generations after recovery from complete submergence of the field.

High percentage survivals were observed in the donor parent (P2), F_1 and BC2 generations of the two crosses. The *Mendelian Analysis* showed that the survival percentages obtained were fitted into the *Mendelian Ratio.*

The generations mean analysis revealed inadequacy of three parameter models to elucidate the inheritance of all the studied traits. High magnitude of the dominance main effects with duplicate epistasis were documented for Plant Height, Days 50% Flowering, Number of Panicle, Panicle Length and Grain Yield. However, the additive genes effect was also considerable and significant for these traits. These findings showed that selection for the traits may be averted by presence of epistasis interaction; although this problem could be overcome through delaying selection to the later generations when the fixable portions of the genes could be easily harnessed.

5.2 Recommendations

Providing rice farmers with a protection against the persistent flooding problems in Nigeria, is like providing a type of 'insurance policy' that can make them feel secured in investing in rice production for the benefits of the country as a whole. Availability of submergence tolerant varieties with desirable grain quality could provide a significant assurance to the resource poor farmers across Nigeria. With this view, the following are recommended:

1. With 54.1% to 66% obtainable grain yield from the tolerant generations after recovery from complete submergence, it is recommended that efforts should be made to advance the crosses made to where adequate selections could be made with the intension to register and release a variety for Nigerian farmers.
2. An ideal rice variety for cultivation must combine quality grain with other commercially acceptable traits; therefore, further screenings of the progenies for traits like pest and disease resistance, and grain quality are recommended.
3. Based on the observed high survival percentage (90-100%) and increased grain yield in F_1, development of submergence tolerant hybrid rice could be a quick way to generate a desirable variety for the Nigerian farmers

5.3 Contribution to knowledge

1. The introgression of Sub-1 gene into major commercial rice varieties of FARO 44 and FARO 57 has increased their tolerance level to submergence for up to 14 days of total submergence.

2. The progenies developed will serve in a breeding program as donor parent lines for the development of new submergence tolerant rice varieties.

3. The introgression of the sub-1 gene demonstrated a considerable improved survival ration of about 54.1% to 66% obtainable grain yield recovery from complete submergence on rice field.

4. The mean generation analysis revealed inadequacies of the three parameters models to elucidate the inheritance of all the study trait. High magnitude of dominance gene effect with duplicate epistasis were observed for plant height, days to 50% flowering, numbers of panicle, panicle length and grain yield.

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APPENDICES

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
P1	1	22.50	0.00	0.00
P1	2	23.20	0.00	0.00
P1	3	23.80	0.00	0.00
P1	4	22.60	0.00	0.00
P1	5	24.10	0.00	0.00
P1	6	24.00	0.00	0.00
P1	7	26.20	0.00	0.00
P1	8	28.20	0.00	0.00
P1	9	23.70	0.00	0.00
P1	10	24.50	0.00	0.00
P1	11	23.40	0.00	0.00
P1	12	24.60	0.00	0.00
P1	13	25.00	0.00	0.00
P1	14	26.20	0.00	0.00
P1	15	24.80	0.00	0.00
P1	16	23.90	0.00	0.00
P1	17	25.10	0.00	0.00
P1	18	24.10	0.00	0.00
P1	19	26.00	0.00	0.00
P1	20	25.70	0.00	0.00
P1	21	24.58	0.00	0.00
P2	1	20.20	21.60	6.93
P2	2	19.40	21.40	10.31
P2	3	21.30	22.30	4.69
P2	4	20.00	20.70	3.50
P2	5	21.50	22.20	3.26
P2	6	19.60	21.00	7.14
P2	7	21.30	22.10	3.76
P2	8	22.10	23.40	5.88
P2	9	21.70	22.80	5.07
P2	10	19.30	20.20	4.66
P2	11	22.00	22.70	3.18
P2	12	19.20	20.40	6.25
P2	13	18.60	19.50	4.84
P2	14	19.70	20.50	4.06
P2	15	18.80	19.80	5.32
P2	16	19.00	20.40	7.37
P2	17	21.40	22.10	3.27
P2	18	0.00	0.00	0.00
P2	19	19.50	21.10	8.21
P2	20	19.50	20.80	6.67
P2	21	20.21	21.32	5.54
F1	1	20.10	22.05	9.72
F1	2	19.15	21.38	11.66
F1	3	22.19	22.88	3.09
F1	4	21.80	22.63	3.78
F1	5	20.01	22.05	10.19
F1	6	23.07	23.87	3.47

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F1	7	22.67	23.40	3.18
F1	8	18.60	18.99	2.12
F1	9	19.30	20.07	3.95
F1	10	18.71	19.54	4.45
F1	11	18.83	20.40	8.34
F1	12	20.75	22.10	6.49
F1	13	19.58	21.44	9.54
F1	14	19.48	20.97	7.69
F1	15	19.70	21.38	8.48
F2	1	30.20	32.91	8.98
F2	2	28.30	28.30	0.00
F2	3	28.20	33.03	17.13
F2	4	26.90	26.90	0.00
F2	5	26.30	28.78	9.41
F2	6	26.10	29.30	12.28
F2	7	25.80	27.00	4.65
F2	8	25.71	29.86	16.16
F2	9	25.30	28.60	13.04
F2	10	24.00	26.40	10.00
F2	11	23.50	23.50	0.00
F2	12	15.45	16.48	6.66
F2	13	15.15	16.53	9.12
F2	14	15.67	17.10	9.12
F2	15	15.83	17.33	9.47
F2	16	16.25	17.33	6.66
F2	17	15.86	17.42	9.82
F2	18	15.99	17.45	9.12
F2	19	16.52	17.62	6.66
F2	20	16.07	17.65	9.82
F2	21	16.37	17.87	9.12
F2	22	16.51	18.01	9.12
F2	23	20.20	22.60	11.88
F2	24	18.20	18.20	0.00
F2	25	17.68	20.54	16.16
F2	26	17.66	20.51	16.16
F2	27	17.40	17.40	0.00
F2	28	16.90	19.93	17.94
F2	29	16.60	16.60	0.00
F2	30	16.40	18.92	15.37
F2	31	16.20	16.20	0.00
F2	32	15.00	17.07	13.81
F2	33	15.01	17.43	16.16
F2	34	15.94	17.68	10.88
F2	35	15.83	17.83	12.64
F2	36	16.37	17.98	9.82
F2	37	16.56	18.19	9.82
F2	38	16.42	18.20	10.88
F2	39	16.29	18.34	12.64
F2	40	16.40	18.47	12.64
F2	41	16.75	18.57	10.88

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	42	16.16	18.77	16.16
F2	43	16.99	19.13	12.64
F2	44	16.88	19.61	16.16
F2	45	17.77	19.87	11.80
F2	46	17.71	19.95	12.64
F2	47	18.01	20.92	16.16
F2	48	18.87	21.25	12.64
F2	49	20.11	22.09	9.82
F2	50	20.00	22.18	10.88
F2	51	20.18	22.38	10.88
F2	52	19.48	22.63	16.16
F2	53	20.71	22.97	10.88
F2	54	20.99	23.27	10.88
F2	55	22.05	24.45	10.88
F2	56	22.24	25.05	12.64
F2	57	23.64	26.46	11.94
F2	58	23.67	26.66	12.64
F2	59	23.84	26.86	12.64
F2	60	24.02	26.89	11.94
F2	61	23.70	27.53	16.16
F2	62	25.60	28.38	10.88
F2	63	25.48	28.48	11.80
F2	64	25.34	28.54	12.64
F2	65	25.78	28.85	11.94
F2	66	25.62	28.86	12.64
F2	67	26.09	29.20	11.94
F2	68	26.32	29.65	12.64
F2	69	26.48	29.82	12.64
F2	70	25.91	30.09	16.16
F2	71	27.03	30.45	12.64
F2	72	27.09	30.51	12.64
F2	73	27.62	30.92	11.94
F2	74	26.65	30.95	16.16
F2	75	28.10	31.42	11.80
F2	76	28.12	31.43	11.80
F2	77	28.13	31.44	11.80
F2	78	27.28	31.69	16.16
F2	79	27.33	31.75	16.16
F2	80	27.64	32.10	16.16
F2	81	28.95	32.61	12.64
F2	82	29.25	32.95	12.64
F2	83	29.81	34.62	16.16
F2	84	22.49	23.35	3.81
F2	85	22.05	25.61	16.16
F2	86	20.67	24.01	16.16
F2	87	20.50	23.89	16.55
F2	88	16.54	18.05	9.12
F2	89	17.21	18.35	6.66
F2	90	16.82	18.48	9.82
F2	91	17.34	18.49	6.66

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	92	17.05	18.67	9.47
F2	93	17.89	19.52	9.12
F2	94	18.04	19.81	9.82
F2	95	19.36	21.19	9.47
F2	96	19.60	21.39	9.12
F2	97	20.04	22.01	9.82
F2	98	20.26	22.25	9.82
F2	99	21.63	23.68	9.47
F2	100	21.88	23.87	9.12
F2	101	21.87	23.94	9.47
F2	102	21.95	23.96	9.12
F2	103	21.92	24.00	9.47
F2	104	23.40	25.70	9.82
F2	105	23.45	25.75	9.82
F2	106	23.64	25.80	9.12
F2	107	23.58	25.82	9.47
F2	108	23.60	25.84	9.47
F2	109	23.84	26.02	9.12
F2	110	24.41	26.63	9.12
F2	111	25.11	26.78	6.66
F2	112	25.62	27.33	6.66
F2	113	25.42	27.82	9.47
F2	114	25.48	27.89	9.47
F2	115	25.67	28.02	9.12
F2	116	25.88	28.24	9.12
F2	117	25.81	28.25	9.47
F2	118	25.90	28.35	9.47
F2	119	26.05	28.61	9.82
F2	120	26.31	28.80	9.47
F2	121	15.13	15.71	3.84
F2	122	15.15	16.30	7.60
F2	123	15.25	15.62	2.43
F2	124	15.25	15.57	2.08
F2	125	15.28	15.65	2.43
F2	126	15.33	15.81	3.14
F2	127	15.45	15.77	2.08
F2	128	15.57	15.89	2.08
F2	129	15.58	15.96	2.43
F2	130	15.63	16.01	2.43
F2	131	15.64	16.24	3.84
F2	132	15.64	15.97	2.08
F2	133	15.72	16.43	4.54
F2	134	15.82	16.70	5.60
F2	135	15.82	16.26	2.78
F2	136	15.84	16.56	4.54
F2	137	15.84	17.04	7.60
F2	138	15.86	16.47	3.84
F2	139	15.90	16.28	2.43
F2	140	15.95	16.56	3.84
F2	141	17.41	17.53	0.67

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	142	17.60	18.59	5.60
F2	143	17.69	19.04	7.60
F2	144	17.71	19.98	12.80
F2	145	17.77	18.45	3.84
F2	146	17.85	18.41	3.14
F2	147	17.89	19.32	8.00
F2	148	17.92	18.35	2.43
F2	149	18.04	18.16	0.67
F2	150	18.21	18.65	2.43
F2	151	18.99	20.06	5.60
F2	152	19.08	19.94	4.54
F2	153	19.11	20.64	8.00
F2	154	19.15	21.52	12.40
F2	155	19.29	20.37	5.60
F2	156	19.29	21.68	12.40
F2	157	19.36	20.24	4.54
F2	158	19.38	20.47	5.60
F2	159	19.38	19.79	2.08
F2	160	19.41	20.15	3.84
F2	161	19.41	19.95	2.78
F2	162	19.44	20.19	3.84
F2	163	19.47	19.87	2.08
F2	164	19.48	20.77	6.66
F2	165	19.48	20.03	2.78
F2	166	19.56	21.05	7.60
F2	167	19.58	20.33	3.84
F2	168	19.82	20.93	5.60
F2	169	19.82	20.72	4.54
F2	170	19.87	22.42	12.80
F2	171	20.04	20.95	4.54
F2	172	20.07	20.56	2.43
F2	173	20.38	21.16	3.84
F2	174	20.38	20.51	0.67
F2	175	20.44	21.37	4.54
F2	176	20.51	21.29	3.84
F2	177	20.67	22.24	7.60
F2	178	20.73	21.53	3.84
F2	179	20.73	21.31	2.78
F2	180	20.80	21.31	2.43
F2	181	20.84	21.35	2.43
F2	182	20.99	22.16	5.60
F2	183	21.76	23.50	8.00
F2	184	21.78	22.31	2.43
F2	185	21.88	22.41	2.43
F2	186	21.93	22.46	2.43
F2	187	21.93	23.68	8.00
F2	188	21.95	22.80	3.84
F2	189	21.97	22.82	3.84
F2	190	21.97	22.43	2.08
F2	191	26.44	29.04	9.82

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	192	26.53	29.14	9.82
F2	193	26.65	29.26	9.82
F2	194	26.73	29.36	9.82
F2	195	27.07	29.73	9.82
F2	196	27.28	29.86	9.47
F2	197	27.61	30.13	9.12
F2	198	27.79	30.43	9.47
F2	199	28.72	30.63	6.66
F2	200	16.95	17.42	2.78
F2	201	16.98	18.33	8.00
F2	202	16.99	17.40	2.43
F2	203	16.99	18.12	6.66
F2	204	17.01	17.54	3.14
F2	205	17.01	17.42	2.43
F2	206	17.16	17.27	0.67
F2	207	17.35	17.71	2.08
F2	208	17.35	19.50	12.40
F2	209	17.41	17.83	2.43
F2	210	22.18	22.72	2.43
F2	211	22.24	23.10	3.84
F2	212	22.32	22.86	2.43
F2	213	23.24	24.29	4.54
F2	214	23.35	24.00	2.78
F2	215	23.38	24.03	2.78
F2	216	23.40	24.71	5.60
F2	217	23.61	25.19	6.66
F2	218	23.61	24.69	4.54
F2	219	23.88	24.46	2.43
F2	220	23.88	26.94	12.80
F2	221	24.04	25.13	4.54
F2	222	24.09	24.76	2.78
F2	223	24.09	27.17	12.80
F2	224	24.18	25.53	5.60
F2	225	24.18	26.12	8.00
F2	226	24.21	25.13	3.84
F2	227	24.98	25.94	3.84
F2	228	25.06	26.46	5.60
F2	229	25.13	26.54	5.60
F2	230	25.13	25.75	2.43
F2	231	25.27	25.80	2.08
F2	232	25.29	26.26	3.84
F2	233	25.32	28.46	12.40
F2	234	25.42	26.03	2.43
F2	235	25.52	26.23	2.78
F2	236	25.52	26.14	2.43
F2	237	25.55	26.98	5.60
F2	238	25.60	26.22	2.43
F2	239	25.75	27.71	7.60
F2	240	25.78	26.77	3.84
F2	241	25.81	27.87	8.00

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	242	25.86	26.57	2.78
F2	243	25.91	26.45	2.08
F2	244	26.00	26.81	3.14
F2	245	26.00	26.72	2.78
F2	246	26.05	27.78	6.66
F2	247	26.09	27.28	4.54
F2	248	26.19	27.19	3.84
F2	249	26.20	27.21	3.84
F2	250	26.24	28.34	8.00
F2	251	26.31	27.32	3.84
F2	252	26.32	27.33	3.84
F2	253	26.35	27.83	5.60
F2	254	26.36	27.10	2.78
F2	255	26.41	27.89	5.60
F2	256	26.43	27.44	3.84
F2	257	26.45	27.10	2.43
F2	258	26.48	29.76	12.40
F2	259	26.53	27.55	3.84
F2	260	26.58	27.79	4.54
F2	261	26.75	26.93	0.67
F2	262	26.77	27.43	2.43
F2	263	26.77	30.09	12.40
F2	264	26.83	27.39	2.08
F2	265	26.84	27.87	3.84
F2	266	27.05	28.09	3.84
F2	267	27.47	28.53	3.84
F2	268	27.49	28.06	2.08
F2	269	27.57	28.63	3.84
F2	270	27.61	28.87	4.54
F2	271	27.92	28.60	2.43
F2	272	27.93	29.79	6.66
F2	273	27.93	28.61	2.43
F2	274	28.10	29.18	3.84
F2	275	28.17	29.06	3.14
F2	276	28.17	28.76	2.08
F2	277	28.35	29.14	2.78
F2	278	28.70	32.37	12.80
F2	279	28.79	32.35	12.40
F2	280	28.99	29.59	2.08
F2	281	29.02	30.64	5.60
F2	282	29.02	31.22	7.60
F2	283	29.12	29.93	2.78
F2	284	29.21	30.54	4.54
F2	285	29.27	30.08	2.78
F2	286	29.50	31.16	5.60
F2	287	29.52	30.24	2.43
F2	288	29.54	30.67	3.84
F2	289	29.59	30.41	2.78
F2	290	29.77	31.12	4.54
F2	291	29.77	30.60	2.78

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	292	29.80	30.52	2.43
F2	293	29.80	30.52	2.43
F2	294	29.81	33.50	12.40
F2	295	31.47	32.68	3.84
F2	296	31.60	32.25	2.08
F2	297	16.19	16.53	2.08
F2	298	16.25	17.49	7.60
F2	299	16.29	16.74	2.78
F2	300	16.37	16.99	3.84
F2	301	16.41	16.81	2.43
F2	302	16.42	17.73	8.00
F2	303	16.55	17.65	6.66
F2	304	16.56	17.49	5.60
F2	305	16.71	17.12	2.43
F2	306	16.75	17.68	5.60
F2	307	16.87	17.28	2.43
F2	308	16.87	18.15	7.60
F2	309	16.88	17.89	5.96
F2	310	22.10	23.08	4.55
F2	311	0.00	0.00	0.00
F2	312	0.00	0.00	0.00
F2	313	0.00	0.00	0.00
F2	314	0.00	0.00	0.00
F2	315	0.00	0.00	0.00
F2	316	0.00	0.00	0.00
F2	317	0.00	0.00	0.00
F2	318	0.00	0.00	0.00
F2	319	0.00	0.00	0.00
F2	320	0.00	0.00	0.00
F2	321	0.00	0.00	0.00
F2	322	0.00	0.00	0.00
F2	323	0.00	0.00	0.00
F2	324	0.00	0.00	0.00
F2	325	0.00	0.00	0.00
F2	326	0.00	0.00	0.00
F2	327	0.00	0.00	0.00
F2	328	0.00	0.00	0.00
F2	329	0.00	0.00	0.00
F2	330	0.00	0.00	0.00
F2	331	0.00	0.00	0.00
F2	332	0.00	0.00	0.00
F2	333	0.00	0.00	0.00
F2	334	0.00	0.00	0.00
F2	335	0.00	0.00	0.00
F2	336	0.00	0.00	0.00
F2	337	0.00	0.00	0.00
F2	338	0.00	0.00	0.00
F2	339	0.00	0.00	0.00
F2	340	0.00	0.00	0.00
F2	341	0.00	0.00	0.00

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	342	0.00	0.00	0.00
F2	343	0.00	0.00	0.00
F2	344	0.00	0.00	0.00
F2	345	0.00	0.00	0.00
F2	346	0.00	0.00	0.00
F2	347	0.00	0.00	0.00
F2	348	0.00	0.00	0.00
F2	349	0.00	0.00	0.00
F2	350	0.00	0.00	0.00
F2	351	0.00	0.00	0.00
F2	352	0.00	0.00	0.00
F2	353	0.00	0.00	0.00
F2	354	0.00	0.00	0.00
F2	355	0.00	0.00	0.00
F2	356	0.00	0.00	0.00
F2	357	0.00	0.00	0.00
F2	358	0.00	0.00	0.00
F2	359	0.00	0.00	0.00
F2	360	0.00	0.00	0.00
F2	361	0.00	0.00	0.00
F2	362	0.00	0.00	0.00
F2	363	0.00	0.00	0.00
F2	364	0.00	0.00	0.00
F2	365	0.00	0.00	0.00
F2	366	0.00	0.00	0.00
F2	367	0.00	0.00	0.00
F2	368	0.00	0.00	0.00
F2	369	0.00	0.00	0.00
F2	370	0.00	0.00	0.00
F2	371	0.00	0.00	0.00
F2	372	0.00	0.00	0.00
F2	373	0.00	0.00	0.00
F2	374	0.00	0.00	0.00
F2	375	0.00	0.00	0.00
F2	376	0.00	0.00	0.00
F2	377	0.00	0.00	0.00
F2	378	0.00	0.00	0.00
F2	379	0.00	0.00	0.00
F2	380	0.00	0.00	0.00
F2	381	0.00	0.00	0.00
F2	382	0.00	0.00	0.00
F2	383	0.00	0.00	0.00
F2	384	0.00	0.00	0.00
F2	385	0.00	0.00	0.00
F2	386	0.00	0.00	0.00
F2	387	0.00	0.00	0.00
F2	388	0.00	0.00	0.00
F2	389	0.00	0.00	0.00
F2	390	0.00	0.00	0.00
F2	391	0.00	0.00	0.00

APPENDIX A: Mean values of screened Progenies of Swarna Sub1 × FARO 44 under Submergence Condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	392	0.00	0.00	0.00
F2	393	0.00	0.00	0.00
F2	394	0.00	0.00	0.00
F2	395	0.00	0.00	0.00
F2	396	0.00	0.00	0.00
F2	397	0.00	0.00	0.00
F2	398	0.00	0.00	0.00
F2	399	0.00	0.00	0.00
F2	400	0.00	0.00	0.00
F2	401	0.00	0.00	0.00
F2	402	0.00	0.00	0.00
BC1	1	21.34	23.41	9.70
BC1	2	23.17	24.19	4.39
BC1	3	21.91	23.41	6.82
BC1	4	23.32	24.68	5.82
BC1	5	18.43	20.51	11.28
BC1	6	19.65	21.84	11.15
BC1	7	20.36	22.39	9.94
BC1	8	21.17	22.92	8.44
BC1	9	0.00	0.00	0.00
BC1	10	0.00	0.00	0.00
BC1	11	0.00	0.00	0.00
BC1	12	0.00	0.00	0.00
BC1	13	0.00	0.00	0.00
BC1	14	0.00	0.00	0.00
BC1	15	0.00	0.00	0.00
BC2	1	20.97	23.19	10.56
BC2	2	20.31	22.58	11.15
BC2	3	21.76	23.93	9.96
BC2	4	21.59	23.78	10.12
BC2	5	21.00	23.23	10.62
BC2	6	22.76	24.92	9.48
BC2	7	0.00	0.00	0.00
BC2	8	18.02	20.25	12.38
BC2	9	19.04	21.24	11.54
BC2	10	18.55	20.78	12.02
BC2	11	19.38	21.63	11.58
BC2	12	20.99	23.14	10.24
BC2	13	20.37	22.59	10.86
BC2	14	19.93	22.16	11.18
BC2	15	20.31	22.51	10.83

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
P1	1	23.94	0.00	0.00
P1	2	24.68	0.00	0.00
P1	3	25.32	0.00	0.00
P1	4	24.05	0.00	0.00
P1	5	25.64	0.00	0.00
P1	6	25.68	26.12	1.71
P1	7	28.03	0.00	0.00
P1	8	30.17	0.00	0.00
P1	9	25.36	0.00	0.00
P1	10	26.22	0.00	0.00
P1	11	25.04	0.00	0.00
P1	12	26.32	26.55	0.87
P1	13	26.75	0.00	0.00
P1	14	28.03	0.00	0.00
P1	15	26.54	0.00	0.00
P1	16	25.57	0.00	0.00
P1	17	26.86	0.00	0.00
P1	18	25.79	0.00	0.00
P1	19	27.82	0.00	0.00
P1	20	27.50	0.00	0.00
P1	21	26.30	0.00	0.00
P2	1	21.74	22.27	7.28
P2	2	20.87	22.06	10.82
P2	3	22.92	22.99	4.93
P2	4	21.52	21.34	3.68
P2	5	23.13	23.02	3.42
P2	6	21.27	21.77	7.50
P2	7	23.11	22.92	3.94
P2	8	23.98	24.26	6.18
P2	9	23.54	23.64	5.32
P2	10	20.94	21.03	4.90
P2	11	24.20	23.63	3.34
P2	12	21.12	21.24	6.56
P2	13	20.46	20.48	5.08
P2	14	21.67	21.53	4.35
P2	15	20.68	20.79	5.69
P2	16	20.90	21.42	7.88
P2	17	23.54	23.21	3.50
P2	18	0.00	0.00	0.00
P2	19	21.45	22.16	8.78
P2	20	21.45	21.84	7.13
P2	21	22.23	22.39	5.93
F1	1	22.11	23.16	10.41
F1	2	21.06	22.45	12.48
F1	3	24.41	24.02	3.30
F1	4	22.02	23.76	4.05
F1	5	20.21	23.15	10.90
F1	6	23.30	25.06	3.71
F1	7	22.90	23.36	3.40
F1	8	18.78	18.96	2.28
F1	9	19.52	20.03	4.26

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F1	10	18.92	19.51	4.79
F1	11	19.04	20.37	8.98
F1	12	20.98	22.06	6.98
F1	13	19.79	21.41	10.35
F1	14	19.92	20.95	8.34
F1	15	20.16	21.35	9.20
F2	1	30.89	32.87	9.74
F2	2	28.95	28.30	0.00
F2	3	28.85	33.36	18.85
F2	4	27.52	27.17	0.00
F2	5	27.09	29.06	9.51
F2	6	26.88	29.60	12.40
F2	7	26.57	27.27	4.70
F2	8	26.48	30.16	16.32
F2	9	26.06	26.41	13.17
F2	10	24.72	25.02	10.10
F2	11	24.21	22.27	0.00
F2	12	15.93	15.62	6.72
F2	13	15.62	15.67	9.21
F2	14	16.15	16.20	9.21
F2	15	16.32	16.43	9.57
F2	16	16.76	16.76	6.73
F2	17	16.35	16.85	9.93
F2	18	16.49	16.88	9.22
F2	19	17.13	17.04	6.73
F2	20	16.67	17.07	9.93
F2	21	16.98	17.28	9.33
F2	22	17.12	17.42	9.33
F2	23	20.95	21.85	12.15
F2	24	18.95	17.60	0.00
F2	25	18.41	19.86	16.53
F2	26	18.38	19.84	16.53
F2	27	18.27	16.83	0.00
F2	28	17.75	19.27	18.48
F2	29	17.43	16.05	0.00
F2	30	17.22	18.30	15.72
F2	31	17.01	15.81	0.00
F2	32	15.75	16.66	14.13
F2	33	15.76	17.01	16.64
F2	34	16.74	17.25	11.21
F2	35	16.62	17.41	13.02
F2	36	17.19	17.55	10.12
F2	37	17.39	17.76	10.12
F2	38	17.24	17.77	11.21
F2	39	17.10	17.91	13.02
F2	40	17.21	18.03	13.03
F2	41	17.59	18.13	11.22
F2	42	16.96	18.32	16.66
F2	43	18.18	18.68	13.03
F2	44	18.07	19.15	16.66
F2	45	19.02	19.40	12.16

F2	46	18.95	19.48	13.03

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	47	19.27	20.44	16.76
F2	48	20.19	20.76	13.11
F2	49	21.52	21.58	10.19
F2	50	21.40	21.66	11.28
F2	51	21.60	21.86	11.28
F2	52	20.85	22.11	16.82
F2	53	22.16	22.44	11.33
F2	54	22.46	22.73	11.33
F2	55	23.59	23.88	11.42
F2	56	23.80	25.81	13.27
F2	57	25.30	27.28	12.53
F2	58	25.32	27.48	13.27
F2	59	25.66	27.69	13.27
F2	60	25.84	27.72	12.53
F2	61	25.50	28.38	16.97
F2	62	27.55	29.26	11.42
F2	63	27.41	29.36	12.38
F2	64	27.49	29.59	13.27
F2	65	27.97	29.92	12.53
F2	66	27.80	29.93	13.27
F2	67	28.31	30.28	12.53
F2	68	28.56	30.74	13.27
F2	69	29.13	31.05	13.27
F2	70	28.50	31.33	16.97
F2	71	29.74	31.70	13.52
F2	72	29.80	32.04	13.52
F2	73	30.39	32.47	12.77
F2	74	29.31	32.50	17.29
F2	75	30.91	32.99	12.62
F2	76	30.93	33.00	12.62
F2	77	30.94	33.02	12.62
F2	78	30.01	33.27	17.29
F2	79	30.06	33.34	17.29
F2	80	30.40	33.71	17.29
F2	81	31.84	34.24	13.52
F2	82	32.18	34.60	13.52
F2	83	32.79	36.46	17.29
F2	84	22.71	24.58	4.07
F2	85	22.27	26.97	17.29
F2	86	20.88	25.28	17.29
F2	87	20.71	25.16	17.80
F2	88	16.71	19.13	9.81
F2	89	17.40	19.46	7.16
F2	90	17.01	19.58	10.57
F2	91	17.53	19.60	7.16
F2	92	17.24	19.79	10.28
F2	93	18.09	20.69	9.90
F2	94	18.46	21.00	10.66
F2	95	19.81	22.47	10.28
F2	96	20.05	22.67	9.90
F2	97	20.50	23.33	10.81

F2	98	20.73	23.59	10.81

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	99	22.13	25.10	10.42
F2	100	22.38	25.31	10.03
F2	101	22.53	25.38	10.42
F2	102	22.61	25.39	10.03
F2	103	22.58	25.44	10.42
F2	104	24.10	27.24	10.81
F2	105	24.15	27.35	10.81
F2	106	24.35	27.40	10.03
F2	107	24.29	27.42	10.42
F2	108	24.34	27.44	10.42
F2	109	24.58	26.28	10.03
F2	110	25.16	26.90	10.03
F2	111	25.89	27.05	7.32
F2	112	26.42	27.60	6.72
F2	113	26.20	28.10	9.57
F2	114	26.27	28.17	9.57
F2	115	26.62	28.33	9.21
F2	116	26.84	28.55	9.21
F2	117	26.76	28.56	9.58
F2	118	26.85	28.67	9.58
F2	119	27.01	28.92	9.93
F2	120	27.39	29.46	9.58
F2	121	15.75	16.07	3.88
F2	122	15.77	16.68	7.77
F2	123	16.02	15.98	2.49
F2	124	16.02	15.93	2.13
F2	125	16.05	16.01	2.49
F2	126	16.10	16.17	3.21
F2	127	16.23	16.25	2.13
F2	128	16.34	16.37	2.13
F2	129	16.36	16.44	2.50
F2	130	16.41	16.49	2.50
F2	131	16.43	16.73	3.96
F2	132	16.43	16.45	2.14
F2	133	16.51	16.93	4.68
F2	134	16.61	17.22	5.77
F2	135	16.61	16.76	2.87
F2	136	16.63	17.07	4.68
F2	137	16.63	17.57	7.84
F2	138	16.66	16.98	3.96
F2	139	15.87	16.79	2.51
F2	140	15.92	17.07	3.96
F2	141	17.38	18.17	0.69
F2	142	17.57	19.27	5.77
F2	143	17.66	19.74	7.88
F2	144	17.68	20.71	13.27
F2	145	17.75	19.14	3.98
F2	146	17.83	19.17	3.25
F2	147	17.86	20.11	8.30
F2	148	17.89	19.10	2.53
F2	149	18.02	19.07	0.70

F2	150	18.21	19.58	2.53

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	151	19.18	21.06	5.88
F2	152	19.27	20.94	4.77
F2	153	19.30	21.67	8.40
F2	154	19.34	22.60	13.02
F2	155	19.48	21.39	5.88
F2	156	19.48	22.77	13.02
F2	157	17.88	21.25	4.77
F2	158	18.37	21.49	5.88
F2	159	18.37	20.77	2.18
F2	160	18.39	21.16	4.03
F2	161	18.39	20.94	2.92
F2	162	18.42	21.19	4.03
F2	163	18.45	21.86	2.18
F2	164	18.83	22.85	6.99
F2	165	18.84	22.03	2.92
F2	166	18.91	23.15	7.98
F2	167	18.93	22.36	3.83
F2	168	19.16	23.02	5.59
F2	169	19.16	22.79	4.54
F2	170	19.22	24.66	12.78
F2	171	19.38	23.04	4.54
F2	172	19.41	22.62	2.43
F2	173	19.70	23.28	3.84
F2	174	19.70	22.57	0.67
F2	175	19.77	23.51	4.54
F2	176	19.83	23.42	3.84
F2	177	19.99	24.47	7.59
F2	178	20.05	21.75	3.84
F2	179	20.24	21.52	2.81
F2	180	20.30	21.52	2.46
F2	181	20.34	21.56	2.46
F2	182	20.48	22.39	5.66
F2	183	21.23	23.76	8.08
F2	184	21.25	22.55	2.46
F2	185	21.36	22.66	2.25
F2	186	21.41	22.71	2.31
F2	187	21.41	23.95	7.58
F2	188	21.43	23.32	3.64
F2	189	21.45	23.34	3.64
F2	190	21.45	22.95	1.97
F2	191	25.81	29.71	9.31
F2	192	25.91	29.81	9.50
F2	193	26.02	29.94	9.50
F2	194	26.10	30.04	9.50
F2	195	26.44	30.62	9.50
F2	196	26.65	30.76	9.16
F2	197	26.97	31.03	8.82
F2	198	27.15	31.34	9.16
F2	199	28.05	31.55	6.44
F2	200	16.56	17.95	2.69
F2	201	16.58	18.88	8.25

F2	202	16.59	17.94	2.51

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	203	16.60	18.69	6.86
F2	204	17.18	18.09	3.25
F2	205	17.18	17.96	2.52
F2	206	17.33	17.81	0.70
F2	207	17.52	18.26	2.16
F2	208	17.52	20.10	12.86
F2	209	17.58	18.49	2.53
F2	210	22.40	23.56	2.53
F2	211	22.47	23.95	4.00
F2	212	22.54	23.70	2.55
F2	213	23.47	25.19	4.77
F2	214	23.59	24.99	2.92
F2	215	23.61	25.02	2.92
F2	216	23.66	25.73	5.88
F2	217	23.88	26.45	6.99
F2	218	23.88	25.92	4.77
F2	219	24.15	25.68	2.55
F2	220	24.15	28.28	13.44
F2	221	24.59	26.38	4.77
F2	222	24.64	26.00	2.92
F2	223	24.64	28.53	13.44
F2	224	24.74	26.81	5.88
F2	225	24.74	27.42	8.40
F2	226	24.76	26.39	4.03
F2	227	25.55	27.24	4.03
F2	228	25.81	27.79	5.99
F2	229	25.89	27.87	5.99
F2	230	25.89	27.03	2.60
F2	231	26.03	27.09	2.23
F2	232	26.05	27.57	4.11
F2	233	26.08	30.45	13.27
F2	234	26.18	27.86	2.60
F2	235	26.31	28.07	2.98
F2	236	26.31	27.97	2.60
F2	237	26.34	28.87	5.99
F2	238	26.39	28.06	2.60
F2	239	26.55	29.65	8.13
F2	240	26.58	28.64	4.11
F2	241	26.61	29.82	8.56
F2	242	26.81	28.44	2.98
F2	243	26.86	28.30	2.23
F2	244	26.95	28.69	3.37
F2	245	26.95	28.59	3.00
F2	246	27.01	29.73	7.16
F2	247	27.16	29.18	4.89
F2	248	27.26	29.10	4.13
F2	249	27.28	29.28	4.17
F2	250	27.55	30.49	8.68
F2	251	27.62	29.40	4.17
F2	252	27.64	29.41	4.17
F2	253	27.67	29.95	6.08

F2	254	27.68	29.40	3.06

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	255	27.73	30.26	6.16
F2	256	27.75	29.77	4.22
F2	257	27.78	29.40	2.68
F2	258	27.80	32.29	13.64
F2	259	27.86	30.31	4.22
F2	260	27.91	30.57	5.00
F2	261	28.09	29.62	0.74
F2	262	28.11	30.17	2.68
F2	263	28.11	33.10	13.64
F2	264	28.17	30.13	2.29
F2	265	28.18	30.66	4.22
F2	266	28.41	30.90	4.22
F2	267	28.85	31.38	4.22
F2	268	28.94	30.86	2.29
F2	269	29.03	31.49	3.88
F2	270	29.07	31.75	4.59
F2	271	29.40	31.46	2.46
F2	272	29.41	32.77	6.72
F2	273	29.61	31.47	2.46
F2	274	29.79	29.47	3.88
F2	275	29.86	29.35	3.17
F2	276	29.86	29.05	2.10
F2	277	30.05	29.43	2.81
F2	278	30.42	32.70	12.94
F2	279	30.51	32.71	12.69
F2	280	30.72	30.68	2.13
F2	281	30.76	31.77	5.73
F2	282	30.76	32.37	7.77
F2	283	30.87	31.16	2.85
F2	284	30.97	31.79	4.65
F2	285	31.02	31.32	2.85
F2	286	31.27	32.71	5.77
F2	287	31.29	31.75	2.50
F2	288	31.31	32.21	3.96
F2	289	31.37	31.93	2.87
F2	290	31.61	32.68	4.68
F2	291	31.61	32.13	2.87
F2	292	31.65	32.05	2.50
F2	293	31.65	32.05	2.51
F2	294	31.66	35.18	12.78
F2	295	33.48	34.31	3.96
F2	296	33.62	33.87	2.14
F2	297	17.23	17.36	2.14
F2	298	17.29	18.36	7.84
F2	299	17.33	17.58	2.87
F2	300	17.51	17.84	3.96
F2	301	17.56	17.65	2.51
F2	302	17.57	18.97	8.25
F2	303	17.70	18.88	6.86
F2	304	0.00	0.00	0.00
F2	305	0.00	0.00	0.00

F2	306	0.00	0.00	0.00

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	307	0.00	0.00	0.00
F2	308	0.00	0.00	0.00
F2	309	0.00	0.00	0.00
F2	310	0.00	0.00	0.00
F2	311	0.00	0.00	0.00
F2	312	0.00	0.00	0.00
F2	313	0.00	0.00	0.00
F2	314	0.00	0.00	0.00
F2	315	0.00	0.00	0.00
F2	316	0.00	0.00	0.00
F2	317	0.00	0.00	0.00
F2	318	0.00	0.00	0.00
F2	319	0.00	0.00	0.00
F2	320	0.00	0.00	0.00
F2	321	0.00	0.00	0.00
F2	322	0.00	0.00	0.00
F2	323	0.00	0.00	0.00
F2	324	0.00	0.00	0.00
F2	325	0.00	0.00	0.00
F2	326	0.00	0.00	0.00
F2	327	0.00	0.00	0.00
F2	328	0.00	0.00	0.00
F2	329	0.00	0.00	0.00
F2	330	0.00	0.00	0.00
F2	331	0.00	0.00	0.00
F2	332	0.00	0.00	0.00
F2	333	0.00	0.00	0.00
F2	334	0.00	0.00	0.00
F2	335	0.00	0.00	0.00
F2	336	0.00	0.00	0.00
F2	337	0.00	0.00	0.00
F2	338	0.00	0.00	0.00
F2	339	0.00	0.00	0.00
F2	340	0.00	0.00	0.00
F2	341	0.00	0.00	0.00
F2	342	0.00	0.00	0.00
F2	343	0.00	0.00	0.00
F2	344	0.00	0.00	0.00
F2	345	0.00	0.00	0.00
F2	346	0.00	0.00	0.00
F2	347	0.00	0.00	0.00
F2	348	0.00	0.00	0.00
F2	349	0.00	0.00	0.00
F2	350	0.00	0.00	0.00
F2	351	0.00	0.00	0.00
F2	352	0.00	0.00	0.00
F2	353	0.00	0.00	0.00
F2	354	0.00	0.00	0.00
F2	355	0.00	0.00	0.00
F2	356	0.00	0.00	0.00
F2	357	0.00	0.00	0.00

F2	358	0.00	0.00	0.00

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	359	0.00	0.00	0.00
F2	360	0.00	0.00	0.00
F2	361	0.00	0.00	0.00
F2	362	0.00	0.00	0.00
F2	363	0.00	0.00	0.00
F2	364	0.00	0.00	0.00
F2	365	0.00	0.00	0.00
F2	366	0.00	0.00	0.00
F2	367	0.00	0.00	0.00
F2	368	0.00	0.00	0.00
F2	369	0.00	0.00	0.00
F2	370	0.00	0.00	0.00
F2	371	0.00	0.00	0.00
F2	372	0.00	0.00	0.00
F2	373	0.00	0.00	0.00
F2	374	0.00	0.00	0.00
F2	375	0.00	0.00	0.00
F2	376	0.00	0.00	0.00
F2	377	0.00	0.00	0.00
F2	378	0.00	0.00	0.00
F2	379	0.00	0.00	0.00
F2	380	0.00	0.00	0.00
F2	381	0.00	0.00	0.00
F2	382	0.00	0.00	0.00
F2	383	0.00	0.00	0.00
F2	384	0.00	0.00	0.00
F2	385	0.00	0.00	0.00
F2	386	0.00	0.00	0.00
F2	387	0.00	0.00	0.00
F2	388	0.00	0.00	0.00
F2	389	0.00	0.00	0.00
F2	390	0.00	0.00	0.00
F2	391	0.00	0.00	0.00
F2	392	0.00	0.00	0.00
F2	393	0.00	0.00	0.00
F2	394	0.00	0.00	0.00
F2	395	0.00	0.00	0.00
F2	396	0.00	0.00	0.00
F2	397	0.00	0.00	0.00
F2	398	0.00	0.00	0.00
F2	399	0.00	0.00	0.00
F2	400	0.00	0.00	0.00
F2	401	0.00	0.00	0.00
F2	402	0.00	0.00	0.00
BC1	1	22.41	25.05	10.06
BC1	2	24.33	25.89	4.56
BC1	3	23.01	25.05	7.07
BC1	4	24.49	26.41	6.04

APPENDIX B: Mean Values of screened Progenies of Swarna Sub1 × FARO 44 under submergence condition in Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
BC1	5	19.35	21.94	11.74
BC1	6	20.63	23.50	11.61
BC1	7	21.38	24.09	10.35
BC1	8	22.23	24.66	8.87
BC1	9	0.00	0.00	0.00
BC1	10	0.00	0.00	0.00
BC1	11	0.00	0.00	0.00
BC1	12	0.00	0.00	0.00
BC1	13	0.00	0.00	0.00
BC1	14	0.00	0.00	0.00
BC1	15	0.00	0.00	0.00
BC2	1	22.23	25.51	11.09
BC2	2	21.53	24.83	11.71
BC2	3	23.07	26.33	10.46
BC2	4	22.89	26.15	10.63
BC2	5	22.26	25.55	11.15
BC2	6	24.13	27.41	9.95
BC2	7	0.00	0.00	0.00
BC2	8	0.00	0.00	0.00
BC2	9	20.18	23.36	12.12
BC2	10	19.67	22.86	12.66
BC2	11	20.54	23.79	12.20
BC2	12	22.25	25.46	10.78
BC2	13	21.60	24.84	11.44
BC2	14	21.13	24.38	11.77
BC2	15	21.57	22.73	11.48

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
P1	1	27.50	0.00	0.00
P1	2	32.30	0.00	0.00
P1	3	28.50	0.00	0.00
P1	4	30.70	0.00	0.00
P1	5	32.60	0.00	0.00
P1	6	27.30	29.79	9.12
P1	7	30.60	0.00	0.00
P1	8	32.10	0.00	0.00
P1	9	31.90	0.00	0.00
P1	10	28.40	0.00	0.00
P1	11	27.90	0.00	0.00
P1	12	29.00	32.67	12.66
P1	13	27.90	0.00	0.00
P1	14	30.10	0.00	0.00
P1	15	31.50	0.00	0.00
P1	16	32.10	0.00	0.00
P1	17	29.30	0.00	0.00
P1	18	30.20	0.00	0.00
P1	19	29.40	0.00	0.00
P1	20	30.60	0.00	0.00
P1	21	30.00	3.12	1.09
P2	1	19.20	21.10	9.90
P2	2	19.30	21.40	10.88
P2	3	21.50	22.30	3.72
P2	4	19.60	20.30	3.57
P2	5	21.30	22.20	4.23
P2	6	18.80	20.10	6.91
P2	7	20.00	21.10	5.50
P2	8	21.30	24.40	14.55
P2	9	22.10	22.10	0.00
P2	10	21.70	23.20	6.91
P2	11	21.50	21.70	0.93
P2	12	19.60	20.70	5.61
P2	13	20.50	22.50	9.76
P2	14	21.20	24.50	15.57
P2	15	20.30	21.20	4.43
P2	16	21.70	22.40	3.23
P2	17	19.30	21.10	9.33
P2	18	22.00	24.10	9.55
P2	19	19.20	21.10	9.90
P2	20	20.00	20.30	1.50
P2	21	20.51	21.89	6.75
F1	1	25.10	25.68	2.31
F1	2	27.34	28.56	4.46
F1	3	26.21	27.91	6.51
F1	4	25.89	27.17	4.93
F1	5	24.99	25.35	1.45
F1	6	26.25	27.72	5.61
F1	7	26.63	28.51	7.08
F1	8	27.53	30.07	9.20
F1	9	26.86	28.67	6.74

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F1	10	26.16	26.77	2.33
F1	11	0.00	0.00	0.00
F1	12	25.21	27.60	9.50
F1	13	26.56	29.59	11.41
F1	14	24.71	27.07	9.54
F1	15	25.77	28.64	11.13
F1	16	0.00	0.00	0.00
F1	17	25.66	27.56	7.40
F1	18	26.30	28.94	10.03
F1	19	25.89	27.06	4.52
F1	20	26.30	28.42	8.08
F1	21	25.73	28.01	8.91
F2	1	22.60	23.90	5.75
F2	2	28.90	30.00	3.81
F2	3	26.90	26.90	0.00
F2	4	26.80	27.10	1.12
F2	5	25.20	27.20	7.94
F2	6	21.20	22.10	4.25
F2	7	19.00	21.20	11.58
F2	8	31.30	32.10	2.56
F2	9	23.40	23.80	1.71
F2	10	21.40	22.50	5.14
F2	11	27.20	30.60	12.50
F2	12	19.90	21.10	6.03
F2	13	26.90	27.60	2.60
F2	14	32.30	32.90	1.86
F2	15	19.30	22.10	14.51
F2	16	31.50	32.40	2.86
F2	17	24.10	25.50	5.81
F2	18	22.10	25.90	17.19
F2	19	21.30	21.40	0.47
F2	20	17.30	19.60	13.29
F2	21	22.60	23.90	5.75
F2	22	28.52	29.61	3.81
F2	23	26.01	26.01	0.00
F2	24	27.07	27.37	1.12
F2	25	26.46	28.56	7.94
F2	26	22.47	23.43	4.25
F2	27	20.33	22.68	11.58
F2	28	31.05	31.85	2.56
F2	29	23.30	23.70	1.71
F2	30	21.28	22.37	5.14
F2	31	26.93	30.29	12.50
F2	32	19.50	20.68	6.03
F2	33	29.59	30.36	2.60
F2	34	31.55	32.14	1.86
F2	35	18.84	21.58	14.51
F2	36	31.45	32.34	2.86
F2	37	23.79	25.17	5.81
F2	38	21.37	25.05	17.19
F2	39	21.13	21.23	0.47

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	40	17.22	19.51	13.29
F2	41	22.60	23.90	5.75
F2	42	28.52	29.61	3.81
F2	43	26.01	26.01	0.00
F2	44	27.07	27.37	1.12
F2	45	26.46	28.56	7.94
F2	46	22.47	23.43	4.25
F2	47	20.33	22.68	11.58
F2	48	31.05	31.85	2.56
F2	49	23.30	23.70	1.71
F2	50	21.28	22.37	5.14
F2	51	26.93	30.29	12.50
F2	52	19.50	20.68	6.03
F2	53	29.59	30.36	2.60
F2	54	31.55	32.14	1.86
F2	55	18.84	21.58	14.51
F2	56	31.45	32.34	2.86
F2	57	23.79	25.17	5.81
F2	58	21.37	25.05	17.19
F2	59	21.13	21.23	0.47
F2	60	17.22	19.51	13.29
F2	61	26.01	26.01	0.00
F2	62	27.07	27.37	1.12
F2	63	26.46	28.56	7.94
F2	64	22.47	23.43	4.25
F2	65	20.33	22.68	11.58
F2	66	31.05	31.85	2.56
F2	67	23.30	23.70	1.71
F2	68	21.28	22.37	5.14
F2	69	26.93	30.29	12.50
F2	70	19.50	20.68	6.03
F2	71	29.59	30.36	2.60
F2	72	31.55	32.14	1.86
F2	73	18.84	21.58	14.51
F2	74	31.45	32.34	2.86
F2	75	23.79	25.17	5.81
F2	76	21.37	25.05	17.19
F2	77	21.13	21.23	0.47
F2	78	17.22	19.51	13.29
F2	79	23.12	24.45	5.75
F2	80	29.41	30.53	3.81
F2	81	26.79	26.79	0.00
F2	82	28.18	28.49	1.12
F2	83	26.72	28.85	7.94
F2	84	23.60	24.60	4.25
F2	85	21.55	24.05	11.58
F2	86	33.23	34.08	2.56
F2	87	23.11	23.51	1.71
F2	88	21.18	22.27	5.14
F2	89	26.77	30.12	12.50
F2	90	19.30	20.47	6.03

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	91	28.99	29.75	2.60
F2	92	31.04	31.61	1.86
F2	93	18.39	21.06	14.51
F2	94	29.80	30.66	2.86
F2	95	21.96	23.24	5.81
F2	96	21.10	24.73	17.19
F2	97	22.19	22.29	0.47
F2	98	17.20	19.49	13.29
F2	99	23.80	25.16	5.75
F2	100	28.84	29.94	3.81
F2	101	28.61	28.61	0.00
F2	102	28.96	29.29	1.12
F2	103	28.71	30.99	7.94
F2	104	23.87	24.88	4.25
F2	105	21.55	24.05	11.58
F2	106	33.04	33.88	2.56
F2	107	24.16	24.57	1.71
F2	108	22.89	24.07	5.14
F2	109	26.04	29.29	12.50
F2	110	19.69	20.88	6.03
F2	111	31.07	31.88	2.60
F2	112	33.44	34.06	1.86
F2	113	20.16	23.09	14.51
F2	114	31.20	32.09	2.86
F2	115	23.68	25.06	5.81
F2	116	21.25	24.90	17.19
F2	117	20.92	21.02	0.47
F2	118	16.88	19.12	13.29
F2	119	28.61	28.61	0.00
F2	120	26.44	26.74	1.12
F2	121	25.83	27.88	7.94
F2	122	22.43	23.39	4.25
F2	123	20.07	22.39	11.58
F2	124	30.03	30.80	2.56
F2	125	23.11	23.51	1.71
F2	126	21.18	22.27	5.14
F2	127	27.54	30.99	12.50
F2	128	20.10	21.32	6.03
F2	129	30.48	31.27	2.60
F2	130	31.37	31.95	1.86
F2	131	18.65	21.36	14.51
F2	132	30.81	31.69	2.86
F2	133	23.40	24.76	5.81
F2	134	20.86	24.44	17.19
F2	135	20.03	20.12	0.47
F2	136	15.90	18.02	13.29
F2	137	22.82	24.14	5.75
F2	138	30.88	32.05	3.81
F2	139	26.76	26.76	0.00
F2	140	29.67	30.00	1.12
F2	141	27.02	29.17	7.94

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	142	25.96	27.06	4.25
F2	143	23.06	25.73	11.58
F2	144	36.05	36.97	2.56
F2	145	24.55	24.97	1.71
F2	146	22.45	23.61	5.14
F2	147	28.48	32.04	12.50
F2	148	20.02	21.22	6.03
F2	149	31.20	32.01	2.60
F2	150	30.01	30.57	1.86
F2	151	18.57	21.27	14.51
F2	152	31.30	32.19	2.86
F2	153	23.28	24.64	5.81
F2	154	22.58	26.46	17.19
F2	155	22.01	22.12	0.47
F2	156	17.13	19.40	13.29
F2	157	23.66	25.02	5.75
F2	158	28.55	29.64	3.81
F2	159	28.04	28.04	0.00
F2	160	31.86	32.22	1.12
F2	161	28.04	30.27	7.94
F2	162	23.30	24.29	4.25
F2	163	21.51	24.00	11.58
F2	164	32.61	33.44	2.56
F2	165	23.84	24.25	1.71
F2	166	22.14	23.28	5.14
F2	167	26.30	29.58	12.50
F2	168	20.68	21.93	6.03
F2	169	32.93	33.79	2.60
F2	170	35.78	36.45	1.86
F2	171	20.00	22.90	14.51
F2	172	31.06	31.95	2.86
F2	173	23.55	24.91	5.81
F2	174	21.03	24.65	17.19
F2	175	20.50	20.59	0.47
F2	176	18.84	21.58	14.51
F2	177	31.45	32.34	2.86
F2	178	23.79	25.17	5.81
F2	179	21.37	25.05	17.19
F2	180	21.13	21.23	0.47
F2	181	17.22	19.51	13.29
F2	182	23.12	24.45	5.75
F2	183	29.41	30.53	3.81
F2	184	26.79	26.79	0.00
F2	185	28.18	28.49	1.12
F2	186	26.72	28.85	7.94
F2	187	23.60	24.60	4.25
F2	188	21.55	24.05	11.58
F2	189	33.23	34.08	2.56
F2	190	23.11	23.51	1.71
F2	191	21.18	22.27	5.14
F2	192	26.77	30.12	12.50

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	193	19.30	20.47	6.03
F2	194	28.99	29.75	2.60
F2	195	31.04	31.61	1.86
F2	196	18.39	21.06	14.51
F2	197	29.80	30.66	2.86
F2	198	21.96	23.24	5.81
F2	199	21.10	24.73	17.19
F2	200	22.19	22.29	0.47
F2	201	17.20	19.49	13.29
F2	202	23.80	25.16	5.75
F2	203	28.84	29.94	3.81
F2	204	28.61	28.61	0.00
F2	205	28.96	29.29	1.12
F2	206	28.71	30.99	7.94
F2	207	23.87	24.88	4.25
F2	208	21.55	24.05	11.58
F2	209	33.04	33.88	2.56
F2	210	24.16	24.57	1.71
F2	211	22.89	24.07	5.14
F2	212	26.04	29.29	12.50
F2	213	19.69	20.88	6.03
F2	214	31.07	31.88	2.60
F2	215	33.44	34.06	1.86
F2	216	20.16	23.09	14.51
F2	217	31.20	32.09	2.86
F2	218	23.68	25.06	5.81
F2	219	21.25	24.90	17.19
F2	220	20.92	21.02	0.47
F2	221	16.88	19.12	13.29
F2	222	28.61	28.61	0.00
F2	223	26.44	26.74	1.12
F2	224	25.83	27.88	7.94
F2	225	22.43	23.39	4.25
F2	226	20.07	22.39	11.58
F2	227	30.03	30.80	2.56
F2	228	23.11	23.51	1.71
F2	229	21.18	22.27	5.14
F2	230	27.54	30.99	12.50
F2	231	20.10	21.32	6.03
F2	232	30.48	31.27	2.60
F2	233	31.37	31.95	1.86
F2	234	18.65	21.36	14.51
F2	235	30.81	31.69	2.86
F2	236	23.40	24.76	5.81
F2	237	20.86	24.44	17.19
F2	238	20.03	20.12	0.47
F2	239	15.90	18.02	13.29
F2	240	22.82	24.14	5.75
F2	241	30.88	32.05	3.81
F2	242	26.76	26.76	0.00
F2	243	29.67	30.00	1.12

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	244	27.02	29.17	7.94
F2	245	25.96	27.06	4.25
F2	246	23.06	25.73	11.58
F2	247	36.05	36.97	2.56
F2	248	24.55	24.97	1.71
F2	249	22.45	23.61	5.14
F2	250	28.48	32.04	12.50
F2	251	20.02	21.22	6.03
F2	252	31.20	32.01	2.60
F2	253	30.01	30.57	1.86
F2	254	18.57	21.27	14.51
F2	255	31.30	32.19	2.86
F2	256	23.28	24.64	5.81
F2	257	22.58	26.46	17.19
F2	258	22.01	22.12	0.47
F2	259	17.13	19.40	13.29
F2	260	23.66	25.02	5.75
F2	261	28.55	29.64	3.81
F2	262	28.04	28.04	0.00
F2	263	31.86	32.22	1.12
F2	264	28.04	30.27	7.94
F2	265	23.30	24.29	4.25
F2	266	21.51	24.00	11.58
F2	267	32.61	33.44	2.56
F2	268	23.84	24.25	1.71
F2	269	22.14	23.28	5.14
F2	270	26.30	29.58	12.50
F2	271	20.68	21.93	6.03
F2	272	32.93	33.79	2.60
F2	273	35.78	36.45	1.86
F2	274	20.00	22.90	14.51
F2	275	31.06	31.95	2.86
F2	276	23.55	24.91	5.81
F2	277	21.03	24.65	17.19
F2	278	20.50	20.59	0.47
F2	279	18.57	21.03	13.29
F2	280	27.95	27.95	0.00
F2	281	25.81	26.10	1.12
F2	282	25.79	27.84	7.94
F2	283	22.14	23.08	4.25
F2	284	19.40	21.65	11.58
F2	285	29.79	30.55	2.56
F2	286	23.01	23.40	1.71
F2	287	21.67	22.78	5.14
F2	288	28.40	31.95	12.50
F2	289	20.71	21.96	6.03
F2	290	31.73	32.55	2.60
F2	291	31.68	32.27	1.86
F2	292	19.58	22.43	14.51
F2	293	32.66	33.60	2.86
F2	294	25.04	26.49	5.81

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	295	20.69	24.25	17.19
F2	296	19.94	20.03	0.47
F2	297	15.81	17.92	13.29
F2	298	22.59	23.89	5.75
F2	299	0.00	0.00	0.00
F2	300	0.00	0.00	0.00
F2	301	0.00	0.00	0.00
F2	302	0.00	0.00	0.00
F2	303	0.00	0.00	0.00
F2	304	0.00	0.00	0.00
F2	305	0.00	0.00	0.00
F2	306	0.00	0.00	0.00
F2	307	0.00	0.00	0.00
F2	308	0.00	0.00	0.00
F2	309	0.00	0.00	0.00
F2	310	0.00	0.00	0.00
F2	311	0.00	0.00	0.00
F2	312	0.00	0.00	0.00
F2	313	0.00	0.00	0.00
F2	314	0.00	0.00	0.00
F2	315	0.00	0.00	0.00
F2	316	0.00	0.00	0.00
F2	317	0.00	0.00	0.00
F2	318	0.00	0.00	0.00
F2	319	0.00	0.00	0.00
F2	320	0.00	0.00	0.00
F2	321	0.00	0.00	0.00
F2	322	0.00	0.00	0.00
F2	323	0.00	0.00	0.00
F2	324	0.00	0.00	0.00
F2	325	0.00	0.00	0.00
F2	326	0.00	0.00	0.00
F2	327	0.00	0.00	0.00
F2	328	0.00	0.00	0.00
F2	329	0.00	0.00	0.00
F2	330	0.00	0.00	0.00
F2	331	0.00	0.00	0.00
F2	332	0.00	0.00	0.00
F2	333	0.00	0.00	0.00
F2	334	0.00	0.00	0.00
F2	335	0.00	0.00	0.00
F2	336	0.00	0.00	0.00
F2	337	0.00	0.00	0.00
F2	338	0.00	0.00	0.00
F2	339	0.00	0.00	0.00
F2	340	0.00	0.00	0.00
F2	341	0.00	0.00	0.00
F2	342	0.00	0.00	0.00
F2	343	0.00	0.00	0.00
F2	344	0.00	0.00	0.00
F2	345	0.00	0.00	0.00

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	346	0.00	0.00	0.00
F2	347	0.00	0.00	0.00
F2	348	0.00	0.00	0.00
F2	349	0.00	0.00	0.00
F2	350	0.00	0.00	0.00
F2	351	0.00	0.00	0.00
F2	352	0.00	0.00	0.00
F2	353	0.00	0.00	0.00
F2	354	0.00	0.00	0.00
F2	355	0.00	0.00	0.00
F2	356	0.00	0.00	0.00
F2	357	0.00	0.00	0.00
F2	358	0.00	0.00	0.00
F2	359	0.00	0.00	0.00
F2	360	0.00	0.00	0.00
F2	361	0.00	0.00	0.00
F2	362	0.00	0.00	0.00
F2	363	0.00	0.00	0.00
F2	364	0.00	0.00	0.00
F2	365	0.00	0.00	0.00
F2	366	0.00	0.00	0.00
F2	367	0.00	0.00	0.00
F2	368	0.00	0.00	0.00
F2	369	0.00	0.00	0.00
F2	370	0.00	0.00	0.00
F2	371	0.00	0.00	0.00
F2	372	0.00	0.00	0.00
F2	373	0.00	0.00	0.00
F2	374	0.00	0.00	0.00
F2	375	0.00	0.00	0.00
F2	376	0.00	0.00	0.00
F2	377	0.00	0.00	0.00
F2	378	0.00	0.00	0.00
F2	379	0.00	0.00	0.00
F2	380	0.00	0.00	0.00
F2	381	0.00	0.00	0.00
F2	382	0.00	0.00	0.00
F2	383	0.00	0.00	0.00
F2	384	0.00	0.00	0.00
F2	385	0.00	0.00	0.00
F2	386	0.00	0.00	0.00
F2	387	0.00	0.00	0.00
F2	388	0.00	0.00	0.00
F2	389	0.00	0.00	0.00
F2	390	0.00	0.00	0.00
F2	391	0.00	0.00	0.00
F2	392	0.00	0.00	0.00
F2	393	0.00	0.00	0.00
F2	394	0.00	0.00	0.00
F2	395	0.00	0.00	0.00
F2	396	0.00	0.00	0.00

APPENDIX C: Mean values of screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the First Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	397	0.00	0.00	0.00
F2	398	0.00	0.00	0.00
F2	399	0.00	0.00	0.00
F2	400	0.00	0.00	0.00
F2	401	0.00	0.00	0.00
F2	402	0.00	0.00	0.00
BC1	1	0.00	0.00	0.00
BC1	2	0.00	0.00	0.00
BC1	3	32.40	33.17	2.38
BC1	4	24.19	24.77	2.43
BC1	5	23.37	23.41	0.17
BC1	6	23.38	23.69	1.32
BC1	7	16.01	16.56	3.41
BC1	8	23.71	23.90	0.80
BC1	9	29.85	29.98	0.44
BC1	10	0.00	0.00	0.00
BC1	11	0.00	0.00	0.00
BC1	12	0.00	0.00	0.00
BC1	13	0.00	0.00	0.00
BC1	14	0.00	0.00	0.00
BC1	15	0.00	0.00	0.00
BC2	1	25.18	27.76	10.24
BC2	2	19.54	24.86	6.74
BC2	3	30.93	33.57	8.52
BC2	4	0.00	0.00	0.00
BC2	5	20.79	26.40	12.55
BC2	6	0.00	0.00	0.00
BC2	7	23.55	27.19	15.47
BC2	8	21.03	23.45	11.47
BC2	9	20.50	22.28	8.68
BC2	10	16.60	18.35	10.50
BC2	11	27.93	29.67	6.24
BC2	12	25.06	28.77	14.80
BC2	13	23.85	28.19	18.19
BC2	14	22.15	26.72	16.14
BC2	15	21.07	23.96	13.70

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
P1	1	28.05	0.00	0.00
P1	2	32.95	0.00	0.00
P1	3	29.07	0.00	0.00
P1	4	31.32	0.00	0.00
P1	5	33.26	0.00	0.00
P1	6	27.85	0.00	0.00
P1	7	31.22	0.00	0.00
P1	8	32.75	0.00	0.00
P1	9	32.54	0.00	0.00
P1	10	28.97	0.00	0.00
P1	11	28.46	0.00	0.00
P1	12	29.58	0.00	0.00
P1	13	28.52	0.00	0.00
P1	14	30.77	0.00	0.00
P1	15	32.20	0.00	0.00
P1	16	32.82	0.00	0.00
P1	17	29.95	0.00	0.00
P1	18	31.61	0.00	0.00
P1	19	30.77	0.00	0.00
P1	20	32.02	0.00	0.00
P1	21	31.39	0.00	0.00
P2	1	20.09	22.69	10.50
P2	2	20.20	23.01	11.54
P2	3	22.50	23.98	3.95
P2	4	20.79	21.83	3.79
P2	5	22.60	23.87	4.48
P2	6	19.94	21.78	7.05
P2	7	21.22	22.87	5.61
P2	8	22.60	26.44	14.85
P2	9	23.45	24.37	0.00
P2	10	23.02	25.58	7.07
P2	11	22.85	23.92	0.95
P2	12	20.83	22.82	5.74
P2	13	21.79	24.81	9.97
P2	14	22.53	27.01	16.29
P2	15	21.58	23.37	4.64
P2	16	23.07	24.70	3.38
P2	17	20.52	23.26	9.76
P2	18	23.65	26.57	9.99
P2	19	20.64	23.26	10.36
P2	20	21.50	22.38	1.57
P2	21	22.05	24.13	7.17
F1	1	27.20	28.31	2.45
F1	2	29.63	31.49	4.73
F1	3	28.40	31.96	6.91
F1	4	28.55	31.11	5.23
F1	5	27.55	29.02	1.53
F1	6	28.94	31.74	5.96
F1	7	29.36	32.65	7.53
F1	8	30.36	34.42	9.77
F1	9	29.61	32.82	7.16

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F1	10	28.84	30.64	2.47
F1	11	25.06	27.67	6.34
F1	12	27.79	31.60	10.10
F1	13	29.28	33.88	12.27
F1	14	27.25	30.99	10.26
F1	15	28.42	32.79	11.97
F1	16	26.14	29.18	6.88
F1	17	28.29	31.55	7.95
F1	18	29.00	33.13	10.87
F1	19	28.55	31.33	4.89
F1	20	28.99	32.91	8.75
F1	21	28.36	32.43	9.82
F2	1	25.06	27.67	6.34
F2	2	32.04	35.32	4.20
F2	3	29.83	31.67	0.00
F2	4	29.72	31.90	1.23
F2	5	28.31	32.02	8.75
F2	6	23.82	26.02	4.68
F2	7	21.35	25.65	12.77
F2	8	35.17	38.84	2.82
F2	9	26.29	28.80	1.88
F2	10	24.05	27.23	5.67
F2	11	30.56	37.03	13.78
F2	12	22.36	25.53	6.65
F2	13	30.22	33.40	2.87
F2	14	36.29	39.81	2.05
F2	15	21.69	26.74	15.99
F2	16	35.39	39.20	3.15
F2	17	27.08	30.86	6.44
F2	18	24.83	31.34	19.07
F2	19	23.93	25.89	0.52
F2	20	19.44	23.72	14.74
F2	21	25.39	28.92	6.38
F2	22	32.17	30.21	4.28
F2	23	29.34	26.54	0.00
F2	24	30.53	27.92	1.26
F2	25	29.84	29.13	8.92
F2	26	25.34	23.90	4.50
F2	27	23.02	23.19	12.28
F2	28	35.15	32.56	2.71
F2	29	26.37	24.22	1.81
F2	30	24.09	22.87	5.45
F2	31	30.48	30.97	13.29
F2	32	22.33	21.64	6.41
F2	33	33.88	31.77	2.77
F2	34	36.12	33.63	1.97
F2	35	21.57	22.58	15.42
F2	36	36.00	33.85	3.04
F2	37	27.23	26.34	6.17
F2	38	24.47	26.21	18.49
F2	39	24.19	22.52	0.50

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	40	19.72	20.70	14.29
F2	41	25.87	25.35	6.18
F2	42	32.66	31.41	4.09
F2	43	29.78	27.60	0.00
F2	44	30.99	29.04	1.21
F2	45	30.29	30.30	8.60
F2	46	25.73	24.90	4.68
F2	47	23.28	24.11	12.77
F2	48	35.55	33.85	2.82
F2	49	26.97	25.19	1.88
F2	50	24.63	23.78	5.67
F2	51	31.17	32.20	13.78
F2	52	22.58	21.98	6.65
F2	53	34.26	32.64	2.87
F2	54	37.14	34.55	2.05
F2	55	22.18	23.20	15.99
F2	56	37.02	34.78	3.15
F2	57	28.00	27.06	6.40
F2	58	25.16	27.14	18.96
F2	59	25.57	23.01	0.52
F2	60	20.84	21.15	14.66
F2	61	31.47	28.68	0.00
F2	62	32.75	30.18	1.28
F2	63	32.02	31.49	9.09
F2	64	27.19	25.83	4.86
F2	65	24.60	25.01	13.26
F2	66	37.57	35.11	2.93
F2	67	28.19	26.12	1.96
F2	68	25.75	24.66	5.89
F2	69	32.58	33.40	14.31
F2	70	23.59	22.79	6.90
F2	71	35.80	33.47	2.98
F2	72	38.18	35.43	2.13
F2	73	22.80	23.79	16.61
F2	74	32.08	35.66	3.27
F2	75	24.26	27.75	6.65
F2	76	21.80	27.61	19.69
F2	77	21.56	21.16	0.54
F2	78	17.57	19.45	15.39
F2	79	23.63	24.36	6.66
F2	80	30.07	30.42	4.41
F2	81	27.39	26.70	0.00
F2	82	28.81	28.40	1.30
F2	83	27.32	28.77	9.34
F2	84	24.69	24.53	5.00
F2	85	22.55	23.98	13.63
F2	86	34.77	33.99	3.01
F2	87	24.19	23.45	2.01
F2	88	22.17	22.27	6.22
F2	89	28.02	30.72	15.13
F2	90	20.20	20.88	6.15

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	91	30.76	30.35	2.65
F2	92	32.93	32.25	1.89
F2	93	19.51	21.48	14.80
F2	94	31.62	31.27	2.91
F2	95	23.30	19.82	5.93
F2	96	22.38	22.21	17.54
F2	97	23.54	20.03	0.48
F2	98	18.28	17.51	13.56
F2	99	25.29	22.61	5.87
F2	100	30.66	26.89	3.88
F2	101	30.42	25.70	0.00
F2	102	30.79	27.39	1.14
F2	103	30.52	28.98	8.11
F2	104	25.37	23.26	4.34
F2	105	23.17	22.48	11.84
F2	106	35.52	31.69	2.61
F2	107	25.97	22.97	1.79
F2	108	24.61	22.51	5.38
F2	109	27.99	27.39	13.08
F2	110	21.34	19.53	6.31
F2	111	33.67	29.81	2.72
F2	112	36.24	31.85	1.94
F2	113	22.23	21.59	15.18
F2	114	34.40	30.01	3.03
F2	115	26.11	23.43	6.16
F2	116	23.43	23.28	17.99
F2	117	23.06	20.02	0.49
F2	118	18.61	18.21	13.91
F2	119	31.55	27.26	0.00
F2	120	29.15	25.47	1.19
F2	121	28.48	26.56	8.42
F2	122	24.73	22.28	4.50
F2	123	22.12	21.34	12.28
F2	124	33.11	29.35	2.71
F2	125	25.48	22.41	1.81
F2	126	23.35	21.23	5.46
F2	127	30.37	29.54	13.29
F2	128	22.16	20.32	6.41
F2	129	34.89	29.81	2.77
F2	130	35.91	30.46	1.97
F2	131	21.35	20.36	15.42
F2	132	35.28	30.21	3.04
F2	133	26.79	23.62	6.25
F2	134	23.88	23.32	18.49
F2	135	22.93	19.20	0.50
F2	136	18.21	17.19	14.29
F2	137	26.13	23.03	6.18
F2	138	35.35	30.58	4.12
F2	139	30.64	25.53	0.00
F2	140	33.97	28.63	1.21
F2	141	30.94	27.83	8.75

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	142	29.72	28.70	4.68
F2	143	26.40	27.35	12.77
F2	144	41.27	39.30	2.82
F2	145	28.42	26.54	1.88
F2	146	26.00	25.09	5.67
F2	147	32.98	34.06	13.78
F2	148	23.17	22.56	6.65
F2	149	36.12	34.03	2.87
F2	150	35.33	32.87	2.05
F2	151	21.87	22.87	15.99
F2	152	36.84	34.61	3.15
F2	153	27.41	26.49	6.40
F2	154	26.58	28.45	18.96
F2	155	26.64	23.97	0.52
F2	156	20.72	21.03	14.66
F2	157	28.63	27.11	6.59
F2	158	34.55	32.67	4.36
F2	159	33.93	30.91	0.00
F2	160	38.55	35.52	1.28
F2	161	33.93	33.37	9.09
F2	162	28.19	26.78	4.86
F2	163	26.03	26.46	13.26
F2	164	39.46	36.87	2.93
F2	165	28.85	26.74	1.96
F2	166	26.79	25.66	5.89
F2	167	31.82	32.62	14.31
F2	168	25.02	24.17	6.90
F2	169	39.85	37.47	2.98
F2	170	36.50	40.42	2.13
F2	171	20.40	25.40	16.61
F2	172	31.69	35.42	3.27
F2	173	24.02	27.62	6.73
F2	174	21.46	27.70	19.91
F2	175	20.96	23.14	0.54
F2	176	19.26	24.24	16.80
F2	177	32.15	36.34	3.31
F2	178	24.32	28.28	6.84
F2	179	21.85	28.14	20.24
F2	180	22.11	23.86	0.55
F2	181	18.03	21.93	15.65
F2	182	24.19	27.47	6.77
F2	183	30.78	34.30	4.61
F2	184	28.04	30.10	0.00
F2	185	29.49	32.01	1.35
F2	186	27.97	32.41	9.60
F2	187	25.03	27.64	5.14
F2	188	22.86	27.02	14.01
F2	189	35.25	38.29	3.09
F2	190	24.52	26.41	2.07
F2	191	22.47	25.12	6.22
F2	192	28.40	33.97	15.13

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	193	20.48	23.08	7.30
F2	194	30.82	33.55	3.15
F2	195	32.99	32.25	2.25
F2	196	19.55	21.48	17.55
F2	197	31.68	31.27	3.46
F2	198	23.35	23.71	5.93
F2	199	22.43	25.22	17.54
F2	200	23.59	22.74	0.48
F2	201	18.49	19.92	13.56
F2	202	25.58	25.73	5.87
F2	203	31.01	30.61	3.89
F2	204	30.76	29.25	0.00
F2	205	31.14	29.94	1.14
F2	206	31.11	32.43	8.11
F2	207	25.86	26.04	4.34
F2	208	23.35	25.16	12.12
F2	209	36.43	35.46	2.67
F2	210	26.63	25.71	1.79
F2	211	25.24	25.19	5.38
F2	212	28.71	30.65	13.08
F2	213	21.71	22.15	6.31
F2	214	34.25	33.82	2.72
F2	215	36.87	36.14	1.97
F2	216	22.23	24.49	15.39
F2	217	34.40	34.04	3.03
F2	218	26.11	26.58	6.16
F2	219	23.43	26.42	18.24
F2	220	23.06	22.34	0.50
F2	221	18.61	20.33	14.10
F2	222	31.55	30.42	0.00
F2	223	29.15	28.42	1.19
F2	224	28.48	29.64	8.44
F2	225	22.36	24.86	4.51
F2	226	20.00	23.80	12.31
F2	227	29.93	33.11	2.72
F2	228	23.03	25.27	1.82
F2	229	21.11	23.95	5.53
F2	230	27.45	33.32	13.44
F2	231	20.05	22.92	6.48
F2	232	30.40	33.89	2.80
F2	233	31.29	34.63	2.00
F2	234	18.60	23.15	15.72
F2	235	30.73	34.94	3.10
F2	236	23.39	27.30	6.30
F2	237	21.28	26.95	18.96
F2	238	20.43	22.19	0.52
F2	239	16.22	19.87	14.66
F2	240	23.28	26.61	6.34
F2	241	31.50	35.34	4.20
F2	242	27.30	29.50	0.00
F2	243	25.30	33.08	1.23

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	244	24.27	32.16	8.75
F2	245	23.32	29.83	4.68
F2	246	20.71	28.37	12.77
F2	247	32.39	40.76	2.82
F2	248	22.05	27.52	1.88
F2	249	20.17	28.57	5.67
F2	250	26.63	38.77	13.78
F2	251	18.72	25.68	6.65
F2	252	29.17	38.73	2.87
F2	253	28.06	36.99	1.85
F2	254	17.37	25.74	14.46
F2	255	29.26	38.95	2.85
F2	256	21.77	29.81	5.79
F2	257	21.11	32.01	17.14
F2	258	20.58	26.76	0.47
F2	259	16.01	23.48	13.26
F2	260	22.12	30.27	5.74
F2	261	26.70	35.86	3.80
F2	262	26.22	33.93	0.00
F2	263	29.79	38.98	1.12
F2	264	26.22	30.88	7.93
F2	265	22.19	24.78	4.33
F2	266	20.49	24.49	11.81
F2	267	31.06	34.12	2.61
F2	268	22.71	24.74	1.74
F2	269	21.09	23.80	5.24
F2	270	25.05	30.24	12.75
F2	271	19.71	22.42	5.14
F2	272	31.39	34.54	2.34
F2	273	34.11	37.26	1.67
F2	274	19.07	23.97	13.03
F2	275	29.61	33.43	2.57
F2	276	22.44	26.07	5.22
F2	277	20.05	25.80	15.45
F2	278	19.54	21.55	0.44
F2	279	17.70	22.01	12.43
F2	280	26.64	29.25	0.00
F2	281	24.63	27.69	1.05
F2	282	24.61	29.53	7.42
F2	283	21.13	24.49	3.97
F2	284	18.51	22.97	10.83
F2	285	28.42	32.41	2.39
F2	286	21.96	24.83	1.60
F2	287	20.68	24.17	5.46
F2	288	27.10	33.96	13.29
F2	289	19.76	23.34	6.41
F2	290	32.37	34.60	2.80
F2	291	32.32	34.30	2.00
F2	292	19.98	23.84	15.60
F2	293	33.32	35.71	3.07
F2	294	25.54	28.16	6.25

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	295	21.11	26.07	18.63
F2	296	0.00	0.00	0.00
F2	297	0.00	0.00	0.00
F2	298	0.00	0.00	0.00
F2	299	0.00	0.00	0.00
F2	300	0.00	0.00	0.00
F2	301	0.00	0.00	0.00
F2	302	0.00	0.00	0.00
F2	303	0.00	0.00	0.00
F2	304	0.00	0.00	0.00
F2	305	0.00	0.00	0.00
F2	306	0.00	0.00	0.00
F2	307	0.00	0.00	0.00
F2	308	0.00	0.00	0.00
F2	309	0.00	0.00	0.00
F2	310	0.00	0.00	0.00
F2	311	0.00	0.00	0.00
F2	312	0.00	0.00	0.00
F2	313	0.00	0.00	0.00
F2	314	0.00	0.00	0.00
F2	315	0.00	0.00	0.00
F2	316	0.00	0.00	0.00
F2	317	0.00	0.00	0.00
F2	318	0.00	0.00	0.00
F2	319	0.00	0.00	0.00
F2	320	0.00	0.00	0.00
F2	321	0.00	0.00	0.00
F2	322	0.00	0.00	0.00
F2	323	0.00	0.00	0.00
F2	324	0.00	0.00	0.00
F2	325	0.00	0.00	0.00
F2	326	0.00	0.00	0.00
F2	327	0.00	0.00	0.00
F2	328	0.00	0.00	0.00
F2	329	0.00	0.00	0.00
F2	330	0.00	0.00	0.00
F2	331	0.00	0.00	0.00
F2	332	0.00	0.00	0.00
F2	333	0.00	0.00	0.00
F2	334	0.00	0.00	0.00
F2	335	0.00	0.00	0.00
F2	336	0.00	0.00	0.00
F2	337	0.00	0.00	0.00
F2	338	0.00	0.00	0.00
F2	339	0.00	0.00	0.00
F2	340	0.00	0.00	0.00
F2	341	0.00	0.00	0.00
F2	342	0.00	0.00	0.00
F2	343	0.00	0.00	0.00
F2	344	0.00	0.00	0.00
F2	345	0.00	0.00	0.00

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	346	0.00	0.00	0.00
F2	347	0.00	0.00	0.00
F2	348	0.00	0.00	0.00
F2	349	0.00	0.00	0.00
F2	350	0.00	0.00	0.00
F2	351	0.00	0.00	0.00
F2	352	0.00	0.00	0.00
F2	353	0.00	0.00	0.00
F2	354	0.00	0.00	0.00
F2	355	0.00	0.00	0.00
F2	356	0.00	0.00	0.00
F2	357	0.00	0.00	0.00
F2	358	0.00	0.00	0.00
F2	359	0.00	0.00	0.00
F2	360	0.00	0.00	0.00
F2	361	0.00	0.00	0.00
F2	362	0.00	0.00	0.00
F2	363	0.00	0.00	0.00
F2	364	0.00	0.00	0.00
F2	365	0.00	0.00	0.00
F2	366	0.00	0.00	0.00
F2	367	0.00	0.00	0.00
F2	368	0.00	0.00	0.00
F2	369	0.00	0.00	0.00
F2	370	0.00	0.00	0.00
F2	371	0.00	0.00	0.00
F2	372	0.00	0.00	0.00
F2	373	0.00	0.00	0.00
F2	374	0.00	0.00	0.00
F2	375	0.00	0.00	0.00
F2	376	0.00	0.00	0.00
F2	377	0.00	0.00	0.00
F2	378	0.00	0.00	0.00
F2	379	0.00	0.00	0.00
F2	380	0.00	0.00	0.00
F2	381	0.00	0.00	0.00
F2	382	0.00	0.00	0.00
F2	383	0.00	0.00	0.00
F2	384	0.00	0.00	0.00
F2	385	0.00	0.00	0.00
F2	386	0.00	0.00	0.00
F2	387	0.00	0.00	0.00
F2	388	0.00	0.00	0.00
F2	389	0.00	0.00	0.00
F2	390	0.00	0.00	0.00
F2	391	0.00	0.00	0.00
F2	392	0.00	0.00	0.00
F2	393	0.00	0.00	0.00
F2	394	0.00	0.00	0.00
F2	395	0.00	0.00	0.00
F2	396	0.00	0.00	0.00

APPENDIX D: Mean Values for screened Progenies of Swarna Sub1 × FARO 57 under submergence condition in the Second Year continued

ENTRY	S/N	BEFORE SUBMERGENCE	AFTER SUBMERGENCE	% SHOOT TIP ELONGATION (CM)
F2	397	0.00	0.00	0.00
F2	398	0.00	0.00	0.00
F2	399	0.00	0.00	0.00
F2	400	0.00	0.00	0.00
F2	401	0.00	0.00	0.00
F2	402	0.00	0.00	0.00
BC1	1	0.00	0.00	0.00
BC1	2	0.00	0.00	0.00
BC1	3	37.52	38.41	2.62
BC1	4	28.00	28.68	2.68
BC1	5	27.51	27.10	0.19
BC1	6	27.52	27.88	1.45
BC1	7	18.85	19.50	3.76
BC1	8	27.91	28.13	0.88
BC1	9	35.13	35.29	0.49
BC1	10	0.00	0.00	0.00
BC1	11	0.00	0.00	0.00
BC1	12	0.00	0.00	0.00
BC1	13	0.00	0.00	0.00
BC1	14	0.00	0.00	0.00
BC1	15	0.00	0.00	0.00
BC2	1	30.46	33.58	11.72
BC2	2	23.64	25.23	7.71
BC2	3	37.43	40.62	9.75
BC2	4	0.00	0.00	0.00
BC2	5	25.15	28.31	14.37
BC2	6	0.00	0.00	0.00
BC2	7	28.49	32.90	17.71
BC2	8	21.46	28.37	13.13
BC2	9	20.91	22.73	9.94
BC2	10	0.00	0.00	0.00
BC2	11	28.49	30.27	7.14
BC2	12	25.56	29.35	16.94
BC2	13	24.39	28.76	21.06
BC2	14	22.64	26.30	18.69
BC2	15	21.54	24.49	15.87

Appendix E: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44)

Conditions	**Year I**						**Year II**					
	Response	Variable:	SW									
	Source	DF	SS	MS	F-Value	P-Value	Source	DF	SS	MS	F-Value	P-Value
Normal	rep	2	0.0064	0.0032	0.57	0.5844	rep	2	0.0156	0.0078	1.66	0.2383
	Entries	5	3.1863	0.6373	113.79	0.0000	Entries	5	2.9253	0.5851	125	0.0000
	Error	10	0.056	0.0056			Error	10	0.0468	0.0047		
	Total	17	3.2486				Total	17	2.9876			
	Response	Variable:	SW									
Submerged	rep	2	0.0407	0.0204	2.82	0.1072	rep	2	0.0715	0.0358	1.2	0.3398
	Entries	5	20.0697	4.0139	555.21	0.0000	Entries	5	22.552	4.5104	151.99	0.0000
	Error	10	0.0723	0.0072			Error	10	0.2968	0.0297		
	Total	17	20.1827				Total	17	22.9203			
	Response	Variable:	GW									
Normal	rep	2	0.0001	0	0.01	0.9930	rep	2	0.0058	0.0029	0.22	0.8089
	Entries	5	0.1728	0.0346	8.83	0.0020	Entries	5	0.1908	0.0382	2.85	0.0748
	Error	10	0.0391	0.0039			Error	10	0.134	0.0134		
	Total	17	0.212				Total	17	0.3306			
	Response	Variable:	GW									
Submerged	rep	2	0.0234	0.0117	0.37	0.6966	rep	2	0.0192	0.0096	0.53	0.6068
	Entries	5	20.0901	4.018	129.03	0.0000	Entries	5	16.1891	3.2378	177.24	0.0000
	Error	10	0.3114	0.0311			Error	10	0.1827	0.0183		
	Total	17	20.4249				Total	17	16.391			
	Response	Variable:	GL									
Normal	rep	2	0.0566	0.0283	0.24	0.7895	rep	2	0.0573	0.0287	0.11	0.8943
	Entries	5	10.4831	2.0966	17.93	0.0001	Entries	5	10.9174	2.1835	8.61	0.0022
	Error	10	1.1691	0.1169			Error	10	2.5367	0.2537		
	Total	17	11.7088				Total	17	13.5115			
	Response	Variable:	GL									
Submerged	rep	2	0.6355	0.3178	1.04	0.3883	rep	2	0.2966	0.1483	0.48	0.6302
	Entries	5	379.1326	75.8265	248.52	0	Entries	5	316.6995	63.3399	206.66	0
	Error	10	3.0512	0.3051			Error	10	3.065	0.3065		
	Total	17	382.8192				Total	17	320.0611			

Appendix E: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44)

Conditions	**Year I**						**Year II**					
	Response	Variable:	FLW									
Normal	rep	2	0.1513	0.0757	0.5	0.6231	rep	2	0.1935	0.0968	0.57	0.5853
	Entries	5	0.4519	0.0904	0.59	0.7067	Entries	5	0.6538	0.1308	0.76	0.5959
	Error	10	1.5251	0.1525			Error	10	1.7114	0.1711		
	Total	17	2.1283				Total	17	2.5587			
	Response	Variable:	FLW									
Submerged	rep	2	0.1183	0.0591	0.23	0.7992	rep	2	0.0811	0.0405	0.2	0.8245
	Entries	5	10.1282	2.0256	7.85	0.0031	Entries	5	8.2841	1.6568	8.04	0.0028
	Error	10	2.5798	0.258			Error	10	2.0601	0.206		
	Total	17	12.8263				Total	17	10.4253			
	Response	Variable:	FLL									
Normal	rep	2	104.6252	52.3126	10.58	0.0034	rep	2	114.8068	57.4034	11.33	0.0027
	Entries	5	107.1435	21.4287	4.33	0.0233	Entries	5	122.5085	24.5017	4.84	0.0166
	Error	10	49.4597	4.946			Error	10	50.6681	5.0668		
	Total	17	261.2284				Total	17	287.9834			
	Response	Variable:	FLL									
Submerged	rep	2	87.6956	43.8478	3.37	0.0759	rep	2	87.6011	43.8006	4.78	0.0349
	Entries	5	4768.495	953.699	73.39	0	Entries	5	3936.171	787.2343	85.94	0
	Error	10	129.9576	12.9958			Error	10	91.6036	9.1604		
	Total	17	4986.148				Total	17	4115.376			
	Response	Variable:	SG									
Normal	rep	2	0.0318	0.0159	2.97	0.0969	rep	2	0.0392	0.0196	3.25	0.0816
	Entries	5	0.6609	0.1322	24.75	0	Entries	5	0.6414	0.1283	21.27	0
	Error	10	0.0534	0.0053			Error	10	0.0603	0.006		
	Total	17	0.746				Total	17	0.7409			
	Response	Variable:	SG									
Submerged	rep	2	0.0258	0.0129	0.68	0.5306	rep	2	0.013	0.0065	0.62	0.5576
	Entries	5	18.0016	3.6003	188.74	0	Entries	5	14.8929	2.9786	283	0
	Error	10	0.1908	0.0191			Error	10	0.1052	0.0105		
	Total	17	18.2182				Total	17	15.0112			

Appendix E: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44)

Conditions	Year I						Year II					
	Response	Variable:	F50.									
Normal	rep	2	3.7864	1.8932	0.84	0.4608	rep	2	12.3654	6.1827	1.02	0.395
	Entries	5	1425.111	285.0221	126.19	0	Entries	5	1637.864	327.5729	54.09	0
	Error	10	22.5871	2.2587			Error	10	60.5613	6.0561		
	Total	17	1451.484				Total	17	1710.791			
	Response	Variable:	F50.									
Submerged	rep	2	18.6897	9.3449	0.34	0.7173	rep	2	18.1896	9.0948	2.31	0.15
	Entries	5	34724.62	6944.924	255.27	0	Entries	5	28810.33	5762.066	1462.02	0
	Error	10	272.0649	27.2065			Error	10	39.4116	3.9412		
	Total	17	35015.38				Total	17	28867.93			
	Response	Variable:	TN									
Normal	rep	2	4.4955	2.2477	0.43	0.6641	rep	2	16.7238	8.3619	1.11	0.3684
	Entries	5	201.854	40.3708	7.66	0.0034	Entries	5	213.4173	42.6835	5.64	0.01
	Error	10	52.6926	5.2693			Error	10	75.6588	7.5659		
	Total	17	259.0421				Total	17	305.7999			
	Response	Variable:	TN									
Submerged	rep	2	2.9318	1.4659	0.1	0.9058	rep	2	2.3127	1.1564	0.1	0.9099
	Entries	5	2582.486	516.4972	35.2	0	Entries	5	2124.256	424.8512	35.03	0
	Error	10	146.7379	14.6738			Error	10	121.2779	12.1278		
	Total	17	2732.156				Total	17	2247.847			
	Response	Variable:	PH									
Normal	rep	2	200.6875	100.3437	2.64	0.12	rep	2	212.2873	106.1437	2.01	0.1846
	Entries	5	743.1731	148.6346	3.91	0.0317	Entries	5	1264.847	252.9693	4.79	0.0171
	Error	10	379.9324	37.9932			Error	10	527.9745	52.7975		
	Total	17	1323.793				Total	17	2005.108			
	Response	Variable:	PH									
Submerged	rep	2	124.092	62.046	0.81	0.4716	rep	2	127.6827	63.8413	1.19	0.3451
	Entries	5	29074.45	5814.89	76.01	0	Entries	5	23724.79	4744.958	88.11	0
	Error	10	765.046	76.5046			Error	10	538.5332	53.8533		
	Total	17	29963.59				Total	17	24391.01			

Appendix E: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44)

Conditions	Year I						Year II					
	Response	Variable:	PN									
Normal	rep	2	8.5	4.25	7.7	0.0095	rep	2	11.3669	5.6834	13.73	0.0014
	Entries	5	253.59	50.718	91.87	0	Entries	5	288.9913	57.7983	139.59	0
	Error	10	5.5204	0.552			Error	10	4.1404	0.414		
	Total	17	267.6103				Total	17	304.4986			
	Response	Variable:	PN									
Submerged	rep	2	3.2125	1.6063	0.88	0.4443	rep	2	3.9303	1.9651	2.05	0.1794
	Entries	5	766.8994	153.3799	84.12	0	Entries	5	676.6601	135.332	141.18	0
	Error	10	18.2341	1.8234			Error	10	9.5855	0.9586		
	Total	17	788.346				Total	17	690.1759			
	Response	Variable:	PL									
Normal	rep	2	12.3431	6.1716	0.95	0.4204	rep	2	16.784	8.392	1.32	0.3105
	Entries	5	119.4776	23.8955	3.66	0.0383	Entries	5	130.5974	26.1195	4.1	0.0276
	Error	10	65.2254	6.5225			Error	10	63.6866	6.3687		
	Total	17	197.0462				Total	17	211.0681			
	Response	Variable:	PL									
Submerged	rep	2	17.502	8.751	2.45	0.1363	rep	2	5.2796	2.6398	0.97	0.4133
	Entries	5	2363.717	472.7434	132.28	0	Entries	5	1964.331	392.8662	143.83	0
	Error	10	35.7381	3.5738			Error	10	27.3145	2.7314		
	Total	17	2416.957				Total	17	1996.925			
	Response	Variable:	IL									
Normal	rep	2	0.8557	0.4278	0.15	0.8589	rep	2	2.2444	1.1222	0.41	0.6744
	Entries	5	217.6078	43.5216	15.72	0.0002	Entries	5	230.9778	46.1956	16.87	0.0001
	Error	10	27.6936	2.7694			Error	10	27.384	2.7384		
	Total	17	246.157				Total	17	260.6062			

Appendix E: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44)

Conditions	**Year I**						**Year II**					
	Response	Variable:	IL									
Submerged	rep	2	4.9464	2.4732	0.72	0.5084	rep	2	3.3201	1.6601	0.66	0.5391
	Entries	5	907.1556	181.4311	53.14	0	Entries	5	731.4052	146.281	57.95	0
	Error	10	34.1395	3.4139			Error	10	25.2435	2.5244		
	Total	17	946.2415				Total	17	759.9689			
	Response	Variable:	SY.g.plant.									
Normal	rep	2	71.785	35.8925	6.72	0.0141	rep	2	38.5467	19.2733	1.31	0.3133
	Entries	5	1965.398	393.0796	73.6	0	Entries	5	2637.38	527.476	35.76	0
	Error	10	53.407	5.3407			Error	10	147.5235	14.7523		
	Total	17	2090.59				Total	17	2823.45			
	Response	Variable:	SY.g.plant.									
Submerged	rep	2	19.514	9.757	1.76	0.2214	rep	2	15.5126	7.7563	2.03	0.1814
	Entries	5	2168.555	433.7109	78.23	0	Entries	5	1878.47	375.6939	98.56	0
	Error	10	55.4394	5.5439			Error	10	38.1194	3.8119		
	Total	17	2243.508				Total	17	1932.102			
	Response	Variable:	CPS									
Submerged	rep	2	0.002	0.001	13.460	0.002	rep	2.000	0.033	0.017	6.200	0.018
	Entries	5	4.631	0.926	12996.370	0.000	Entries	5.000	5.228	1.046	387.950	0.000
	Error	10	0.001	0.000			Error	10.000	0.027	0.003		
	Total	17	4.633				Total	17.000	5.289			

Appendix F: Combined ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44) over the two years

		Submerged				Normal			
Response	Variable:	SW				SW			
Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
Conditions	1	0.000	0.000	0.000	0.958	0.007	0.007	1.220	0.332
Rep	4	0.112	0.028	1.520	0.234	0.022	0.006	1.07	0.3996
Entries	5	41.964	8.393	454.830	0.000	6.095	1.219	237.130	0.000
Conditions: Entries	5	0.658	0.132	7.130	0.001	0.017	0.003	0.650	0.662
Pooled	20	0.369	0.019			0.103	0.005	0.005	
Total	35	43.103				6.243			
Response	Variable:	GW				GW			
Conditions	1	0.471	0.471	44.310	0.003	0.1313	0.1313	89.59	0.0007
Rep	4	0.043	0.011	0.430	0.785	0.0059	0.0015	0.17	0.9515
Entries	5	36.143	7.229	292.610	0.000	0.3394	0.0679	7.84	0.0003
Conditions: Entries	5	0.136	0.027	1.100	0.390	0.0243	0.0049	0.56	0.7289
Pooled	20	0.494	0.025			0.1731	0.0087		
Total	35	37.287				0.6739			
Response	Variable:	GL				GL			
Conditions	1	4.748	4.748	20.380	0.011	2.9115	2.9115	102.22	0.0005
Rep	4	0.932	0.233	0.760	0.562	0.1139	0.0285	0.15	0.9591
Entries	5	693.851	138.770	453.780	0.000	20.0109	4.0022	21.6	0
Conditions: Entries	5	1.981	0.396	1.300	0.305	1.3896	0.2779	1.5	0.2343
Pooled	20	6.116	0.306			3.7058	0.1853		
Total	35	707.628				28.1317			
Response	Variable:	FLW				FLW			
Conditions	1	0.170	0.170	3.410	0.139	0.0191	0.0191	0.22	0.6625
Rep	4	0.199	0.050	0.210	0.927	0.3449	0.0862	0.53	0.7131
Entries	5	18.358	3.672	15.830	0.000	1.0846	0.2169	1.34	0.288
Conditions: Entries	5	0.054	0.011	0.050	0.999	0.0211	0.0042	0.03	0.9996
Pooled	20	4.640	0.232			3.2364	0.1618		
Total	35	23.422				4.7061			
Response	Variable:	FLL				FLL			
Conditions	1	93.272	93.272	2.130	0.218	8.0121	8.0121	0.15	0.7218
Rep	4	175.297	43.824	3.960	0.016	219.432	54.858	10.96	0.0001
Entries	5	8679.104	1735.821	156.690	0.000	229.2042	45.8408	9.16	0.0001
Conditions: Entries	5	25.563	5.113	0.460	0.800	0.4478	0.0896	0.02	0.9999
Pooled	20	221.561	11.078			100.1278	5.0064		
Total	35	9194.797				557.2239			
Response	Variable:	SG				SG			
Conditions	1	0.317	0.317	32.630	0.005	0.0361	0.0361	2.03	0.2273
Rep	4	0.039	0.010	0.660	0.630	0.071	0.0178	3.12	0.0378
Entries	5	32.801	6.560	443.260	0.000	1.3019	0.2604	45.79	0.00
Conditions: Entries	5	0.094	0.019	1.260	0.318	0.0003	0.0001	0.010	1.000
Pooled	20	0.296	0.015			0.1137	0.0057		
Total	35	33.546				1.523			
Response	Variable:	F50.				F50.			
Conditions	1	564.296	564.296	61.200	0.001	61.5808	61.5808	15.25	0.0175
Rep	4	36.879	9.220	0.590	0.672	16.1518	4.0379	0.97	0.4451
Entries	5	63340.329	12668.066	813.420	0.000	2999.294	599.8588	144.29	0
Conditions: Entries	5	194.620	38.924	2.500	0.065	63.681	12.7362	3.06	0.0326
Pooled	20	311.477	15.574			83.1484	4.1574		

ppendix F: Combined ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 44) over the two years

		Submerged				Normal			
Total	35	64447.601				3223.856			
Response	Variable:	TN				TN			
Conditions	1	57.119	57.119	43.560	0.003	35.7459	35.7459	6.74	0.0603
Rep	4	5.245	1.311	0.100	0.982	21.2192	5.3048	0.83	0.5237
Entries	5	4694.938	938.988	70.070	0.000	410.7724	82.1545	12.8	0
Conditions: Entries	5	11.804	2.361	0.180	0.968	4.499	0.8998	0.14	0.9808
Pooled	20	268.016	13.401			128.3514	6.4176		
Total	35	5037.121				600.5879			
Response	Variable:	PH				PH			
Conditions	1	669.364	669.364	10.630	0.031	121.377	121.377	1.180	0.339
Rep	4	251.775	62.944	0.970	0.448	412.975	103.244	2.270	0.097
Entries	5	52628.403	10525.681	161.490	0.000	1905.729	381.146	8.400	0.000
Conditions: Entries	5	170.840	34.168	0.520	0.755	102.290	20.458	0.450	0.808
Pooled	20	1303.579	65.179			907.907	45.395		
Total	35	55023.961				3450.278			
Response	Variable:	PN				PN			
Conditions	1	7.921	7.921	4.440	0.103	8.068	8.068	1.620	0.272
Rep	4	7.143	1.786	1.280	0.310	19.867	4.967	10.280	0.000
Entries	5	1441.881	288.376	207.320	0.000	541.182	108.236	224.070	0.000
Conditions: Entries	5	1.678	0.336	0.240	0.939	1.400	0.280	0.580	0.715
Pooled	20	27.820	1.391			9.661	0.483		
Total	35	1486.443				580.177			
Response	Variable:	PL				PL			
Conditions	1	48.127	48.127	8.450	0.044	6.157	6.157	0.850	0.410
Rep	4	22.782	5.695	1.810	0.167	29.127	7.282	1.130	0.371
Entries	5	4316.448	863.290	273.830	0.000	248.985	49.797	7.730	0.000
Conditions: Entries	5	11.600	2.320	0.740	0.605	1.090	0.218	0.030	0.999
Pooled	20	63.053	3.153			128.912	6.446		
Total	35	4462.009				414.271			
Response	Variable:	IL				IL			
Conditions	1	15.088	15.088	7.300	0.054	1.026	1.026	1.320	0.314
Rep	4	8.267	2.067	0.700	0.604	3.100	0.775	0.280	0.887
Entries	5	1632.829	326.566	109.990	0.000	448.251	89.650	32.550	0.000
Conditions: Entries	5	5.732	1.146	0.390	0.852	0.335	0.067	0.020	1.000
Pooled	20	59.383	2.969			55.078	2.754		
Total	35	1721.299				507.789			
Response	Variable:	SY.g.plant.				SY.g.plant.			
Conditions	1	31.021	31.021	3.540	0.133	72.811	72.811	2.640	0.180
Rep	4	35.027	8.757	1.870	0.155	110.332	27.583	2.750	0.057
Entries	5	4040.132	808.026	172.730	0.000	4560.771	912.154	90.790	0.000
Conditions: Entries	5	6.893	1.379	0.290	0.910	42.007	8.402	0.840	0.540
Pooled	20	93.559	4.678			200.930	10.047		
Total	35	4206.630				4986.851			

Appendix G: Pooled ANOVA for Cross I (Swarna sub1 × FARO 44) traits of evaluated under normal and submerged conditions for the two seasons

Source	DF	SS	MS	F-Value	P-Value
Response	Variable:	SW			
Conditions	3	6.210	2.070	123.460	0.000
Rep	8	0.134	0.017	1.420	0.218
Entries	5	20.840	4.168	353.320	0.000
Conditions : Entries	15	27.893	1.860	157.640	0.000
Pooled	40	0.472	0.012		
Total	71	55.549			
Response	Variable:	GW			
Conditions	3	5.910	1.970	325.530	0.000
Rep	8	0.048	0.006	0.360	0.934
Entries	5	19.255	3.851	230.870	0.000
Conditions : Entries	15	17.388	1.159	69.490	0.000
Pooled	40	0.667	0.017		
Total	71	43.268			
Response	Variable:	GL			
Conditions	3	69.804	23.268	177.960	0.000
Rep	8	1.046	0.131	0.530	0.825
Entries	5	360.064	72.013	293.270	0.000
Conditions : Entries	15	357.168	23.811	96.970	0.000
Pooled	40	9.822	0.246		
Total	71	797.905			
Response	Variable:	FLW			
Conditions	3	1.133	0.378	5.550	0.024
Rep	8	0.544	0.068	0.350	0.942
Entries	5	13.762	2.752	13.980	0.000
Conditions : Entries	15	5.756	0.384	1.950	0.047
Pooled	40	7.876	0.197		
Total	71	29.072			
Response	Variable:	FLL			
Conditions	3	589.431	196.477	3.980	0.052
Rep	8	394.729	49.341	6.140	0.000
Entries	5	4457.615	891.523	110.860	0.000
Conditions : Entries	15	4476.704	298.447	37.110	0.000
Pooled	40	321.689	8.042		
Total	71	10240.167			
Response	Variable:	SG			
Conditions	3	5.130	1.710	124.530	0.000
Rep	8	0.110	0.014	1.340	0.252
Entries	5	12.812	2.562	250.160	0.000
Conditions : Entries	15	21.385	1.426	139.180	0.000
Pooled	40	0.410	0.010		
Total	71	39.846			

Appendix G: Pooled ANOVA for Cross I (Swarna sub1 × FARO 44) traits of evaluated under normal and submerged conditions for the two seasons

Source	DF	SS	MS	F-Value	P-Value
Response	Variable:	F50.			
Conditions	3	3646.345	1215.448	183.360	0.000
Rep	8	53.031	6.629	0.670	0.713
Entries	5	42356.181	8471.236	858.660	0.000
Conditions: Entries	15	24241.743	1616.116	163.810	0.000
Pooled	40	394.625	9.866		
Total	71	70691.925			
Response	Variable:	TN			
Conditions	3	668.503	222.834	67.360	0.000
Rep	8	26.464	3.308	0.330	0.948
Entries	5	3161.394	632.279	63.810	0.000
Conditions: Entries	15	1960.620	130.708	13.190	0.000
Pooled	40	396.367	9.909		
Total	71	6213.347			
Response	Variable:	PH			
Conditions	3	4826.345	1608.782	19.360	0.001
Rep	8	664.749	83.094	1.500	0.187
Entries	5	19367.847	3873.569	70.060	0.000
Conditions: Entries	15	35439.416	2362.628	42.730	0.000
Pooled	40	2211.486	55.287		
Total	71	62509.844			
Response	Variable:	PN			
Conditions	3	195.654	65.218	19.320	0.001
Rep	8	27.010	3.376	3.600	0.003
Entries	5	1505.979	301.196	321.440	0.000
Conditions: Entries	15	480.162	32.011	34.160	0.000
Pooled	40	37.481	0.937		
Total	71	2246.285			
Response	Variable:	PL			
Conditions	3	550.553	183.518	28.280	0.000
Rep	8	51.909	6.489	1.350	0.247
Entries	5	1764.628	352.926	73.540	0.000
Conditions: Entries	15	2813.495	187.566	39.080	0.000
Pooled	40	191.965	4.799		
Total	71	5372.549			
Response	Variable:	IL			
Conditions	3	106.081	35.360	24.890	0.000
Rep	8	11.367	1.421	0.500	0.851
Entries	5	1411.552	282.311	98.660	0.000
Conditions: Entries	15	675.594	45.040	15.740	0.000
Pooled	40	114.461	2.862		
Total	71	2319.054			
Response	Variable:	SY.g.plant.			
Source	DF	SS	MS	F-Value	P-Value
Conditions	3	4649.269	1549.756	85.290	0.000
Rep	8	145.358	18.170	2.470	0.028
Entries	5	6383.070	1276.614	173.400	0.000
Conditions: Entries	15	2266.733	151.116	20.530	0.000
Pooled	40	294.489	7.362		
Total	71	13738.920			

Appendix H: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57)

			Year I				Year II			
Conditions	Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
	Response	Variable	SW							
Normal	Rep	2	0.001	0.001	0.490	0.624	0.007	0.003	1.510	0.267
	Entries	5	2.581	0.516	475.460	0.000	2.343	0.469	206.740	0.000
	Error	10	0.011	0.001			0.023	0.002		
	Total	17	2.593				2.373			
	Response	Variable:	SW							
Submerged	rep	2	0.088	0.044	4.460	0.041	0.039	0.020	4.100	0.050
	Entries	5	19.191	3.838	389.090	0.000	15.714	3.143	661.380	0.000
	Error	10	0.099	0.010			0.048	0.005		
	Total	17	19.377				15.800			
	Response	Variable:	GW							
Normal	rep	2	0.001	0.001	0.890	0.441	0.005	0.002	1.390	0.293
	Entries	5	0.033	0.007	10.840	0.001	0.134	0.027	16.120	0.000
	Error	10	0.006	0.001			0.017	0.002		
	Total	17	0.040				0.155			
	Response	Variable:	GW							
Submerged	rep	2	0.003	0.002	0.050	0.948	0.008	0.004	0.190	0.830
	Entries	5	16.061	3.212	114.930	0.000	13.442	2.688	131.750	0.000
	Error	10	0.280	0.028			0.204	0.020		
	Total	17	16.344				13.654			
	Response	Variable:	GL							
Normal	rep	2	0.032	0.016	1.010	0.399	0.022	0.011	0.990	0.407
	Entries	5	6.146	1.229	78.460	0.000	8.876	1.775	159.690	0.000
	Error	10	0.157	0.016			0.111	0.011		
	Total	17	6.334				9.009			
	Response	Variable:	GL							
Submerged	rep	2	0.256	0.128	0.190	0.832	0.430	0.215	0.320	0.733
	Entries	5	240.091	48.018	70.510	0.000	203.714	40.743	60.830	0.000
	Error	10	6.810	0.681			6.698	0.670		
	Total	17	247.157				210.842			

Appendix H: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57)

			Year I				Year II			
Conditions	Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
	Response	Variable:	FLW							
Normal	rep	2	0.134	0.067	0.610	0.564	0.120	0.060	0.490	0.627
	Entries	5	0.333	0.067	0.600	0.700	0.447	0.090	0.730	0.616
	Error	10	1.106	0.111			1.223	0.122		
	Total	17	1.573				1.791			
	Response	Variable:	FLW							
Submerged	rep	2	0.226	0.113	0.840	0.460	0.169	0.084	0.890	0.441
	Entries	5	6.720	1.344	9.990	0.001	5.413	1.083	11.420	0.001
	Error	10	1.346	0.135			0.948	0.095		
	Total	17	8.292				6.530			
	Response	Variable:	FLL							
Normal	rep	2	80.810	40.405	11.190	0.003	86.649	43.324	11.400	0.003
	Entries	5	80.366	16.073	4.450	0.022	89.642	17.928	4.720	0.018
	Error	10	36.117	3.612			38.012	3.801		
	Total	17	197.293				214.302			
	Response	Variable:	FLL							
Submerged	rep	2	48.124	24.062	1.920	0.197	41.386	20.693	2.590	0.124
	Entries	5	2995.928	599.186	47.880	0.000	2426.378	485.276	60.780	0.000
	Error	10	125.151	12.515			79.838	7.984		
	Total	17	3169.203				2547.602			
	Response	Variable:	SG							
Normal	rep	2	0.023	0.012	2.710	0.115	0.027	0.013	3.370	0.076
	Entries	5	0.506	0.101	23.560	0.000	0.497	0.099	25.100	0.000
	Error	10	0.043	0.004			0.040	0.004		
	Total	17	0.573				0.563			
	Response	Variable:	SG							
Submerged	rep	2	0.140	0.070	0.900	0.438	0.078	0.039	0.760	0.493
	Entries	5	13.539	2.708	34.630	0.000	11.564	2.313	45.030	0.000
	Error	10	0.782	0.078			0.514	0.051		
	Total	17	14.462				12.155			

Appendix H: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57)

			Year I				Year II			
Conditions	Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
	Response	Variable:	F50.							
Normal	rep	2	3.661	1.830	0.810	0.473	9.521	4.760	0.940	0.424
	Entries	5	1422.781	284.556	125.620	0.000	1646.883	329.377	64.770	0.000
	Error	10	22.653	2.265			50.857	5.086		
	Total	17	1449.095				1707.260			
	Response	Variable:	F50.							
Submerged	rep	2	21.153	10.576	3.260	0.081	2.873	1.437	0.710	0.516
	Entries	5	20551.044	4110.209	1268.680	0.000	16710.865	3342.173	1648.500	0.000
	Error	10	32.398	3.240			20.274	2.027		
	Total	17	20604.594				16734.013			
	Response	Variable:	TN							
Normal	rep	2	4.589	2.295	0.600	0.566	6.966	3.483	0.650	0.544
	Entries	5	124.801	24.960	6.550	0.006	155.602	31.120	5.780	0.009
	Error	10	38.090	3.809			53.829	5.383		
	Total	17	167.480				216.397			
	Response	Variable:	TN							
Submerged	rep	2	15.289	7.644	1.360	0.301	13.198	6.599	1.870	0.205
	Entries	5	2143.176	428.635	76.100	0.000	1727.824	345.565	97.780	0.000
	Error	10	56.326	5.633			35.341	3.534		
	Total	17	2214.790				1776.363			
	Response	Variable:	PH							
Normal	rep	2	154.741	77.370	2.870	0.104	151.709	75.854	2.010	0.185
	Entries	5	464.427	92.886	3.440	0.046	868.659	173.732	4.600	0.019
	Error	10	269.960	26.996			377.399	37.740		
	Total	17	889.128				1397.768			
	Response	Variable:	PH							
Submerged	rep	2	189.079	94.540	1.810	0.214	134.484	67.242	1.810	0.213
	Entries	5	25721.481	5144.296	98.220	0.000	20743.746	4148.749	111.890	0.000
	Error	10	523.745	52.375			370.789	37.079		
	Total	17	26434.306				21249.018			

Appendix H: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57)

			Year I				Year II			
Conditions	Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
	Response	Variable:	PN							
Normal	rep	2	6.219	3.110	10.110	0.004	6.922	3.461	9.710	0.005
	Entries	5	172.129	34.426	111.900	0.000	188.912	37.783	105.970	0.000
	Error	10	3.076	0.308			3.565	0.357		
	Total	17	181.424				199.399			
	Response	Variable:	PN							
Submerged	rep	2	2.690	1.345	1.170	0.350	2.053	1.026	1.240	0.329
	Entries	5	652.529	130.506	113.240	0.000	556.875	111.375	134.990	0.000
	Error	10	11.525	1.153			8.251	0.825		
	Total	17	666.744				567.178			
	Response	Variable:	PL							
Normal	rep	2	10.567	5.283	1.170	0.350	11.014	5.507	1.130	0.361
	Entries	5	93.378	18.676	4.130	0.027	97.738	19.548	4.010	0.029
	Error	10	45.227	4.523			48.709	4.871		
	Total	17	149.172				157.461			
	Response	Variable:	PL							
Submerged	rep	2	20.120	10.060	0.860	0.451	14.872	7.436	0.990	0.406
	Entries	5	1814.348	362.870	31.160	0.000	1465.303	293.061	38.950	0.000
	Error	10	116.464	11.646			75.244	7.524		
	Total	17	1950.932				1555.420			
	Response	Variable:	IL							
Normal	rep	2	1.238	0.619	0.310	0.738	1.868	0.934	0.410	0.673
	Entries	5	165.968	33.194	16.800	0.000	164.995	32.999	14.570	0.000
	Error	10	19.756	1.976			22.642	2.264		
	Total	17	186.961				189.504			
	Response	Variable:	IL							
Submerged	rep	2	1.661	0.830	0.430	0.661	0.532	0.266	0.130	0.876
	Entries	5	687.155	137.431	71.530	0.000	566.868	113.374	57.150	0.000
	Error	10	19.214	1.921			19.838	1.984		
	Total	17	708.029				587.239			

Appendix H: Individual ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57)

			Year I				Year II			
Conditions	Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
	Response	Variable:	SY							
Normal	rep	2	36.101	18.051	10.060	0.004	27.086	13.543	5.250	0.028
	Entries	5	1375.476	275.095	153.380	0.000	1695.062	339.012	131.340	0.000
	Error	10	17.936	1.794			25.811	2.581		
	Total	17	1429.513				1747.959			
	Response	Variable:	SY							
Submerged	rep	2	13.010	6.505	1.590	0.252	14.886	7.443	2.810	0.107
	Entries	5	1519.776	303.955	74.260	0.000	1303.938	260.788	98.530	0.000
	Error	10	40.932	4.093			26.468	2.647		
	Total	17	1573.718				1345.292			
	Response	Variable:	CPS							
Submerged	rep	2	0.019	0.009	21.320	0.000	0.002	0.001	7.420	0.011
	Entries	5	3.193	0.639	1470.530	0.000	7.127	1.426	14444.870	0.000
	Error	10	0.004	0.000			0.001	0.000		
	Total	17	3.216				7.130			

Appendix I: Combined ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57) over the two years

		Normal				Submerged			
Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
Response	Variable:	SW							
Conditions	1	0.020	0.020	10.030	0.034	0.386	0.386	12.180	0.025
Rep	4	0.008	0.002	1.180	0.349	0.127	0.032	4.340	0.011
Entries	5	4.916	0.983	586.570	0.000	34.795	6.959	952.220	0.000
Conditions: Entries	5	0.008	0.002	0.960	0.467	0.110	0.022	3.010	0.035
Pooled	20	0.034	0.002			0.146	0.007		
Total	35	4.985				35.564			
Response	Variable:	GW							
Conditions	1	0.128	0.128	89.900	0.001	0.278	0.278	103.250	0.001
Rep	4	0.006	0.001	1.260	0.319	0.011	0.003	0.110	0.977
Entries	5	0.121	0.024	21.240	0.000	29.427	5.886	243.430	0.000
Conditions: Entries	5	0.046	0.009	8.150	0.000	0.076	0.015	0.630	0.681
Pooled	20	0.023	0.001			0.484	0.024		
Total	35	0.323				30.276			
Response	Variable:	GL							
Conditions	1	1.360	1.360	101.690	0.001	3.724	3.724	21.730	0.010
Rep	4	0.054	0.013	1.000	0.431	0.686	0.171	0.250	0.904
Entries	5	14.229	2.846	212.520	0.000	442.722	88.544	131.100	0.000
Conditions : Entries	5	0.793	0.159	11.840	0.000	1.083	0.217	0.320	0.895
Pooled	20	0.268	0.013			13.508	0.675		
Total	35	16.703				461.723			
Response Variable: FLW									
Conditions	1	0.020	0.020	0.310	0.606	0.155	0.155	1.570	0.278
Rep	4	0.254	0.064	0.540	0.705	0.395	0.099	0.860	0.504
Entries	5	0.773	0.155	1.330	0.293	12.097	2.419	21.100	0.000
Conditions : Entries	5	0.008	0.002	0.010	1.000	0.037	0.007	0.060	0.997
Pooled	20	2.329	0.116			2.294	0.115		
Total	35	3.383				14.977			
Response	Variable:	FLL							
Conditions	1	7.461	7.461	0.180	0.695	69.050	69.050	3.090	0.154
Rep	4	167.459	41.865	11.300	0.000	89.511	22.378	2.180	0.108
Entries	5	169.807	33.962	9.160	0.000	5403.507	1080.701	105.440	0.000
Conditions : Entries	5	0.200	0.040	0.010	1.000	18.799	3.760	0.370	0.865
Pooled	20	74.129	3.706			204.989	10.249		
Total	35	419.057				5785.854			
Response Variable: SG									
Conditions	1	0.028	0.028	2.220	0.211	0.186	0.186	3.400	0.139
Rep	4	0.050	0.013	3.030	0.042	0.218	0.055	0.840	0.514
Entries	5	1.003	0.201	48.590	0.000	25.058	5.012	77.370	0.000
Conditions : Entries	5	0.000	0.000	0.010	1.000	0.045	0.009	0.140	0.982
Pooled	20	0.083	0.004			1.296	0.065		
Total	35	1.164				26.803			
Response	Variable:	F50.							
Conditions	1	96.450	96.450	29.270	0.006	414.777	414.777	69.060	0.001
Rep	4	13.181	3.295	0.900	0.484	24.026	6.007	2.280	0.096
Entries	5	3026.220	605.244	164.670	0.000	37139.159	7427.832	2820.430	0.000
Conditions : Entries	5	43.443	8.689	2.360	0.077	122.750	24.550	9.320	0.000
Pooled	20	73.510	3.676			52.672	2.634		
Total	35	3252.804				37753.384			

Appendix I: Combined ANOVA for traits evaluated under normal and submerged conditions for Cross I (Swarna sub1 × FARO 57) over the two years

	Normal					Submerged			
Source	DF	SS	MS	F-value	P-value	SS	MS	F-value	P-value
Response	Variable:	TN							
Conditions	1	21.189	21.189	7.330	0.054	42.120	42.120	5.910	0.072
Rep	4	11.555	2.889	0.630	0.648	28.486	7.122	1.550	0.225
Entries	5	278.104	55.621	12.100	0.000	3857.304	771.461	168.320	0.000
Conditions : Entries	5	2.299	0.460	0.100	0.991	13.696	2.739	0.600	0.702
Pooled	20	91.919	4.596			91.667	4.583		
Total	35	405.066				4033.273			
Response	Variable:	PH							
Conditions	1	150.569	150.569	1.970	0.234	611.075	611.075	7.550	0.052
Rep	4	306.450	76.612	2.370	0.087	323.563	80.891	1.810	0.167
Entries	5	1282.932	256.586	7.930	0.000	46307.945	9261.589	207.070	0.000
Conditions : Entries	5	50.155	10.031	0.310	0.901	157.282	31.456	0.700	0.628
Pooled	20	647.359	32.368			894.535	44.727		
Total	35	2437.464				48294.399			
Response	Variable:	PN							
Conditions	1	7.698	7.698	2.340	0.201	8.654	8.654	7.300	0.054
Rep	4	13.141	3.285	9.890	0.000	4.742	1.186	1.200	0.342
Entries	5	360.678	72.136	217.220	0.000	1207.220	241.444	244.180	0.000
Conditions : Entries	5	0.363	0.073	0.220	0.950	2.184	0.437	0.440	0.814
Pooled	20	6.642	0.332			19.776	0.989		
Total	35	388.522				1242.577			
Response	Variable:	PL							
Conditions	1	6.834	6.834	1.270	0.323	43.490	43.490	4.970	0.090
Rep	4	21.581	5.395	1.150	0.363	34.992	8.748	0.910	0.476
Entries	5	190.978	38.196	8.130	0.000	3268.846	653.769	68.200	0.000
Conditions : Entries	5	0.139	0.028	0.010	1.000	10.805	2.161	0.230	0.947
Pooled	20	93.937	4.697			191.709	9.585		
Total	35	313.467				3549.842			
Response	Variable:	IL							
Conditions	1	1.000	1.000	1.290	0.320	11.365	11.365	20.730	0.010
Rep	4	3.105	0.776	0.370	0.830	2.193	0.548	0.280	0.887
Entries	5	330.592	66.118	31.190	0.000	1250.670	250.134	128.100	0.000
Conditions : Entries	5	0.371	0.074	0.030	0.999	3.354	0.671	0.340	0.880
Pooled	20	42.398	2.120			39.052	1.953		
Total	35	377.465				1306.632			
Response	Variable:	SY							
Conditions	1	57.283	57.283	3.630	0.130	15.379	15.379	2.210	0.212
Rep	4	63.187	15.797	7.220	0.001	27.895	6.974	2.070	0.123
Entries	5	3049.389	609.878	278.820	0.000	2818.435	563.687	167.260	0.000
Conditions : Entries	5	21.149	4.230	1.930	0.133	5.278	1.056	0.310	0.899
Pooled	20	43.747	2.187			67.401	3.370		
Total	35	3234.755				2934.389			

Appendix J: Pooled ANOVA for Cross I (Swarna sub1 × FARO 57) traits of evaluated under normal and submerged conditions for the two seasons

Source	DF	SS	MS	F-value	P-value
Response	Variable:	SW			
Conditions	3	4.032	1.344	79.750	0.000
Rep	8	0.135	0.017	3.750	0.002
Entries	5	18.165	3.633	808.750	0.000
Conditions : Entries	15	21.663	1.444	321.500	0.000
Pooled	40	0.180	0.005		
Total	71	44.175			
Response	Variable:	GW			
Conditions	3	2.839	0.946	459.240	0.000
Rep	8	0.017	0.002	0.160	0.995
Entries	5	15.006	3.001	237.140	0.000
Conditions : Entries	15	14.664	0.978	77.250	0.000
Pooled	40	0.506	0.013		
Total	71	33.031			
Response	Variable:	GL			
Conditions	3	61.991	20.664	223.680	0.000
Rep	8	0.739	0.092	0.270	0.973
Entries	5	224.114	44.823	130.150	0.000
Conditions : Entries	15	234.713	15.648	45.440	0.000
Pooled	40	13.776	0.344		
Total	71	535.333			
Response	Variable:	FLW			
Conditions	3	1.187	0.396	4.880	0.033
Rep	8	0.649	0.081	0.700	0.688
Entries	5	9.074	1.815	15.700	0.000
Conditions : Entries	15	3.840	0.256	2.220	0.023
Pooled	40	4.623	0.116		
Total	71	19.373			
Response	Variable:	FLL			
Conditions	3	815.475	271.825	8.460	0.007
Rep	8	256.969	32.121	4.600	0.001
Entries	5	2694.799	538.960	77.240	0.000
Conditions : Entries	15	2897.514	193.168	27.680	0.000
Pooled	40	279.118	6.978		
Total	71	6943.875			
Response	Variable:	SG			
Conditions	3	4.274	1.425	42.470	0.000
Rep	8	0.268	0.034	0.970	0.470
Entries	5	10.761	2.152	62.470	0.000
Conditions : Entries	15	15.345	1.023	29.690	0.000
Pooled	40	1.378	0.035		
Total	71	32.027			
Response	Variable:	F50.			
Conditions	3	1905.557	635.186	136.570	0.000
Rep	8	37.207	4.651	1.470	0.197
Entries	5	27511.847	5502.369	1744.280	0.000
Conditions : Entries	15	12819.726	854.648	270.930	0.000
Pooled	40	126.181	3.155		
Total	71	42400.518			

Appendix J: Pooled ANOVA for Cross I (Swarna sub1 × FARO 57) traits of evaluated under normal and submerged conditions for the two seasons

Source	DF	SS	MS	F-value	P-value
Response	Variable:	TN			
Conditions	3	343.676	114.559	22.890	0.000
Rep	8	40.042	5.005	1.090	0.390
Entries	5	2638.531	527.706	114.980	0.000
Conditions : Entries	15	1512.872	100.858	21.980	0.000
Pooled	40	183.586	4.590		
Total	71	4718.707			
Response	Variable:	PH			
Conditions	3	1422.624	474.208	6.020	0.019
Rep	8	630.012	78.752	2.040	0.066
Entries	5	17589.659	3517.932	91.260	0.000
Conditions : Entries	15	30208.655	2013.910	52.250	0.000
Pooled	40	1541.894	38.547		
Total	71	51392.843			
Response	Variable:	PN			
Conditions	3	97.049	32.350	14.470	0.001
Rep	8	17.883	2.235	3.380	0.005
Entries	5	1204.455	240.891	364.740	0.000
Conditions : Entries	15	365.990	24.399	36.940	0.000
Pooled	40	26.418	0.660		
Total	71	1711.795			
Response	Variable:	PL			
Conditions	3	348.535	116.178	16.430	0.001
Rep	8	56.573	7.072	0.990	0.458
Entries	5	1353.513	270.703	37.910	0.000
Conditions : Entries	15	2117.254	141.150	19.770	0.000
Pooled	40	285.645	7.141		
Total	71	4161.520			
Response	Variable:	IL			
Conditions	3	86.367	28.789	43.470	0.000
Rep	8	5.298	0.662	0.330	0.952
Entries	5	1106.432	221.286	108.670	0.000
Conditions : Entries	15	478.554	31.904	15.670	0.000
Pooled	40	81.449	2.036		
Total	71	1758.100			
Response	Variable:	SY.g.plant.			
Conditions	3	3197.416	1065.805	93.610	0.000
Rep	8	91.083	11.385	4.100	0.001
Entries	5	4342.642	868.528	312.570	0.000
Conditions : Entries	15	1551.610	103.441	37.230	0.000
Pooled	40	111.148	2.779		
Total	71	9293.897			
Response	Variable:	CPS			
Conditions	1	0.248	0.248	49.540	0.002
Rep	4	0.020	0.005	18.750	0.000
Entries	5	9.169	1.834	6881.640	0.000
Conditions : Entries	5	1.151	0.230	864.080	0.000
Pooled	20	0.005	0.000		
Total	35	10.593			

Appendix K: Pooled ANOVA for traits evaluated under normal and submerged conditions for the two Crosses

Source	DF	SS	MS	F-Value	P-Value
Response	Variable:	SW			
Conditions	7	13.120	1.874	111.510	0.000
Rep	16	0.269	0.017	2.060	0.018
Entries	5	38.919	7.784	955.730	0.000
Conditions : Entries	35	49.643	1.418	174.160	0.000
Pooled	80	0.652	0.008		
Total	143	102.602			
Response	Variable:	GW			
Conditions	7	12.224	1.746	430.550	0.000
Rep	16	0.065	0.004	0.280	0.997
Entries	5	33.670	6.734	459.100	0.000
Conditions: Entries	35	32.642	0.933	63.580	0.000
Pooled	80	1.174	0.015		
Total	143	79.775			
Response	Variable:	GL			
Conditions	7	217.661	31.095	278.710	0.000
Rep	16	1.785	0.112	0.380	0.984
Entries	5	567.405	113.481	384.720	0.000
Conditions: Entries	35	608.654	17.390	58.960	0.000
Pooled	80	23.598	0.295		
Total	143	1419.103			
Response	Variable:	FLW			
Conditions	7	4.334	0.619	8.300	0.000
Rep	16	1.193	0.075	0.480	0.951
Entries	5	22.419	4.484	28.700	0.000
Conditions: Entries	35	10.013	0.286	1.830	0.014
Pooled	80	12.499	0.156		
Total	143	50.457			
Response	Variable:	FLL			
Conditions	7	2489.114	355.588	8.730	0.000
Rep	16	651.698	40.731	5.420	0.000
Entries	5	6986.681	1397.336	186.060	0.000
Conditions: Entries	35	7539.950	215.427	28.690	0.000
Pooled	80	600.807	7.510		
Total	143	18268.250			
Response	Variable:	SG			
Conditions	7	12.897	1.842	77.930	0.000
Rep	16	0.378	0.024	1.060	0.408
Entries	5	22.861	4.572	204.600	0.000
Conditions: Entries	35	37.442	1.070	47.870	0.000
Pooled	80	1.788	0.022		
Total	143	75.366			
Response	Variable:	F50.			
Conditions	7	9562.007	1366.001	242.200	0.000
Rep	16	90.238	5.640	0.870	0.609
Entries	5	68894.723	13778.945	2116.560	0.000
Conditions: Entries	35	38034.774	1086.708	166.930	0.000
Pooled	Error	80.000	520.806	6.510	
Total	143	117102.548			

Appendix K: Pooled ANOVA for traits evaluated under normal and submerged conditions for the two Crosses

Source	DF	SS	MS	F-Value	P-Value
Response	Variable:	TN			
Conditions	7	1560.994	222.999	53.650	0.000
Rep	16	66.506	4.157	0.570	0.895
Entries	5	5739.292	1147.858	158.340	0.000
Conditions: Entries	35	3534.124	100.975	13.930	0.000
Pooled	80	579.953	7.249		
Total	143	11480.869			
Response	Variable:	PH			
Conditions	7	9657.590	1379.656	17.050	0.000
Rep	16	1294.762	80.923	1.720	0.058
Entries	5	36914.532	7382.907	157.360	0.000
Conditions: Entries	35	65691.044	1876.887	40.000	0.000
Pooled	80	3753.380	46.917		
Total	143	117311.307			
Response	Variable:	PN			
Conditions	7	432.338	61.763	22.010	0.000
Rep	16	44.893	2.806	3.510	0.000
Entries	5	2693.679	538.736	674.490	0.000
Conditions: Entries	35	862.907	24.655	30.870	0.000
Pooled	80	63.898	0.799		
Total	143	4097.715			
Response	Variable:	PL			
Conditions	7	1293.861	184.837	27.260	0.000
Rep	16	108.481	6.780	1.140	0.338
Entries	5	3061.531	612.306	102.560	0.000
Conditions: Entries	35	4987.359	142.496	23.870	0.000
Pooled	80	477.610	5.970		
Total	143	9928.842			
Response	Variable:	IL			
Conditions	7	306.219	43.746	42.000	0.000
Rep	16	16.665	1.042	0.430	0.972
Entries	5	2504.989	500.998	204.580	0.000
Conditions: Entries	35	1167.143	33.347	13.620	0.000
Pooled	80	195.910	2.449		
Total	143	4190.926			
Response	Variable:	SY.g.plant.			
Conditions	7	8649.294	1235.613	83.610	0.000
Rep	16	236.441	14.778	2.910	0.001
Entries	5	10623.702	2124.740	419.040	0.000
Conditions: Entries	35	3920.352	112.010	22.090	0.000
Pooled	80	405.637	5.071		
Total	143	23835.425			

Appendix l: Result of Soil Analysis at the Three Study Locations

Samples description		Study sites		
	Units	Crossing Block	Submergence tank	Control field
pH		6.40	6.60	6.5
Organic Carbon	(%)	1.39	2.40	1.32
Organic Matter	(%)	2.42	4.18	2.30
Total Nitrogen	(%)	0.09	0.19	0.3
Available P	(ppm)	13.10	18.21	11.15
Exchangeable Cat ions Na	(Cmolkg^{-4})	0.34	1.38	0.40
K	(Cmolkg^{-4})	0.20	0.31	0.12
Ca	(Cmolkg^{-4})	3.54	3.64	3.30
Mg	(Cmolkg^{-4})	2.61	2.52	2.14
EA	(Cmolkg^{-4})	0.33	0.27	0.36
CEC	(Cmolkg^{-4})	7.02	8.12	6.26
Sand	(%)	60.00	88.26	86.31
Silt	(%)	12.80	4.46	3.21
Clay	(%)	27.20	7.28	11.32

Plate IV: (a): parents and progeny of family 1 (FARO 44, Swarna SUB1 and F1 progeny)
(b): parents and progeny of family 2 (FARO 57, Swarna SUB1 and F1 progeny)

Source: field Photograph

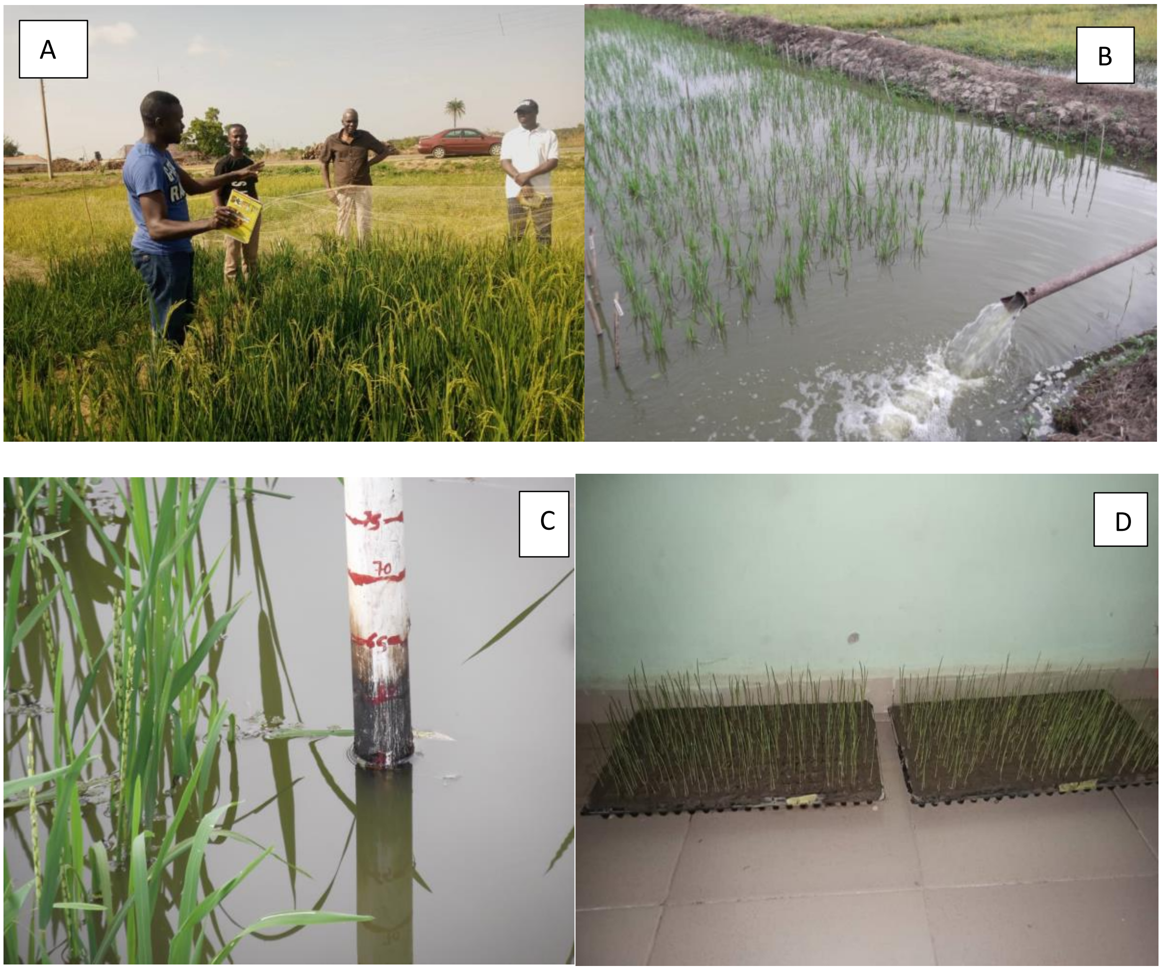

Plate V: (A): Field evaluation of 6 generations for the two families of crosses
(B): Field Evaluation under stress condition for the two families of crosses
(C): Calibrated pole used to guide the depth of flooding under stress condition.
(D): Recovery of seedling after submergence stress condition

Source: field Photograph