# SCREENING OF INTRODUCED BARLEY LINES AND THEIR INHERITANCE FOR SEEDLING AND ADULT PLANT RESISTANCE TO STEM RUST RACE *Ug99*

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Mercy N. Wamalwa.

Reg.No: KM12/2451/09

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This work has been submitted with our approval as supervisors.

Signature: ---------- Date: 22/4/13

Dr. James Owuoche (Department of Crops Horticulture and Soils)

Signature: ---------- Date: 23/4/2013

Professor. Christopher Ndirangu (Department of Crops Horticulture and Soils)

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## DEDICATION

This thesis is dedicated to my husband Peter and our children Salem and Rehoboth for their patience.

## ABSTRACT

Stem rust (*Puccinia graminis* pers. f. sp. *tritici)* is a disease of economic importance in barley (*Hordeum vulgare* L.) and wheat (*Triticum aestivum* L.) worldwide. Barley accessions are valuable genetic resources for improving the genetic base for resistance to biotic and abiotic stresses in barley. The objectives of this study were to determine the seedling and adult plant resistance in barley to stem rust race *Ug99* and to determine the mode of inheritance of resistant genes conferring resistance to race *Ug99*. Two hundred and eighty barley introductions from North America, Latin America, Europe, Asia and East Africa were screened for seedling resistance in the greenhouse and adult plant resistance in the field for two seasons. Variable disease severity response to *Ug99* was observed from "0" to 70S with 40% of the germplasm showing slow disease progress and these introductions could be considered as a source of resistance in barley. Although, the disease severity depended on the season, over 60% of the introduced varieties were susceptible to *Ug99*. At seedling stage, 67% of the germplasm exhibited low infection types with no sporulating uredinia. However, germplasm originating from Canada, Bangladesh, England, North Dakota State University, Utah State University and Wisconsin USA had infection type of "$2^{+}$" to X and this constituted 33% of the germplasm. Although all the hybrids were resistant to *Ug99* with IT ranging from "0" to "$1^{+}$", $F_1$ population from a cross of Karne × 09-N2-19 were susceptible to stem rust. The observed resistant (R):susceptible (S) ratio of the $F_2$ populations [HKBL-1385-13 × 08-UT-86 ($\chi^2_{0.05}$ = 0.480, p≥0.488, df = 99)] [HKBL-1385-13 × 09-N2-19 ($\chi^2_{0.05}$ = 0.641, p≥0.424, df = 99)] [ND2649 × 09-AB-78 ($\chi^2_{0.05}$ = 1.05, p≥0.309, df = 101)] and [ND25882 × 09-AB-78 ($\chi^2_{0.05}$ = 3.599, p≥0.058, df= 48)] exhibited segregation ratio of 2.6R:1S suggesting that the resistance is conferred by major genes at seedling stage. In addition, $F_2$ population that conformed to phenotypic ratio of 10.3R:6.3S indicates that there are genes modifying the resistant genes to *Ug99* which are duplicate recessive epistatis, aa epistatic to B, b; bb epistatic to A, a. Barley evaluated in 2010 were 30% taller than those grown in 2011, but biomass weight was 60% more in 2011 than those of barley in 2010. The mean biomass was high in germplasm from East Africa. Barley from North America, Asia and East Africa differed significantly in mean grain yield. Current study indicates that there is limited germplasm resistant to *Ug99* and efforts to identify and characterize new sources of resistance are imperative to prevent future losses and to maintain diversity for resistance.

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# TABLE OF CONTENTS

**DECLARATION AND RECOMMENDATION** ..... ii
**COPYRIGHT** ..... iii
**ACKNOWLEDGEMENT** ..... iv
**DEDICATION** ..... v
**ABSTRACT** ..... vi
**TABLE OF CONTENTS** ..... vii
**LIST OF FIGURES** ..... xi
**LIST OF PLATES** ..... xii
**LIST OF ABBREVIATIONS/ACRONYMS** ..... xiii
**CHAPTER ONE** ..... 1
**INTRODUCTION** ..... 1
1.1 Background Information ..... 1
1.2 Statement of the Problem ..... 2
1.3 Objectives ..... 3
1.4 Null Hypotheses ..... 3
1.5 Justification ..... 3
1.6 References ..... 5
**CHAPTER TWO** ..... 7
**LITERATURE REVIEW** ..... 7
2.1 Botany and Genetics of Barley ..... 7
2.2 Stem Rust (Puccinia graminis Pers. f. sp. tritici Eriks) Disease ..... 8
2.3 Stem Rust Epidemiology ..... 9
2.4 Biology of Rust and Host ..... 9
2.5 Barley Stem Rust Resistant Genes ..... 10
2.6 Evaluation of Germplasm for Stem rust ..... 11
2.7 Host - Pathogen Relationship ..... 11
2.8 Multiple and Durable Resistance ..... 12
2.9 Global Threat of Stem Rust Race Ug99 ..... 13
2.10 Genetics of Diseases ..... 13
2.11 References ..... 15



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**CHAPTER THREE** ..... 21

**EVALUATION OF BARLEY (*HORDEUM VULGARE* L.) INTRODUCTION LINES FOR ADULT PLANT RESISTANCE TO STEM RUST (*PUCCINIA GRAMINIS* PERS. F. SP. *TRITICI* ERIKS AND E. HENN) RACE *UG99*** ..... 21

3.1 Abstract ..... 21

3.2 Introduction ..... 22

3.3 Materials and Methods ..... 23

3.3.1 Experimental Site ..... 23

3.3.2 Genotypes ..... 23

3.3.3 Experimental Procedure ..... 23

3.4 Data Collection ..... 24

3.5 Data Analysis ..... 25

3.6 Results ..... 25

3.6.1 Reaction of barley germplasm to stem rust infection ..... 25

3.6.2 Agronomic Traits ..... 27

3.8 Conclusion ..... 32

**CHAPTER FOUR** ..... 38

**GENETIC ANALYSIS OF BARLEY (*HORDEUM VULGARE* L.) SEEDLING RESISTANCE TO STEM RUST (*PUCCINIA GRAMINIS* PERS. F. SP. *TRITICI* ERIKS AND E. HENN) RACE *UG99*** ..... 38

4.1 Abstract ..... 38

4.2 Introduction ..... 38

4.3 Materials and Methods ..... 40

4.3.1 Experimental Site ..... 40

4.3.2 Genotypes and Development of $F_2$ Population ..... 40

4.3.3 Experimental Procedure ..... 41

4.4 Disease Assessment ..... 41

4.5 Data Analysis ..... 42

4.6 Results ..... 42

4.7 Discussion ..... 52

4.8 Conclusion ..... 54

4.9 References ..... 55

**CHAPTER FIVE** ..... 58
**GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS** ..... 58
5.1 General Discussion ..... 58
5.2 Conclusions ..... 60
5.3 Recommendations ..... 60
**APPENDICES** ..... 61
**Appendix 1: Disease reaction to Puccinia graminis sp. tritici race Ug99 on barley lines at seedling stage in the greenhouse at Njoro in 2011** ..... 61
**Appendix2: Means of agronomic traits for different barley (Hordeum vulgare) lines for season one at Njoro in 2010** ..... 68
**Appendix 3: Means of agronomic traits for barley (Hordeum vulgare L.) lines for Season two at Njoro in 2010 and 2011** ..... 74
**Appendix4 SAS Procedure for $\chi^2$ and Npar1way analysis** ..... 78

## LIST OF TABLES

Table 3.1 Monthly mean rainfall and temperature of barley (*Hordeum vulgare* L.) evaluated at Njoro during August 2010 to March.....29

Table 3.2 Severity of stem rust race *Ug99* and area under the disease progress curve (AUDPC) on barley (*Hordeum vulgare* L.) germplasm from different regions evaluated at Njoro in 2010 and 2011.....30

Table 3.3 Means of two seasons for different agronomic parameters and area under the disease progress curve (AUDPC) of barley (*Hordeum vulgare* L. ) germplasm from different origins at Njoro .....33

Table 3.4 Means of agronomic parameters and area under the disease progress curve (AUDPC) of barley (*Hordeum vulgare* L.) germplasm from different origins at Njoro.....34

Table 4.1 Seedling reaction (most common IT) of barley (*Hordeum vulgare* L.) germplasm from 18 regions to stem rust (*Puccinia graminis* sp. *tritici*) race *Ug99* in the green house at Njoro in 2011.....45

Table 4.2 Seedling reaction of the barley parents, $F_1$ and $F_2$ genotypes to stem rust *Puccinia graminis* sp. *tritici*) race *Ug99* in 2011 and 2012.....50

## LIST OF FIGURES

Figure 3.1 Seedling reaction of barley (*Hordeum vulgare* L.) parents and $F_1$ population to stem rust race *Ug99* in the green house.....47

Figure 3.2 Frequencies of seedling infection type of barley (*Hordeum vulgare* L.) for $F_2$ population to stem rust (*Puccinia graminis* sp. *tritici*) race *Ug99* in the greenhouse.....48

## LIST OF PLATES

Plate 3.1 Stem rust seedling infection types for barley genotypes from "0", to "X", on 08-N2-58, Swiss HV627, ND25882 × 09-AB-78, HKBL-1385, ND26249, 09-N2-19, PI21486..... .....44

## LIST OF ABBREVIATIONS/ACRONYMS

| | |
|---|---|
| ACI | Average Coefficient of Infection |
| APR | Adult Plant Resistance |
| AVr | Avirulence |
| AUDPC | Area under the Disease Progress Curve |
| BYDV | Barley Yellow Dwarf Virus |
| CIMMYT | International Maize and Wheat Improvement Centre |
| cm | Centimeters |
| HTMJ | Stem rust race in barley |
| JCMN | Stem rust race in barley |
| ICARDA | International Center for Agricultural Research in the Dry Areas |
| KARI | Kenya Agricultural Research Institute |
| M | Meters |
| MCCF | Stem rust race in barley |
| MR | Moderately Resistant |
| MS | Moderately Susceptible |
| PI | Plant Introduction |
| QCCJ | Stem rust race in barley |
| R | Resistant |
| RH | Relative humidity |
| Rpg | gene resistant to *Puccinia graminis* |
| S | Susceptible |
| SAS | Statistical Analysis Software |
| Sr | Stem rust gene |
| TTKS | Acronym for *Ug99* according to the American nomenclature |
| *Ug99* | Stem rust race discovered in Uganda on wheat in 1999 |
| USDA | United States Department of Agriculture |
| USA | United States of America |
| $\chi^2$ | Chi-square |

# CHAPTER ONE

# INTRODUCTION

## 1.1 Background Information

Barley (*Hordeum vulgare* L.) is grown across a wide range of environments (Poehlman, 1985). Stem rust (*Puccinia graminis* f.sp. *tritici*) is a devastating fungal disease that attacks wheat (*Triticum aestivum* L.), barley and barley grass (*Hordeum leporium* Link) (Luig and Watson, 1972). Since 1970s, stem rust problem in barley and wheat has been solved through breeding for resistant varieties. Stem rust is a foliar disease of economic importance in barley and wheat growing areas and has caused major loses worldwide. In 1989, severe epidemic of stem rust occurred in barley in North Dakota and West Central Minnesota causing a yield loss of 60% (Roelfs *et al.,* 1990). Although application of fungicides is a short term remedial measure and is less effective in reducing the overall size of stem rust population (Park, 2008), this method has proved to be expensive for barley and wheat farmers. Therefore, protection of barley from stem rust infection using genetic resistance remain the most economical means of controlling rust to sustain productivity and malting qualities.

Three types of stem rust resistance occur in barley. The first is overall resistance that operates during all growth stages of the plant and is effective under a wide range of environmental conditions. The second is seedling resistance that operates during seedling stage only, and may be influenced by environmental conditions (Ellingboe, 1981). Adult plant resistance (APR) is the third type of resistance, which depends on minor genes. Genetic resistance is the most efficient method of reducing yield losses. Besides, resistance to rust diseases can be utilized by knowledge of resistant genes in commonly used parental germplasm and released cultivars. Moreover, identification of the rust resistance genes allows efficient incorporation of these genes into germplasm pools, hence avoiding release of genetically uniform cultivars.

Various wheat breeding programs in North America, Mexico and Australia have produced cultivars with long-lasting, effective resistance to rust diseases (Shang and Samborki, 1986; Kolmer *et al.,* 1991). Genetic resistance occurs when a resistance allele is present in a host in response to avirulent gene in the pathogen. However, durable resistance is often confronted by

genetic adaptation in the pathogen hence increase in frequency of the virulent race leading to resistance break down (McIntosh, 1988; Johnson and Knott, 1992).

Seedling resistance protects the plant against virulent pathogen isolate during their entire growing period and it is race specific controlled by major genes (Parlevliet, 2001). However, when used extensively over along period of time, new races usually overcomes it leading to susceptibility of the released germplasm (Knott, 1982; Rajaram *et.al.,* 1988). Germplasm with adult plant resistance are susceptible at seedling stages and develop resistance in post - seedling phases (Roelfs, 1985). General resistance is effective against all races of the pathogen, while specific resistance is effective against some and ineffective against others (Knott, 1982). Partially recessive genes control the inheritance of longer latent period. In a population involving three genes; one of the genes controls the inheritance for instance in leaf rust three to twenty one genes controlled slow leaf rusting and its components were considered for selection of resistant individuals (Chen *et al.,* 1995; Chen *et al.,* 2002).

**1.2 Statement of the Problem**

In 1999, a new stem rust race *Ug99* was detected in Uganda on wheat germplasm (Pretorius *et al.,* 2000). The emergence of the new race poses a major threat to most of barley and wheat areas of the world. According to surveys, virulence for *Sr31* is now widespread in the Eastern African Highlands. During 2001, the cultivar Shirma became susceptible to stem rust in Ethiopia as well as the two major cultivars grown (56% of small scale production). In 2002, the yield losses in Kenya were estimated to be 71% under experimental conditions. In 2007, plant pathologists announced that *Ug99* had crossed the red sea into the Arabian Peninsula and that it now threatens the major barley and wheat production areas of Asia. About 70% of U.S. wheat varieties are thought to be susceptible to *Ug99*. Between 70 and 75% of wheat cultivars grown in India, Pakistan China and Egypt are also susceptible. The race has a broad virulence and it migrated to Ethiopia and Kenya especially in the Kenyan Highlands causing devastating effect on wheat. At the moment, this foliar disease is causing major losses on barley crops grown in low, mid and high altitude areas in Kenya. This is a serious threat to food security in Africa and Asia. Consequently, identification of resistant genes that control durable resistance for introgression and determination of inheritance after incorporation of these genes into adapted cultivars is absolutely necessary.

## 1.3 Objectives

### Broad Objective

To contribute to improved barley yields in Kenya through development of cultivars with durable resistance to stem rust.

### Specific Objectives

1. To evaluate barley lines for adult field plant resistance to stem rust.

2. To evaluate the barley lines for resistance to stem rust race *Ug99* at seedling stage (Feekes stage 1) in the greenhouse.

3. To determine the inheritance of resistance gene to stem rust race *Ug99* in barley.

## 1.4 Null Hypotheses

1. The introduced barley lines did not have field resistant to stem rust.

2. The introduced barley lines were not resistant to stem rust race *Ug99* at seedling stage.

3. The to stem rust race *Ug99* resistant genes were not monogenically inherited in barley.

## 1.5 Justification

The new stem rust race (*Ug99*) is currently a major global threat to barley and wheat farmers worldwide. Since the seventh decade in the last century, stem rust problem in barley and wheat has been solved through breeding varieties resistant to stem rust. The short term solution of applying fungicide to the barley crop to restrict development and devastation of this pathogen is expensive to farmers.

Although barley is mainly used for malting purposes, it is one of the cereals that are used to make breakfast food. In addition to wheat and maize (*Zea mays* L.), barley is one of the cereals grown by farmers in North, Central, and South Rift Valley of Kenya and significantly consequently contributes to reduction of poverty. As a result there is need to identify and develop barley cultivars that are resistant to stem rust. The knowledge of source of resistant genes, epidemiology and race of the stem rust is of utmost importance in achieving this goal. This TTKSK (*Ug99*) is predicted to spread to the world's most important wheat and barley growing regions in the near future (Singh *et al.*, 2008). Before the *Ug99* reaches across the Saudi Arabian

Peninsula, South Asia, East Asia and eventually the Americas, plant breeders and pathologists still have time to identify resistant genotypes, introgress the genes and multiply the seed for farmers. This can reduce the devastating effect of the pathogen on susceptible cereals. Therefore, there is need to control race TTKSK before it reverses the gains of green revolution achieved in the $7^{th}$ - $8^{th}$ decade in the last century.

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# CHAPTER TWO

# LITERATURE REVIEW

## 2.1 Botany and Genetics of Barley

Barley (*Hordeum vulgare* L.), one of the most important temperate cereals grown worldwide belongs to the family Poaceae/Gramineae and genus Hordeum and has been subject to considerable genetic study (Abeledo *et al.,* 2003). It is a large-genome, self-fertilizing monocotyledon and a true diploid (2n = 2x = 14) (Caldwell *et al.,* 2004). Barley is one of the first domesticated cereals originating in the Fertile Crescent area of the Near East (Pourkheirandish and Komatsuda, 2007). It is the fourth most produced cereal worldwide (after maize, wheat and rice), mainly used for animal feed, human food and malting (Belcredi et al., 2009). Although almost half of the area where barley is grown is a high-risk area where crop failures are common and resources are limited, it has remained a predominant grain crop and a source of livelihood to many this makes breeding for increased yield imperative (Shakhatreh *et al.,* 2001; Pswarayi *et al.,* 2008).

The growth and development of barley, like other crops is influenced by the genetic make up and the environment hence a single plant will produce three to six stems which are 10 cm to more than 150 cm in length. In barley a single leaf consist of a sheath, ligule, auricle, ablade and leaf node of which is borne alternatively on opposite sides. Each spikelet has one flower consisting of two glumes and floret. Three spikelets are attached at each node of the rachis. In two – rowed barley, only the central floret is fertile, while in six-rowed barleys, all three florets are fertile. The number of kernels that develop per head varies from 25 to 60 in six – rowed types and from 15 to 30 in two-rowed types (Mathre, 1982).

Barley has dominant genes such as *Rpg1* that controlled stem rust epidemic in Northern Great plains since 1942. This gene was mapped to the short arm of barley chromosome 1 (7H) from cultivar Morex (Steffenson, 1992). Moreover, the knowledge on allele sequencing confirmed that *Rpg1* had 14 exons in 4,466 bp of genomic sequence encoding an 837 amino acid protein. However, barley cultivars indicated no amino acid sequence polymorphism (Brueggeman *et al.,* 2002).

## 2.2 Stem Rust (Puccinia graminis Pers. f. sp. tritici Eriks) Disease

The stem rust fungus (*Puccinia graminis* Pers. f. sp. *tritici* Eriks and E. Henn) belongs to the genus *Puccinia*, family Pucciniaceae, order Uredinales and class Basidiomycetes that causes disease on almost all major families of cereals (Agrios, 2005). Stem rust disease infects wheat and barley worldwide. The disease appears as uredinia on the leaf sheaths, stem tissue, awns, glumes and leaves of barley plant (Agrios, 2005). The urediniospores are brownish red in colour and converted into telia, changing colour from red/dark brown to black as plant matures, hence the name black rust was given. The orange red lesions are oval or elongated blister in shape, and are visible on both sides of the leaf (Roelfs, 1985). The degree of damage includes the tearing of outer layers of plant tissue that is visible without magnification. It bears many physiological races generated mainly by mutation (Roelfs, 1985). Puccinia is the largest genius of the rust fungi and its species appear as uredinia on the leaf sheaths, stem tissue, awns, glumes and leaves of cereals maize, barley, wheat, oat (*Avena sativa L.*) and rye (*Secale cereale* L.) causing significant economic losses that result in famines (Swann *et al.*, 2001; Cummins and Hiratsuka, 2003).

A new stem rust race that originated from the Pacific Northwest, with a devastating magnitude of 60% on yield of barley was observed in the upper Midwest barley growing area of the United States in 1989 (Roelfs *et al.*, 1990; Roelfs *et al.*, 1991; Roelfs *et al.*, 1993). Because the rust produces new races through asexual and parasexual reproduction, development and growing of resistant cultivars has reduced losses in rust - prone areas of the United States, Northern New South Wales and Queensland of Australia (Park, 2008).

Stem rust has been a serious threat to cereal production for more than 50 years, however since detection of the race *Ug99* in Kenya and Ethiopia in 2005 it causes yield losses up to 100% in Kenya (CIMMYT, 2005; Wanyera *et al.*, 2006). Recently, virulent race of stem rust TTKSK emerged and it was first isolated from Uganda, spread through East Africa then to Middle East (Nazari *et al.*, 2009). If not checked, this race will spread to the most important wheat and barley growing regions across the world (Singh *et al.*, 2008).

Stem rust resistance research has been confined to wheat, barley, rye and oat (*Avena sativa* L.) (Steffenson, 1992). Stem rust epidemics on barley were rare unless the nearby wheat fields were severely attacked (Roelfs, 1985). In North America epidemics occurred from 1989 to

1991 with losses of 1 to 3% due to race *QCCJ* (Steffenson, 1992). Apart from stem rust, other rust diseases of barley include barley stripe rust (*Puccinia striiformis* westend. f.sp. *hordei* Eriks and Henn) which is destructive in many barley-growing regions worldwide (Hassebrauk and Robbelen, 1975). Stripe rust pathogen grows parallel to the leaf axis to produce long stripes with pustules. On seedlings, an individual infection is not confirmed by leaf veins and may grow to produce pustules that completely cover the leaf. Stripe rust has no alternate host, and the telial stage has no known function (Hassebrauk and Robbelen, 1975).

**2.3 Stem Rust Epidemiology**

Stem rust mainly infects barley late maturing cultivars, sown late at low altitudes. In high altitude of North America, spring- sown wheat is vulnerable to stem rust if the source of inoculum is from a high location (Alexopolous *et al.,* 1996). The disease is an obligate biotroph, heteroecioous in its life cycle and heterothallic in mating type (Alexopolous *et al.,* 1996). Stem rust alternates between a telial host in Poaceae and an aecial host in Berberidaceae and macrocyclic. The primary hosts are bread wheat, durum wheat, barley and triticale (*X. triticosecale*) while barberry, (*B. vulgaris*) is the most important alternate host (Roelfs, 1985). Urediospores infect nearby plants and disseminated by wind a cross Great Plains of Australia to New Zealand, Southern Africa to Australia (Luig, 1985). The minimum, optimum and maximum temperature for urediniospore germination are 15, 24 and 30 °C, respectively and for sporulation 5, 30 and 40 °C, respectively (Roelfs *et al.,* 1992). The modes of pathogen dispersal include the long distance dispersal that results in pathogen colonization of new region (Brown and Hovmøller, 2002), contaminated cloths (Leonard, 2001; Hugh - Jones, 2002), and stepwise range expansion (Singh *et al.,* 2006). Lastly, this pathogen is dispersed by extinction and recolonization like the "Puccinia Pathways" of North America (Stakman *et al.,* 1930; Brown and Hovmøller, 2002).

**2.4 Biology of Rust and Host**

The rust pathogen nomenclature includes: *Puccinia graminis* Pers. f. sp. *tritici,* the pathogen of stem rust (black rust); *Puccinia recondita* Rob. ex Desm. f. sp. *tritici* the pathogen of leaf rust (brown rust); *Puccinia striiformis* westend. f. sp. *tritici*, the pathogen of stripe rust (yellow rust). *Puccinia graminis* and *P. recondita* f.sp. *tritici* are macrocyclic and heteroecious

(McIntosh *et al.,* 1995). There is a distant relationship among the formae specialis of *Puccinia recondita* f.sp *tritici* (Roelfs *et al.,* 1992). However, the relationship of the cereals and grasses attacking pathogens differs, for example *P. graminis*. f. sp. *tritici* and *P. graminis*. f. sp. *secalis* are closely related and they hybridize with *P. graminis*. f. sp. *avenae*. *P. graminis* f.sp. *tritici* also infects rye while both formae specials and their hybrids may infect barley and various species of *Aegilops* and Agropyron (Kleinhofs *et al.*,2009). In *Puccinia striiformis* which is close to formae specialis hordei, mutation and asexual recombination brings about the source of pathogenic variability (Zadoks, 1961). Stem rust has a complex cycle featuring alternation of generations, the completion of its life cycle requires barberry as well as a cereal species, (Schumann and Leonard, 2000). Urediniospore germinates and infects cereals by penetrating through the stomata in spring and summer. Rust produces teliospores which remains dormant until spring when it undergoes meiosis to produce basidiospore that leads to production of urediniospores that ruptures the plant's epidermis (Schumann and Leonard, 2000).

**2.5 Barley Stem Rust Resistant Genes**

Genes for resistant to *Puccinia graminis* f. sp. *tritici* in barley have been identified and designated as *RPg1, RPg2 , RPg3 , rPg4 , RPg5, rPgBH* and *rPg6* (Fetch *et al.,* 2008). Among these genes *RPg1, rPg4* and *RPg5* have been investigated at molecular level. The *rPg6* a recessive gene is located on a translocational chromosome 6H from *Hordeum bulbosum* (and is resistant to race *QCCJ* (Fetch *et al.,* 2008). *RPg1* has been resistant to stem rust races for over 50 years but is currently susceptible to races *QCCJ* and TTKSK (*Ug99*) (Sun and Steffenson, 2005; Steffenson and Jin, 2006; Fetch *et al.,* 2008). Durability of *RPg1* was confirmed during the release of Kindred barley in 1942 and even during the severe epidemics of rust in 1953 and 1954 (Kleinhofs *et al.,* 2009). Barley cultivar Chevron (CIho 1111) and Peatland (CIho 5267) are other sources of *RPg1* gene (Brueggeman *et al.,* 2002).

*RPg2,* derived from cultivar Heitpas - 5, is an adult and seedling resistance gene to stem rust races HTMJ and JCMN but susceptible to most stem rust races at seedling stage (Sun and Steffenson, 2005). Gene *RPg3* derived from PI382313, confers an intermediate level of seedling resistance but is susceptible to race *QCCJ* (Sun and Steffenson, 2005). In a study carried out on 18,000 barley accessions from the USDA National Small Grains collection, Q21816 was identified as the most resistant line the *rPg4* gene (Jin *et al.,* 1994). The resistant expression of

*rPg4* depends on temperature, notably effective at 17-22 °C but ineffective above 27 °C (Jin *et al.*, 1994). Accession Q21861 is also resistant to rye stem rust *P. graminis* f. sp. *secalis* and wheat stem rust race TTKSK (Steffenson, 1992). *RPg5* and *rPg4* gene function dependently and the former is required for resistance to stem rust races MCCF and TTKSK in addition to *QCCJ.* Since the *rPg4* gene is recessive and temperature dependent, it may have a negative function on the ability of fungus to establish itself within the plant (Brueggeman *et al.*, 2009). The wild and cultivated relatives of wheat and barley offer a potential source of stem rust resistance. Landraces are priority, as they may possess a wide range of variation, specific adaptation to the different environments in their regions of growth and resistance or tolerance to diseases and insect pests (Alex *et al.*, 1997; Mujeeb- Kazi and Rajaram, 2000).

**2.6 Evaluation of Germplasm for Stem rust**

The screening of barley and wheat germplasm against a new variant TTKSK which is a major threat in the highlands, particularly in Eastern Africa (Kenya and Ethiopia) is going on (Bonman *et al.*, 2007). In any rust breeding program, the aims of germplasm screening are to evaluate the scope of virulence of the new stem rust races and secondly, to identify the source of resistance to stem rust in a large number of germplasm (Jin and Singh, 2006). In Australia, germplasm screening and advancement of generations involves routine tests against infection. This includes two greenhouse seedling and single adult plant field evaluations to all three rust pathogens (Park, 2008). An enhancement involves the incorporation of resistant genes through backcrossing of advanced lines to the recurrent parent done at $F_1BC_5$ or $F_1BC_6$ and evaluation of seedling and adult plants. Adult plant resistant (APR) genes are considered to be more durable than seedling resistance (major genes) (Singh, 1992). Stem rust resistance genes *Sr2, QSr-sun-7DS* and *QSr-sun-5BL* confer APR genes to stem rust in winter wheat cultivars Forno and Arina (Bansal *et al.*, 2008).

**2.7 Host - Pathogen Relationship**

The host – parasite complex was first demonstrated by Flor (1955) and this explained the importance of gene – for – gene hypothesis. As a result of Flor's hypothesis, Eriksson and Henning (year) used the hypothesis to propose the new formae speciales as a sub-species of *Puccinia graminis* (Schafer *et al.*, 1984). In 1905, Briffin came up with a monogene concept of

resistance which was dependent on single gene located in the host (Bushnell and Roelfs, 1984). In the interaction between a host and a pathogen that follow a gene-for-gene relationship, the expression of resistance or susceptibility of the host to a pathogen depends on the pathogen's degree of virulence to the host (Crute and Pink, 1996).

In crosses between rye and wheat, most hybrids behave like Triticum parents and several intermediates between rye and wheat are formed and this is attributed to the constitution of the genome (Stakman *et al.,* 1930). Race genotypes can be distinguished by the virulence pattern or the level of resistance to the host plants. On the other hand, the studies on spores (teliospores, basidiospores and urediniospores) resulted in the emergence of classical and molecular genetics of the rust (D'silva, 1997). The concept of physiological races explains why a cultivar Ceres could be resistant to stem rust in one geographical location but susceptible in another (Stakman *et al.,* 1930).

**2.8 Multiple and Durable Resistance**

Vanderplank introduced the concept of two kinds of resistance; vertical resistance controlled by one gene and is race specific and horizontal resistance is polygenically controlled and species specific (Ellingboe, 1981). Qualitative or vertical resistance is conferred by a single major resistance gene, also referred to as a race or genotype specific gene (Nelson, 1978). Durable resistance is resistance that is effective in a cultivar during its widespread cultivation for a long sequence of generations or a period of time, in an environment favorable to the disease (Johnson, 1984; Park, 2008). Since the 1960s, stem rust has been controlled by the incorporation of more than one resistant genes into cultivars. However, other factors which may contribute to the long-lasting disease control includes early maturing barley crop (Steffenson, 1992). Partial resistant gene to leaf rust (*Puccinia hordei*) is found in barley cultivar Minerva and Vada (Parlevliet, 2001).

Although combining many genes each of small effects is more likely to achieve durable resistance, it should not lead to the neglect of the opportunities presented by the increasing number of major genes (Parlevliet, 2001). In the past, major genes such as *Lr24/Sr24, Sr26* and polygenic resistance have been used successfully to control cereal rust diseases in Australia (Park, 2008). Moreover, a colouration of major genes in spring and winter wheat have been utilized to confer APR resistance to stem rust leaf rust and stripe rust (Singh *et al.,* 2008). The

APR genes show intermediate responses and often combinations of more than three genes are required to attain commercially acceptable level of resistance (Bansal *et al.*, 2008). Durable resistance to stem rust has been provided by recessively inherited *Sr2* gene (Mishra *et al.*, 2005). The association between melanism (pseudo-black chaff) on the ear head is used as morphological marker for the *Sr2* gene in adult wheat plant while leaf chlorosis in seedlings (Have and McIntosh, 1979; Brown, 1997). The occurrence of a new race of stem rust with virulence for many of the known major genes for resistance in Eastern Africa indicates the need to focus on finding new sources of minor gene resistance to this pathogen (Singh *et al.*, 2006).

### 2.9 Global Threat of Stem Rust Race *Ug99*

Rust diseases are some of the most devastating biotic stresses in small grains. Among the three rusts in barley, stem rust is the most damaging disease (Bansal *et al.*, 2008). Race *Ug99* has spread throughout East Africa and recently to the Middle East (Singh *et al.*, 2008; Nazari *et al.*, 2009). The global production of wheat and barley is at risk due to the emergence of devastating race *Ug99* which has caused yield losses ranging from 30 to 70% in the case of susceptible varieties in East African highlands (Ephrem *et al.*, 2000; Pretorius *et al.*, 2000; Singh *et al.*, 2006). Unlike other rusts, this only partially affects crop yields, the destruction of *Ug99* results in yield loss ranging 80-100% (CIMMYT, 2005). The *Sr2, Sr30* and *Sr31* are among the 45 stem rust genes that have been evaluated for virulence in different wheat backgrounds (Bansal *et al.*, 2008). It is evident that race *Ug99* is virulent to genotypes possessing *Sr31* gene (Pretorius *et al.*, 2000; Singh *et al.*, 2006). The *Ug99* race is a threat to barley production globally hence search for new and potentially durable sources of resistance is essential.

### 2.10 Genetics of Diseases

Normally, there is a corresponding locus in the pathogen with alternate alleles that condition virulence for each resistance gene in the host. However, for some corresponding gene pairs the interactions differ from the classical one-to-one relationship. For instance in wheat *P.triticina* avirulence to alleles *Lr2a*, *Lr2b* and *Lr2c* is conditioned by a single allele , although a dominant gene at an independent locus inhibits the expression of resistant gene (Samborski *et, al.*, 1968; Statler and Jin, 1991). Gene postulations assume gene-for gene rules in developing

probable resistant genes present in the host genotypes. For instance a specific gene in a host can be postulated from arrays of pathogen cultures with known avirulence and virulence symptoms (Peterson, 1959). Expression of resistant genes in the host ranged from completely dominant to recessive, depending on whether the pathogen was homozygous or heterozygous for avirulence. Like-wise, expression of avirulence in the pathogen depended on whether the host was homozygous or heterozygous for resistance (Haggag *et al.,* 1973). In an experiment to determine inheritance of resistance to fusarium in pigeon pea (*Cajanus cajan* L.) two complementary genes, single dominant, 2 genes, major genes, duplicate gene and single recessive gene were observed (Pawar and Mayee, 1986; Jain and Reddy, 1995; Okiror, 2002; Kotresh *et al.,* 2006;). Finally, all types of gene actions are generally observed (additive, dominance and epistasis), and multiple types of gene actions can occur in the same resistance phenotype in a single disease system (Randle *et al.,* 1984).

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# CHAPTER THREE

# EVALUATION OF BARLEY (*Hordeum vulgare* L.) INTRODUCTION LINES FOR ADULT PLANT RESISTANCE TO STEM RUST (*Puccinia graminis* pers. f. sp. *tritici* Eriks and E. Henn) RACE *Ug99*

## 3.1 Abstract

Stem rust (*Puccinia graminis* pers. f. sp. *tritici)* is one of important foliar diseases in barley (*Hordeum vulgare* L.) worldwide. The objective of this study was to determine the adult plant resistance (APR) of barley lines to stem rust race *Ug99.* Two hundred and eighty barley introductions were evaluated in a two - season field experiment at KARI - Njoro. The effect of season on severity of stem rust was clearly manifested on most of the germplasm. Severity of rust was more in 2011 than 2010 in all the germplasm. The 21% of germplasm that were susceptible exhibited AUDPC (Area Under Disease Progressive Curve) ranging from 1098 – 1130. On the other hand, 68% of the germplasm were relatively resistant with AUDPC ranging from 510 – 945. Among the barley germplasm from 19 origins, 40% showed low disease progression hence could be considered for use in improvement of barley varieties. Infection ranged between 1R to 70S in the two seasons. About, 90% of the germplasm were susceptible to *Ug99,* however, Swiss HV673, 08-AB-17, Chevron and Q21861 were resistant. The seasonal effects were manifested on agronomic parameters. The barley genotypes were 30% taller in 2010 than in 2011; the biomass weight was 60% higher in 2011 than in 2010. Furthermore, the mean spike length and number of spikes per ear for germplasm from North America and Europe were higher than from barley derived from other regions. The mean biomass was high in germplasm from East Africa. Barley from North America, Asia and East Africa differed in mean grain yield. In addition, the germplasm from Latin America and Europe were similar in mean grain yield. This study implies that resistance to stem rust race *Ug99* is influenced by the host and environment as the latter was manifested in the two seasons.

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## 3.2 Introduction

Stem rust (*Puccinia graminis* f.sp. *tritici*) is a destructive fungal disease that attacks wheat (*Triticum aestivum* L), barley and barley grass (*Hordeum leporium* Link) (Luig and Watson, 1972). Since 1970's, stem rust problem in wheat has been checked by incorporation of *Sr2* gene into most of the wheat germplasm and *Rpg1* gene in barley. However, in 1989, severe epidemic of stem rust occurred in barley in North - central and North - eastern part of United States resulting in 60% yield loss (Roelfs *et al.*, 1990). Germplasm with adult plant resistance (APR) are sometimes susceptible at seedling stage and develop resistance in post – seedling phases; Adult plant resistance which is under the control of minor genes is effective against some races and ineffective against others (Knott, 1982; Roelfs, 1985). The emergence of stem rust race *Ug99* in 1999 rendered all Kenyan wheat cultivars with *Sr2* gene susceptible and was capable of reducing wheat yields by 60% (Ephrem *et al.*, 2000).

Although fungicides can be used as a short term measure to control this foliar disease, it is less effective in reducing stem rust infection and increase the cost of barley production (Park, 2008). Therefore, it is necessary to deploy resistant adapted cultivars to minimize the devastating effect of stem rust in order to sustain barley production and malting qualities. Seedling, adult-plant and slow rusting resistance to stem rust have been observed in barley and wheat (Knott, 1982). Watson (1970) proposed that virulence is controlled by specific genes whose products interact with those of corresponding resistance genes in the host, under a relatively simple genetic system. Nonetheless, growth rate, lesion size, spore production, aggressiveness and characters related to pathogenicity are controlled by a polygenic system. Slow rusting results from limited growth in the host after penetration has been observed (Martin *et al.*, 1977). According to Palmer and Wilcoxon (1982), frequency of infection and latent period are not affected by the plant anatomy and morphological characteristics, but the enlargement of uredinia and sporulation of the pathogen could be affected by the plant structure.

Resistance occurs when resistant allele is present in the host along with a corresponding a virulence gene in the pathogen (Johnson and Knott, 1992). Due to the constant evolution of rust races, there must be a constant search for germplasm possessing resistance to the cereal rusts. Cultivars, landraces, wild or cultivated relatives of barley and mutation are some of specific sources of resistance genes to stem rust (Dyck and Kerber, 1992). Numerous sources of resistance genes exist to rust diseases, although not all are of equal value (McIntosh *et al.*, 1995).

sources of resistance genes to stem rust (Dyck and Kerber, 1992). Numerous sources of resistance genes exist to rust diseases, although not all are of equal value (McIntosh *et al.*, 1995). Breeding for resistance aims at producing durable resistant germplasm that depend on APR genes. Incorporation of several genes into a germplasm often provides resistance to more than one race of stem rust (Knott, 1982). However, effective deployment of resistant genes depends on availability of resistant genetic stock. Moreover, resistance that is not race specific and controlled by several of genes is long lasting because of minimal selection pressure on the pathogen (McIntosh, 1995). The objective of this experiment was to evaluate the adult plant resistance of barley germplasm to stem rust race *Ug99* and to identify the resistant genotypes.

## 3.3 Materials and Methods

### 3.3.1 Experimental Site

Field experiment was conducted at Kenya Agricultural Research Institute (KARI) - Njoro ($0^{o}$ 20'S $35^{o}$ 56'E) situated at an elevation of 2185m above sea level. This institute experiences an average annual rainfall of 939.3 mm (average of 61 years) (Kenya Meteorological Station Identification Number 9031021) and an average minimum and maximum temperature of 9 and 24°C, respectively. The Njoro site was chosen because environmental conditions favours stem rust infection and is a representative of wheat and barley growing areas (Singh *et al.*, 2006).

### 3.3.2 Genotypes

Two hundred and eighty barley germplasm from North America, Ukraine, Europe, Latin America, East Africa and Asia and 4 Kenyan cultivars Karne, Nguzo, HKBL-13 and HKBL-12 were evaluated (Appendix 1). Wheat germplasm with *Sr24* gene complex was planted as a susceptible check.

### 3.3.3 Experimental Procedure

A two-season field experiment was established on land previously under grass ley. The land was disc ploughed and harrowed to fine tilth suitable for barley planting. Each entry was sown in double rows measuring 0.2 × 0.75m in August 2010 and December 2010. The experimental units were separated by 0.3 m and 0.5 m wide alleyways within and between the blocks, respectively. Sowing was done by hand at an equivalent seeding rate of 33.33 kg $ha^{-1}$. To facilitate inoculum build-up and uniform dissemination within the nursery, a continuous row of

stem rust spreader carrying *Sr24* gene was planted perpendicular to all entries. At planting time, diammonium phosphate (DAP) fertilizer was applied at the rate of 155 kg $ha^{-1}$ in order to supply an equivalent of 27.9 kg N $ha^{-1}$ and 31.5 kg P $ha^{-1}$. Growth of weeds was restricted by applying both pre - and post - emergent herbicides. Immediately after sowing, Stomp® 500 EC (pendimethalin) a broad spectrum, pre-emergent herbicide was applied at a rate of 830g $ha^{-1}$. At tillering stage (Zadok's Growth stage 20-29) (Zadok *et al.*, 1974) the plots were sprayed with Buctril MC (bromoxynil + MCPA) at the rate of 450g $ha^{-1}$ to control broad-leaved weeds. The trial was top dressed with Calcium Ammonium Nitrate (CAN) at stem elongation stage (Zadok's GS 30) (Zadok, 1974) at the rate of 100 kg $ha^{-1}$ in order to supply additional 33 kg N $ha^{-1}$. Bulk of urediniospores was collected from experimental plots of wheat variety *Sr24* genes grown within the field where the experiments were carried out. The inoculum was collected from (a mixture of susceptible *cvs.* carrying *Sr24* gene) from the disease nursery in the field. The plants were cut into pieces and suspended in Soltrol (Chevron Philips Chemical Co. No.0113172) at an approximate concentration of $4\times10^{10}$spores per ml. The inoculum was filtered and drained in a dispenser then sprayed on the test germplasm in the evening using an atomizer machine.

**3.4 Data Collection**

Plant response to rust infection at the adult plant stage was termed "infection response". According to the size of the pustules and associated necrosis or chlorosis infection responses were classified into four categories; R = resistant, MR = moderately resistant, MS = moderately susceptible and S = susceptible (Roelfs *et al.*,1992). Stem rust severity was assessed following the modified Cobb scale (Peterson *et al.*, 1948). Entries were evaluated for response to infection and stem rust severity three times between heading (Zadok GS58) and plant maturity (Zadok GS70-89). At physiological maturity 5 plants $plot^{-1}$ were selected randomly from the two rows and used to estimate plant height (from plant base to the tip of spike excluding awns), the number of spikes $plant^{-1}$, and kernels $spike^{-1}$ and spike length. Spike length was measured from the base of the ear to the tip of the spike (excluding the awns) based on an evaluation of all the spikes from the five plants. Harvesting was done in December 2010 and March 2011. Each plot was harvested by hand by cutting the plants at the base and biomass determined using a weighing balance. Ear from each plot was threshed and kernel weight determined. A sample of 1000 kernels was taken and weighed in order to determine 1000-kernel weight.

### 3.5 Data Analysis

Area under disease progress curve (AUDPC) was computed using the following formula:

$$AUDPC = \sum[t(i+1) - ti][y(i+1) + yi]/2$$ (http://www.apsnet.org.)

Where

*ti* is the first assessment date of two consecutive assessment

*yi* is the disease severity on assessment date *ti*

*t (i+1)* is the second assessment date of two consecutive assessment

*y (i+1)* is the disease severity on assessment date *t (i+1)*

Non-parametric analysis with Wilcoxon was done on all agronomic data using the SAS version (SAS Institute, Inc. 2001) (Appendix 4b). Standard error was calculated using the following formula

$$SE = \frac{Sd}{\sqrt{N}}$$

Where SE=standard error, sd = standard deviation and N= the number of germplasm.

### 3.6 Results

The temperature and rainfall experienced during the growth period of the crop varied. The temperature ranged from 20 - 24°C in first season while in the second season the temperature range was between 25 and 26°C. The mean precipitation ranged from 14.3 – 240 mm for the four months in 2010 while in 2011, the mean rainfall ranged from 3.9 to 130 mm (Table 3.1).

#### 3.6.1 Reaction of barley germplasm to stem rust infection

Generally, the effect of weather related factors influenced disease severity on all the germplasm. The stem rust infection was more severe in 2011 than 2010 based on disease notes (Table 3.2). Moreover, low (TR) and moderate (MR) disease incidences were observed in 2010 (Table 3.2). Stem rust severity was different on germplasm from different regions; with those from Africa and Asia exhibiting a susceptible reaction of 70S while a low disease incidence of 0

and AUDPC 0 was observed on germplasm from Canada and USA (Table 3.2). Among the tested germplasm, 21% were susceptible to stem rust exhibiting the highest AUDPC ranging from 1098 – 1130, while 68% of the germplasm were relatively resistant with AUDPC value ranging from 510 – 945 (Table 3.2). Severity of disease was high on germplasm from East Africa and Asia with an AUDPC above 1000 but Canadian germplasm were resistant with an AUDPC of 195 (Table 3.2). Nonetheless, germplasm from North America (Alberta Canada, North Dakota and Wisconsin) exhibited a susceptibility reaction of 30S. Stem rust race *Ug99* was avirulent on germplasm from Latin America and part of North America (Switzerland, England, Montana, Aberdeen and CIMMYT) exhibiting intermediate levels of stem rust severity from TR to 40 MRMS which constituted 42% of the germplasm.

It was clear from this study that infection type of stem rust on germplasm from Asia ranged from TR to 20MSS. Although seasonal effects were observed, there was genetic variation among the germplasm due to stem rust resistance within each season. The highest variation between seasons ranged from TR – 60S; 15S – 40MSS from Asia and North America regions, respectively.

The effect of year on disease severity was observed on QSM039 with disease severity of "0" and 30MSS in 2010 and 2011(Table 3.2). *Ug99* was virulent on QSM039 with severity of "0" and 15MS in 2010 and 2011, respectively. Although the seasonal variation on stem rust infection was also detected on PI45242, the reaction to stem rust ranged from 40S to 60S in 2011. In addition, stem rust was avirulent on 08-UT-47 (5MS) and Hietpas 5 (TS) but virulent on 08-UT-86 with reaction of 30 - 50MSS in the second season. Most of the germplasm from North America were resistant to stem rust with 08-AB-17 showing reaction of TR while 09-AB-89 and 06WA-406.27 had susceptible reaction of 40M and 30MSS, respectively in 2011. In addition, 08-MT-28 (TR) and 08-MT-32 (40MSS) showed variable reaction to stem rust infection. Q21861 DHP, Q21861 and Q125 were resistant to stem rust with severity ranging from 0 - 25MR. Similarly, germplasm (PI14971, PI14934 and PI21481) from Tajikistan exhibited the same infection type ranging from MSS- S while 14971 was susceptible (5S).

Despite the fact that SwissHV644 from Switzerland was resistant (0) to stem rust in the first season, it exhibited susceptibility reaction of 25S in the second season. Disease severity was high in the second season on germplasm KENP12 and 08-BA-69 from Bangladesh with susceptible

reaction of 50S and 70S, respectively. Germplasm 5045, 17024 and Q125 had disease severity of TR, 70S and 0, respectively (Table 3.2). Stem rust was virulent on germplasm 21481 with 60S reaction in 2011 From East Africa, Ethiopian germplasm showed low disease severity of 10MR on PI386458 in season one and susceptibility reaction above 60S on 23027. The Kenyan germplasm HKBL-13 and Nguzo were susceptible to stem rust with severity of 70S and 40S, respectively.

### 3.6.2 Agronomic Traits

The effects of season on agronomic traits of barley were also clearly manifested. Although barley evaluated in 2010 were taller than those grown in 2011, the weight of biomass was 60% more in 2011 than those of barley in 2010 (Table 3.3). However, for the two seasons, the spike length and number of spikelet ear $^{-1}$ were not different. The plant height, mean grain yield, thousand kernel weight and AUDPC were higher in 2011 than 2010 (Table 3.4). From this study, it has been observed that agronomic parameters from East African germplasm were higher than barley from any other region (Table 3.4) (Appendix 2 and 3). The tallest barley plants were observed for germplasm from North America (51.060 cm), Asia (50.170 cm) and East Africa (51.180 cm) (Table 3.4). The highest number of spikelets ear $^{-1}$ was observed on East African barley (40.14) and Latin American barley (40.12) (Table 3.4) (Appendix 2) with the longest spike length being observed on the former (11.43cm). Nevertheless, the mean barley spike length and number of spikes per ear from North America and Europe were significantly different from barley obtained from other regions (Table 3.4). The tallest barley from East Africa produced the highest biomass (1480g) followed by barley from North and Latin America (1310g). Barley from North America, Asia and East Africa produced grain yield ranging from 22g to 349g. However, with respect to grain yield, Latin America and Europe barley produced the same. Thousand kernel weight was similar in all germplasm across all the regions. The mean AUDPC was high on barley from East Africa (671.090) but least in Europe (315.55) (Table 3.4) (Appendix 3).

## 3.7 Discussion

The two seasons differed in weather related factors (Table 3.1). The mean rainfall and temperature during the crop cycles ranged between 14.3 - 240mm and 8 - 22°C in 2010. In 2011 rainfall and temperature ranges were 3.9 - 130.3 mm and 8 - 25°C, respectively. In a study on

resistant genes for leaf, stem and stripe rust in wheat, it was found that expression of these genes is influenced by temperature (Leonard and Szabo, 2005; Datta *et al.*, 2009). Temperature effect has also been observed on expression of stem rust resistant gene *Sr15* as it changed from resistant at 15°C to nearly full susceptible at 20°C (Roelfs, 1988). Park *et. al.* (1992) found that the resistant gene to stripe rust conferred by *Yr18* is temperature sensitive and is effective at high temperature above 40°C.

Further studies showed that stripe rust epidemics are often elevated by increased pathogen aggressiveness at higher temperature, this contribute to adaptation of stripe rust to warm environments (Milus *et al.*, 2009). This study suggests that stem rust infection was influenced by the variation of temperature and precipitation which contributed to increase in relative humidity. Consequently temperature range of 8- 9°C and 23 - 26°C favoured stem rust infection on barley.

In Canada, Boland *et. al.* (2004) reported that rusts do not survive winter temperatures but mild winter enhanced earlier rust epidemics making them more severe. Pittock *et. al.* (2008) in Australia found that increased off-season rainfall increased rust infection on wheat. Consequently, the difference in stem rust severity observed between the two years could have been probably due to temperature variation and it can be further deduced that the warm and moist environmental conditions favoured rust development during the second year. In a study on effect of climate change on wheat rusts, it was noted that rainfall distribution must be considered in assessing the effects of environmental changes on rust (Chakraborty and Newton, 2011).

Table 3.1: Monthly mean rainfall and temperature for two seasons during the crop cycle of barley (*Hordeum vulgare*) evaluated at Njoro during August 2010 to March 2011.

| Monthly Mean | August | September | October | November | December | January | February | March |
|---|---|---|---|---|---|---|---|---|
| | ----------2010---------- | | | | | ----------2011---------- | | |
| Max. Temp (°C) | 20.0 | 22.0 | 22.0 | 22.6 | 23.6 | 25.0 | 26.0 | 26.0 |
| Min. Temp (°C) | 8.0 | 8.0 | 10.0 | 8.4 | 8.1 | 8.0 | 8.0 | 9.0 |
| Rainfall (mm) | 240.0 | 172.2 | 109.9 | 53.1 | 14.3 | 3.9 | 9.5 | 130.3 |

Table 3.2: Severity of stem rust race *Ug99* and AUDPC on 10% of barley (*Hordeum Vulgare* L.) germlasm from different regions evaluated at KARI - Njoro in 2010 and 2011.

| ORIGIN | CULTIVAR | 2010 | | | | 2011 | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | 1st score | 2nd score | 3rd score | AUDPC | 1st score | 2nd score | 3rd score | AUDPC |
| Alberta Canada | Diamond | 5S | 10S | 15S | 181.50 | 20MSS | 30MSS | 30MSS | 510.00 |
| BARI | KENP12 | 10MSS | 10MSS | 30S | 255.00 | 40S | 30S | 50S | 510.00 |
| BARI | 08-BA-69 | TS | 5S | 5S | 6.50 | 10M | 20M | 30M | 662.50 |
| BARI | 08-BA-77 | TR | TS | 5M | 109.50 | 5MSS | 15MSS | 20MSS | 565.00 |
| Canada | Q21861 | 0 | TS | TS | 6.50 | 5M | 15M | 15M | 185.00 |
| Canada | QSM001 | 5MSS | 15MSS | 15M | 157.50 | 0 | TR | TR | 18.50 |
| Canada | QSM039 | 0 | 0 | 0 | 0.00 | 5MS | 10MS | 15MS | 195.00 |
| CIMMYT, Mexico | Q21861 | 0 | 0 | 0 | 0.00 | 5MR | 10MS | 15MS | 195.00 |
| CIMMYT, Mexico | Q21861 | 0 | 0 | TR | 57.50 | 10M | 20M | 20M | 460.00 |
| CIMMYT, Mexico | Q21861 | TR | TR | 10MR | 310.00 | 15M | 30M | 30M | 640.00 |
| England | P1452421a | TS | TS | TS | 18.50 | 40S | 50S | 60S | 945.00 |
| Ethiopia | P1347245 | 15MSS | 20MS | 20MS | 310.00 | 20MSS | 30MSS | 30MSS | 510.00 |
| Ethiopia | P1386458 | TR | 5MR | 10MR | 77.00 | 50S | 60S | 70S | 1130.00 |
| Ethiopia | 23027 | 5S | 25S | 30S | 255.00 | 50S | 60S | 60S | 975.00 |
| Kazakhstan | 17024 | 5M | 20MS | 20MSS | 190.00 | 50S | 60S | 70S | 1130.00 |
| Kazakhstan | 15517 | TS | 5S | 15S | 109.50 | 20M | 30MSS | 40MSS | 575.00 |
| Kazakhstan | 5045 | TR | TR | TR | 18.50 | 30S | 40S | 50S | 760.00 |
| Kenya | Karne | 30S | 40S | 60S | 945.00 | 40M | 50MS | 50S | 880.00 |
| Kenya | Nguzo | 25S | 35S | 60S | 825.00 | 25M | 40M | 40S | 673.00 |
| Kenya | HKBL-13 | 40S | 50S | 70S | 1130.00 | 50S | 60S | 65S | 1098.00 |
| Kyrgyzstan | 18358 | 5S | 10S | 15S | 157.50 | 40M | 50M | 50M | 880.00 |
| Kyrgyzstan | 18360 | TS | 5S | 15S | 109.50 | 40M | 50MS | 50MS | 880.00 |
| Minnesota USA | FEG192-16 | 5MS | 10MSS | 15MR | 157.50 | 40MSS | 50MSS | 50S | 880.00 |
| Minnesota USA | Shech/Ha079 | TS | TS | TS | 18.50 | 30M | 40M | 40MSS | 695.00 |
| Minnesota USA | Q125 | 0 | 0 | 0 | 0.00 | 5MR | 15MR | 25MR | 417.50 |
| Montana State Uni. | 08-MT-28 | 5S | 10M | 5MR | 181.50 | 10M | 20M | 30M | 580.00 |
| Montana | 08-MT-32 | 0 | 0 | TR | 6.50 | 30MSS | 40MSS | 40MSS | 520.00 |
| Montana | 08-MT-92 | 5MR | 10M | 5R | 125.00 | 20MSS | 30MSS | 10MS | 385.00 |
| North Dakota State Uni | 08-N2-87 | 0 | 0 | 10MSS | 6.50 | 20M | 30MSS | 35MSS | 542.50 |
| North Dakota StateUni.. | 09N2-64 | 10S | 15S | 30S | 25.00 | 10MS | 20MS | 30MS | 542.50 |
| North Dakota State Uni. | 09N6-08 | TS | 10S | 15S | 207.00 | 10MS | 20MS | 40MSS | 640.00 |
| Switzerland | Swiss HV525 | TS | 5S | 5S | 57.50 | 15M | 20M | 20MR | 325.00 |
| Switzerland | SwissHV644 | 0 | 0 | 0 | 0.00 | 15MS | 25MSS | 25S | 417.50 |
| Switzerland | SwissHV673 | 0 | TMR | TMR | 18.50 | 5MR | 10MR | 10MR | 162.50 |
| Tajikistan | 14971 | TR | 2R | 5R | 44.50 | 15MSS | 25MSS | 40MSS | 530.00 |
| Tajikistan | 14934 | TS | 5S | 15S | 109.50 | 30MSS | 40MSS | 50MSS | 760.00 |
| Tajikistan | 21481 | 5S | 15MSS | 20MSS | 214.00 | 30S | 40S | 60S | 1020.00 |
| Ukraine | C15541A | TMS | 5MS | 10MS | 77.00 | 40MSS | 50MSS | 50MSS | 893.00 |
| USDA-ARSAberdeen | 08-AB-17 | 0 | 0 | TR | 77.00 | 5MR | 10MR | 10MR | 422.50 |
| USDA-ARSAberdeen | 09AB-79 | TS | 5S | 5S | 157.50 | 10MSS | 20MSS | 30MSS | 640.00 |
| USDA-ARSAberdeen | 09AB-89 | TR | 5MR | 5MR | 18.50 | 10M | 20M | 40M | 737.50 |
| Utah State University | U04B2041-14 | 5MSS | 10MSS | 10MSS | 149.00 | 10MSS | 20MSS | 30MSS | 542.50 |
| Utah State University | 08-UT-47 | 0 | TS | 5MS | 6.50 | 20MSS | 30MSS | 40MSS | 640.00 |
| Utah State University | 08-UT-86 | 10MSS | 15MSS | 15MSS | 500.00 | 30MSS | 40MSS | 50MSS | 760.00 |
| WashingtonState Uni. | 06WA-406.27 | TMR | 5MR | 5MR | 57.50 | 30M | 30MSS | 30MSS | 510.00 |
| Washington State Uni. | 06WA-427.12 | 0 | TR | TMR | 18.50 | 10M | 15M | 25M | 417.50 |
| Washington State Uni. | 09WA-35 | TS | 5MS | 10MS | 18.50 | 5M | 10MS | 10MS | 422.50 |

AUDPC = area under the disease progress curve; 0 = immune, MT = Maturity. R = resistant, MR = moderately resistant, MS = moderately susceptible, S = susceptible, TR= trace resistant, TS = trace susceptible, TMR= trace moderately resistant, TMS= trace moderately susceptible, MSS = moderately susceptible and susceptible, M=MRMS (Roelfs *et al.*, 1992). Uni = university.

A modeling study on crop pathogen predicted a range shift with rising temperature and other weather variables for black sigatoka (*Mycosphaerella fujiensis*) in banana (*Musa* spp.) (Ghini *et al.*, 2008).

Variability of virulence of stem rust on the germplasm was clearly manifested from AUDPC. In this study, germplasm from East Africa exhibited high AUDPC because Kenya and Ethiopia are areas where prevalence of stem rust is high and germplasm are exposed to broad range of virulent genes hence lose of variability normally occurs (Dubin and Rajaram, 1996). The high severity of stem rust on germplasm from Canada, Bangladesh, Ethiopia, Kenya, Kyrgyzstan, North Dakota, Wisconsin, indicates that no resistant genes to *Ug99* was present. Consequently, there is an urgent need to tap other genes from other gene pools. The susceptible varieties mighty have only single race specific type of resistance (Ellingboe, 1981).

In an epidemiological study, Roelfs et al., (1994) noted that the movement of race 24 of *P. striiformis* f.sp. *hordei* on barley from South America to Mexico then to the United States, showed that cereal rusts can move North of the America. The evidence of rust movement has been observed on coffee rust (*Hemileia vastatrix*), which moved northwards from South America to Mexico and dissemination of the rust was attributed to both wind and human activities (Scheiber and Zentmeyer, 1984). Majority of barley lines from CIMMYT among others remained moderately resistant due to either inadequate stem rust inoculum or presence of race that lacked virulence for the resistant genes contained in the germplasm (Njau *et al.*, 2009).

Germplasm from Kazakhstan, North Dakota, USDA-ARS, Washington State and Montana among others showed seasonal variation an indication of genetic variation in germplasm from these regions. Germplasm with the same severity (PI14971, PI14934 and PI21481) and (Q21861 DPH, Q21861 and Q125) indicates that they may have a common origin as the later comes from Asia which is tropical lowland with an elevation of 10 – 40 masl and humid conditions. This suggests that they may have same genes hence similar reaction to rust infection (Dubin and Rajaram, 1996). Seven different barley stem rust genes are now catalogued, *RPg1, RPg2 , RPg3 , rPg4 , RPg5, rPgBH* and *rPg6* (Fetch *et al.*, 2008). Germplasm Q21861 from CIMMYT that contain *rPg4* gene was among the resistant lines to stem rust. This recessive gene is temperature sensitive and is effective at 17-22 °C but ineffective above 27 °C (Jin *et al.*, 1994). Because the temperature experienced during growth period is within this range,

conferment of resistance of this gene to stem rust was effective. Whether the same gene confers resistance to *P. graminis secalis* would be an interesting area for further investigation.

The agronomic and AUDPC traits were measured under two contrasting moisture conditions in 2010 and 2011. Biomass, 1000-kernel weight was significantly different in 2011 due to low disease severity and favourable weather conditions. The high means in agronomic parameters in East Africa is due to the fact that East African highlands (Ethiopia) is an area of cereal diversity majorly wheat hence well adapted. The mean plant height was also high in barleys from Asia and North America, and the same germplasm differed significantly in the mean grain yield as a result of day length sensitivity enhanced in the germplasm from this regions.

Regions with the same means in agronomic parameters, biomass and grain yield are speculated to have the same agro - ecological zones. For instance, Latin and North America are tropical highland with high rainfall, temperate environments with an average of more than 500mm of rainfall during the crop cycle with an elevation of 1000 masl (Rajaram and Van Ginkel, 1994). A thousand kernel weight was similar in all the germplasm across all the regions. In contrast to this result, Harder and Legge (2000) reported a loss in kernel weight in barley for resistant and susceptible varieties, respectively. Herrera – Foessel *et. al.* (2006) reported an average loss in kernel weight of 13.3 and 10.3% in durum wheat (*Triticum turgidum* L.).

**3.8 Conclusion**

This study demonstrated that Hietpas 5, 09-AB-78, Q21861, 09-N2-52 and Chevron have valuable stem rust resistance genes that could be useful for barley improvement as far as resistance to stem rust is concerned. Despite the fact that most of the barley genotypes were infected by the rust, some did not show a high AUDPC which suggest that polygenic genes plays a crucial role in conferring resistance. The evidence from this study showed that there is lose of variability in East African barley due to mutation of the stem rust pathogen race *Ug99* which so far has eight variants.

Table 3.3: Mean of two seasons for different agronomic parameters and area under the disease progress curve (AUDPC) of Barley (*Hordeum vulgare*) germplasm from different origin in Njoro.

| Season | | Mean height | Spike length | No. of spikelet/ear | Biomass | Grain yield | 1000-kernel weight | AUDPC |
|---|---|---|---|---|---|---|---|---|
| | | ----------cm---------- | | | ----------g---------- | | -------g----- | |
| Year 2010 | Mean | 60.52±0.700 | 8.66±0.16 | 34.83±0.89 | 64.00±0.01 | 50.00±0.004 | 30.00±0.001 | 147.19±9.72 |
| | N | (278) | (278) | (278) | (278) | (278) | (278) | (278) |
| | Range | 30 - 90 | 3.15 – 12.65 | 6.24 – 71.20 | 0.07 – 1.49 | 0.06 – 0.25 | 0- 0.25 | 0 - 630 |
| Year 2011 | Mean | 38.60±9.05 | 8.52±0.25 | 32.28±0.91 | 191.00±0.07 | 70.00±0.004 | 40.00±0.001 | 735.59±14.43 |
| | N | (266) | (266) | (266) | (266) | (266) | (266) | (266) |
| | Range | 13 - 2424 | 2.7 – 72.40 | 10.8 – 87.20 | 0.04 – 5.75 | 0.07 – 0.95 | 0.03 – 0.37 | 18.50 - 1282 |

Means ± Standard Error; N = the number of germplasm, Grain yield area = $0.15m^2$

Table 3.4: Means of agronomic traits and area under the disease progress curve (AUDPC) of barley (*Hordeum vulgare*) lines from different origin evaluated at Njoro in 2010 and 2011.

| Origin | | Mean height | Spike length | No. of spikelets/ear | Biomass | Grain yield | 1000-kernel weight | AUDPC |
|---|---|---|---|---|---|---|---|---|
| | | ----------cm---------- | | | ----------g---------- | | ------g----- | |
| N. America | Mean | 51.06±6.89 | 8.21±0.07 | 30.80±0.71 | 1310±0.05 | 60.00±0.003 | 40.00±0.001 | 436.20±19.4 |
| | N | (350) | (350) | (349) | (349) | (349) | (349) | (353) |
| | Range | 179.5 - 266 | 1 – 98.5 | 0 -88.5 | 190 - 265 | 130 - 260 | 1 - 195 | 103 - 185 |
| L. America | Mean | 46.28±2.59 | 9.68±1.24 | 40.12±2.25 | 1310±0.15 | 50.00±0.005 | 40.00±0.001 | 487.40±52.67 |
| | N | (52) | (52) | (52) | (52) | (52) | (52) | (52) |
| | Range | 99 – 168.8 | 188 - 266 | 168 - 264 | 89 - 189 | 90.5 – 178.5 | 96 - 175 | 103 - 185 |
| Europe | Mean | 42.23±3.01 | 7.59±0.165 | 33.31±2.59 | 860.0±0.1 | 50.00±0.007 | 40.00±0.002 | 315.55±44.08 |
| | N | (42) | (42) | (42) | (42) | (42) | (42) | (42) |
| | Range | 2 - 85 | 1 - 98.5 | 91.5 - 168 | 3 - 88 | 90.5 – 178.5 | 178 - 265 | 9.5 - 100 |
| Asia | Mean | 50.17±2.21 | 9.32±0.18 | 39.63±1.84 | 1150±0.11 | 40.00±0.003 | 40.00±0.003 | 395.42±32.41 |
| | N | (78) | (78) | (78) | (78) | (78) | (78) | (78) |
| | Range | 99 – 168.5 | 100.5 - 185 | 160 - 260 | 89 - 189 | 2 – 88.5 | 9.5 – 99.5 | 9.5 - 100 |
| East Africa | Mean | 51.18±4.29 | 11.43±1.62 | 40.14±3.51 | 1480±0.19 | 80.00±0.05 | 40.00±0.002 | 671.09±88.75 |
| | N | (22) | (22) | (22) | (22) | (22) | (22) | (22) |
| | Range | 2 - 85 | 188 - 266 | 168 - 264 | 168 - 264 | 190 - 265 | 181 - 265 | 195 – 266.5 |

Mean± Standard Error; N = the number of germplasm, Grain yield area = $0.15m^2$

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# CHAPTER FOUR

# GENETIC ANALYSIS OF BARLEY (*Hordeum vulgare* L.) SEEDLING RESISTANCE TO STEM RUST (*Puccinia graminis* pers. f. sp. *tritici* Eriks and E. Henn) RACE *Ug99*

## 4.1 Abstract

Stem rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks and E. Henn) race *Ug99* is a devastating disease in barley (*Hordeum vulgare* L.) worldwide. This study was set to determine the seedling resistance in barley to stem rust race *Ug99* and to determine the mode of inheritance of resistant genes conferring resistance to race *Ug99*. Two hundred and eighty barley introductions from North America, Latin America, Europe, Asia and East Africa were evaluated for seedling resistance to stem rust race *Ug99* in the greenhouse. Seedlings were inoculated with stem rust inoculum 7-10 days after planting when the first leaf was fully emerged (Feekes stage 1). At seedling stage, 67% of the germplasm exhibited low infection types (IT) "0" to "$1^{+}$" with no sporulating uredinia. However, race *Ug99* was virulent to germplasm from Canada, Bangladesh, England, and USA. Although all the hybrids were resistant to *Ug99* with IT ranging from "0" to "$1^{+}$", $F_1$ population from the cross Karne × 09-N2-19 were susceptible to stem rust. The observed resistant (R):susceptible (S) ratio of the $F_2$ populations; HKBL-1385-13 × 08-UT-86 ($\chi^2_{0.05}$= 0.480, p≥0.488, df = 99); HKBL-1385-13 × 09-N2-19 ($\chi^2_{0.05}$= 0.641, p≥0.424, df = 99, df = 99) and [ND2649 × 09-AB-78 ($\chi^2_{0.05}$= 1.05, p≥0.309, df = 48) exhibited Mendelian segregation of 3R:1S suggesting that the resistance is conferred by major genes at seedling stage. In addition, $F_2$ population derived from crosses Karne × 09-N2-19 ($\chi^2_{0.05}$= 1.343 p≥0.246, df = 99), Nguzo × 09-AB-78 ($\chi^2_{0.05}$= 0.429, p≥0.512, df =99) and ND26249 × 09-N2-52 ($\chi^2_{0.05}$= 2.576, p≥0.111, df =108) conformed to phenotypic ratio of 9:7 indicating the common epistatic ratio. The results of this study suggest that there are valuable major genes for stem rust resistance that could be used to develop resistant barley germplasm.

## 4.2 Introduction

Stem rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks and E. Henn) race *Ug99* (TTKSK) is virulent to most wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) cultivars grown worldwide (Singh *et al.*, 2008). Seedling resistance is monogenic and race specific, however the pathogens often evolve to overcome these genes with time leading to "boom and bust cycles" (Parlevliet, 2001). There is possibility that seedling resistance genes provide

resistance at all stages of plant growth unlike polygenic genes which are detected in post seedling stages (Parlevliet, 2001). Race specificity resistance uncovers Mendelian inheritance however, experimental precaution is required on quantitative inheritance. Since the emergence of race *Ug99* that causes 30 – 70% yield loss more than a decade ago, the global production of barley is at risk (Ephrem *et al.,* 2000; Pretorius *et al.,* 2000; Singh *et al.,* 2006). Unlike stripe rust (*Puccinia striiformis*) and leaf rust (*Puccinia triticina*) rust, that partially affects crop yields, *Ug99* reduces yield by 80-100%, (Leonard, 2001; CIMMYT, 2005; Singh *et al.,* 2006). Moreover, the rust pathogens are highly mobile trans - boundary diseases which can spread rapidly over long distance, either by wind or accidental human aided transmission (Brown and Hovmøller, 2002).

In barley, genes conferring resistance to *Puccinia graminis* f. sp. *tritici* have been identified and designated as *RPg1, RPg2, RPg3, rPg4, RPg5, rPgBH* and *rPg6* (RPg means resistant to *Puccinia graminis*) (Fetch *et al.,* 2008). Among these genes, *RPg1, rPg4* and *RPg5* have been investigated at molecular level (Han *et al.,* 1999). The *rPg6* gene derived from *Hordeum bulbosum* and located on chromosome 6H is resistant to race *QCCJ* (Fetch et. al. 2008). Cultivars Chevron (CIho 1111) and Peatland (CIho 5267) are other sources of resistance to stem rust in barley that possess the *RPg1* gene (Brueggeman *et al.,* 2002). Gene *RPg2* from Heitpas- 5 is resistant to stem rust race HTMJ and JCMN at seedling stage but susceptible to most stem rust races despite the fact that it is reported to be an adult - plant resistance gene (Sun and Steffenson, 2005). Gene *RPg3* derived from PI 382313 has an intermediate level of seedling resistance but is susceptible to race *QCCJ* (Sun and Steffenson, 2005). In a study carried out on 18,000 barley accessions from the USDA National Small Grains, gene in Q21816 containing the gene *rPg4* was identified as the most resistant germplasm. The gene was effective at 17-22 °C but ineffective above 27 °C (Jin *et al.,* 1994). Barley accession Q21861 was also resistant to rye (*Secale cereale*) stem rust (*P. graminis* f. sp. *secalis)* (Steffenson, 1992).

Since the *rPg4* gene is a recessive gene and temperature sensitive, it may have a negative function on the ability of fungus to establish itself within the plant, (Brueggeman *et al.,* 2009). The wild and cultivated relatives of wheat and barley such as triticale (*X. triticosecale*) offer useful sources of stem rust resistance. In addition, landraces are valuable genetic resources for cultivar improvement, as they may possess a wide range of variation, specific adaptation to the different environments in their regions of growth and resistance to diseases and insect pests

(Alex *et al.*, 1997; Mujeeb- Kazi and Rajaram, 2000). Though molecular investigation and identification of location of gene *RPg1* has been done, it is important to focus research on the durability and mode of action of this gene (Kleinhofs *et al.*, 2009).

In wheat, evaluation of 45 stem rust genes has been done including *Sr2, Sr30* and *Sr31* among others (Bansal *et al.*, 2008). Among the designated genes in wheat, *Sr2* is race specific and is expressed at both seedling and adult plants as it is also effective in slowing the development of rust (Sunderwirth and Roelfs, 1980; McIntosh *et al.*, 1995). However the resistance conferred by the *Sr2* gene has broken down and wheat cultivars became susceptible to *Ug99* at the end of last century (Ephrem *et al.*, 2000). Race *Ug99* is also virulent on genotypes carrying stem rust resistant gene *Sr31* (Pretorius *et al.*, 2000; Singh *et al.*, 2006). Therefore it is important to search for new and potentially durable sources of resistance. Objectives of this study were to assess barley genotypes for resistance to stem rust and to determine the mode of inheritance of seedling resistance to stem rust race *Ug99*. Gene postulation was beyond the scope of this study.

## 4.3 Materials and Methods

### 4.3.1 Experimental Site

A greenhouse experiment was conducted at Kenya Agricultural Research Institute (KARI) - Njoro (0° 20'S 35° 56'E) situated at an elevation of 2185 m above sea level. This site experiences annual rainfall of 939.3 mm (average of 61 years) and an average minimum and maximum temperature of 9 and 24°C, respectively (Kenya Meteorological Station Identification Number 9031021). The site was chosen because environmental conditions are conducive for stem rust infection and it is a representative of wheat and barley growing areas (Singh *et al.*, 2006.

### 4.3.2 Genotypes and Development of $F_2$ Population

Two hundred and eighty barley germplasm from North America, Europe, Eastern Europe and Eastern Africa were evaluated for seedling resistance to stem rust in the greenhouse. Wheat genotype with *Sr24* gene was planted together with test genotypes as a susceptible check. Fifteen $F_1$ populations were developed through one way cross by crossing Plant Introduction (PI) × Plant Introduction (PI) (ND26249 × 08-UT-86, ND26249 × 09-AB-78, ND26249 × 09-N2-52,

ND25882 × 09-AB-78) and Kenyan barley variety × PI (KARNE × 09-N2-19, NGUZO × 09-AB-78, NGUZO × 09-N2-19, HKBL1385-13 × 08-UT-86, HKBL-1385-13 × 09-N2-19, HKBL-1385-13 × 09-N2-20) in the cage.

### 4.3.3 Experimental Procedure

The 284 barley germplasm and $F_1$ populations were planted in plastic pots measuring 6 cm × 6 cm filled with about 200g of a mixture of soil and sand in a ratio of 3:1. The pots were placed in a greenhouse that was maintained at 23°C and 60% RH. In each pot, ten seeds were planted at approximately 2 cm deep and pots were then placed in large non-draining aluminum trays measuring 60 cm × 240 cm and watered to field capacity. From each $F_2$ population (120-150 seeds) were planted, 3-4 seeds were sowed in each pots measuring 6 cm × 6 cm pots and filled with Hygro mix seedling growing media (REG. NR./NO.84/00638/07).

Uredinal of one stem rust race, *Ug99* obtained from Kenya Agricultural Research Institute (KARI – Njoro) was used for inoculation. The virulent race was collected from differential hosts in the greenhouse using portable sunction pump, packed in vials, sealed under vacuum, and stored at - 20°C. Inoculation was done in November 2011 for the barley lines and April 2012 for the populations at four in the evening. Uredinospores were removed from - 20□C and heat shocked in a water bath at 40°C for 3 minutes. The spores were suspended in soltrol (Chevron Philips Chemical Co. No.0113172) at a concentration of $4\times10^{10}$ spores per ml. The seedlings were inoculated by hand sprayer with urediniospores at feekes stage 1 in isolation room and placed in dark chamber with 100% RH maintained at 13°C for 18 hours. Seedlings were then transferred to a growth chamber that was maintained at about 22°C day and 20 - 21□C night temperature. Illumination in the greenhouse was supplemented with halogen lamps for 15 hour photoperiod.

## 4.4 Disease Assessment

Seedlings were assessed for disease severity 14 days later (Feekes 1) after inoculation using 0 - 4 infection types (IT) scale when uredinia on the susceptible line appeared fully developed (McIntosh *et.al.*, 1995). A susceptible host with large uredina without chlorosis or necrosis was denoted by"3" and "4", whereas flecking, chlorosis and necrosis was shown by ";" "C" and "N", respectively. Variation with less or more than the average of class was indicated by

the use of superscript "+" for pustules that were larger or "_" for those pustules that were smaller than the normal size limiting in reference to 0 - 4 infection types (IT) scale.

### 4.5 Data Analysis

The results for PI, $F_1$, $F_2$ and adapted Kenyan genotypes (Karne, Nguzo, and HKBL-13 and HKBL-12) were evaluated for seedling resistance in the greenhouse. The seedlings were categorized as resistant if they had infection type ranging from "0" to "$2^+$" and susceptible if they had a score ranging from "3" to "4" when uredinia on the susceptible line appeared fully developed according to (Roelfs *et al.,* 1994; McIntosh *et al.,* 1995). Inheritance to stem rust in the $F_2$ population was determined by using the Chi-squared ($\chi^2$) formula below:

$$\chi^2 = \frac{\sum(Observed - Expected)^2}{Expected}$$

The data were analyzed using the (SAS Institute, Inc 2001) procedure (Appendix 4 a):
Where the figures in parenthesis in this SAS procedure represent the expected proportions.

### 4.6 Results

The germplasm evaluated for seedling resistance exhibited variable infection types. The infection types observed ranged from 0 - 4 (Table 4.1). The check variety showed an infection type "4" (Plate 4.1).The variation observed also varied with the origin of the germplasm. At seedling stage (Feekes 1), 67%, exhibited IT "0" to "2" and were considered resistant to stem rust race *Ug99*. This included germplasm from North America, Latin America, East Africa, Asia, Europe and Ukraine. Race *Ug99* used for inoculation on the germplasm was virulent with IT ranging from "3" to "4" on 33% of the germplasm. About 22% of the germplasm evaluated mainly from North America were resistant to stem rust. However, some of the germplasm exhibited heterogeneous infection type "X" (Table 4.1).

Even though "X" infection type was observed on the germplasm from 18 origins, this infection type was not common. It was observed that the virulence of *Ug99* on the germplasm from North Dakota showed susceptible infection type "4". Germplasm from North America, Latin America, Asia (Kazakhstan), East Africa (Kenya) and Europe (Switzerland) exhibited the

most common IT of "0"(Table 4.1). The susceptibility of germplasm Diamond, QSM058 and QSM059 to stem rust were noted with infection type "$3^+$" although IT of "0" was expressed on most of the QSM cultivars (Appendix 1). In addition, the resistant reaction of "0" was observed on FEG183-53, Schech/Harr079 and QSM127 despite the fact that FEG192-15 from the same region had "X" reaction.

In this work, race *Ug99* was avirulent to cultivars 08-N2-22, 08-N2-47, 08-N2-87 and 09-N6-08 from North Dakota with low IT of "0". However, the virulence of this race on genotypes 09-N2-52, 09-N2-23, and 09-N2-20 was observed with susceptibility IT of "4". Four genotypes (08-AB-17, 08-AB-28 and 08-AB-31) from USDA - ARS Arbedeen were resistant to stem rust with IT "0.", but 09-AB-79 and 09-AB-80 exhibited heterogeneous reaction of "X" and IT of "4", respectively (appendix 1). Two genotypes 08-UT-91 and 08-UT-72 from Utah were resistant to *Ug99* with IT of "0" but 08-UT-73 showed susceptibility with IT "3". Germplasm from Washington showed variable reaction to stem. Genotypes 08-WA-01, 09-WA-10 and 09-WA-63 were resistant with infection type "0" while 06-WA-427.12 and 06-WA-437.14 were susceptible (Appendix 1). Six out of eight germplasm from Switzerland (SwissHV504, SwissHV611, SwissHV630, SwissHV658, SwissHV673 and Chevron) were resistant to *Ug99* with infection type "0" and two PC84a and SwissHV664 were susceptible to stem rust with infection type "3" and "$3^+$". Remarkably, all germplasm from Bangladesh, Kazakhstan, Kenya and Ethiopia were resistant with IT of "0". Moreover, IT of "$1^+$" and ";" were expressed by germplasm CI5541a from Ukraine and PI14905 from Tajikistan and germplasm PI22482 was susceptible with IT of "4".

Among the eleven barley germplasm used for genetic analysis, 56% were found to be resistant and 44% were susceptible to stem rust at seedling stage. In general, about 90% of the $F_1$ populations were resistant to stem rust at seedling stage while 10% was susceptible. Among the fifteen crosses obtained, $F_1$ derived from HKBL-1385-13 × 09-N2-20; ND25882 × 08-UT-86, Steptoe × 08-UT-86 and ND26249 × 09AB-78 reacted showed an infection type of "0",";" to "1"(Table 4.2). The hybrids ed from HKBL-1385-13 × 08-UT-86, Nguzo × 09-N2-19, ND26249 × 08-UT-86 and ND25882 × 09-AB-78 were resistant with slightly larger uredinia surrounded by necrosis than expected for this infection type. In general, about 90% of the $F_1$

populations were resistant to stem rust at seedling stage while 10% was susceptible. Among the fifteen crosses obtained, $F_1$ derived from HKBL-1385-13 × 09-N2-20 showed an infection type of "0". While $F_1$ from crosses ND25882 × 08-UT-86, Steptoe × 08-UT-86 and ND26249 × 09AB-78 reacted to stem rust with an IT of exhibited ";" to "1"(Table 3.2). The hybrids developed from HKBL-1385-13 × 08-UT-86, Nguzo × 09-N2-19, ND26249 × 08-UT-86 and ND25882 × 09-AB-78 were resistant with slightly larger uredinia surrounded by necrosis than expected for this infection type. The hybrids from Karne × 09-N2-19 was the most susceptible cross with infection type "3". Among the susceptible crosses, $F_1$ derived from Karne × 09-N2-19 was the most susceptible. However, there were no "X" reactions observed among the evaluated $F_1$ genotypes.

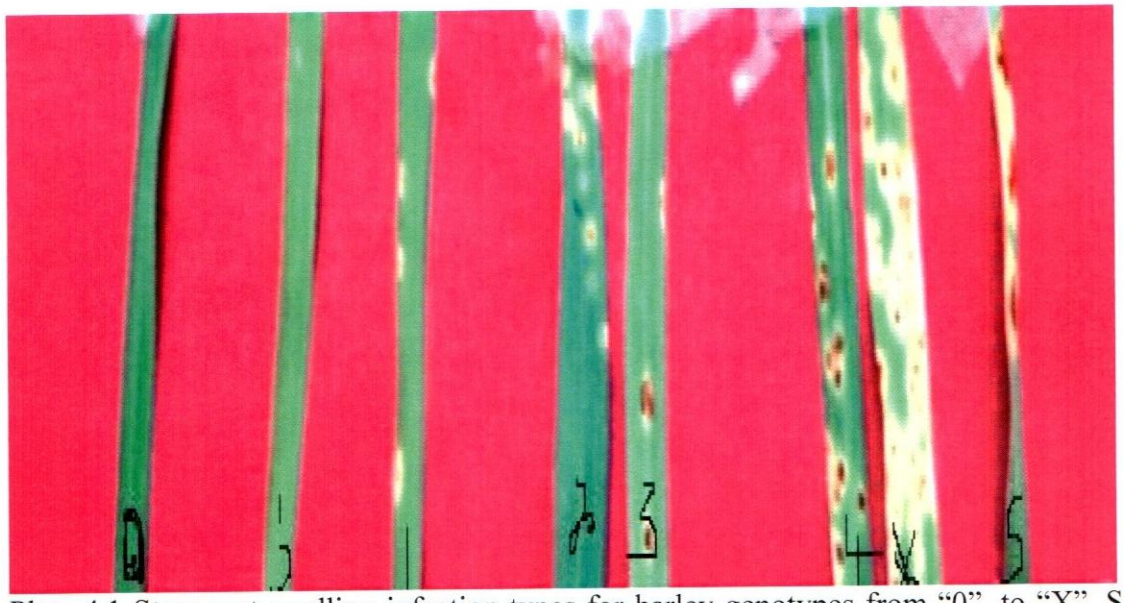


Plate 4.1 Stem rust seedling infection types for barley genotypes from "0", to "X", S is the spreader on 08-N2-58,Swiss HV627, ND25882 × 09-AB-78,HKBL-1385-13,ND26249, 09-N2-19,PI21486.

Table 4.1 Seedling reaction (Most common IT) of barley (*Hordeum vulgare L.*) germplasm from 18 regions to stem rust (*Puccinia graminis* sp. *tritici*) race *Ug99* in the green house at Njoro in 2011.

| Origin | Country/State | No. of Genotypes | Infection types (IT) (0-4 Scale)[1] | | Resistance (%) |
|---|---|---|---|---|---|
| | | | Most Common | Range | |
| North America | Alberta Canada | 1 | 3+ | --[2] | --[2] |
| Asia | Bangladesh | 13 | 2+ | 0 - 2+ | 53 |
| North America | Minnesota USA | 10 | 1+ | 0 – X | 80 |
| North America | Montana | 9 | ; | 0 – 4 | 55 |
| North America | North Dakota State University | 23 | 4 | 0 – 4 | 65 |
| North America | USDA-ARS Aberdeen | 16 | 1+,2+ | 0 – X | 68 |
| North America | Utah State University | 8 | 3 | 0 – 3 | 83 |
| North America | Washington State University | 46 | 0 | 0 – X | 59 |
| North America | Wisconsin USA | 1 | 2+ | --[2] | --[2] |
| North America | Canada | 72 | 0 | 0-3+ | 58 |
| Latin America | CIMMYT, Mexico | 22 | 0 | 0 – 3 | 95 |
| Europe | Switzerland | 40 | 0 | 0 - 3+ | 67 |
| Europe | England | 1 | 2+ | --[2] | --[2] |
| Asia | Tajikistan | 9 | ; | ; -X | 55 |
| Asia | Kazakhstan | 3 | 0 | 0 | 100[3] |
| East Africa | Ethiopia | 6 | 1+ | 0 - 2+ | 83 |
| East Africa | Kenya | 4 | 0 | 0 - 1+ | 75[3] |
| Asia | Ukraine | 1 | 1+ | --[2] | --[2] |

[2] Country of seed origin with only one cultivar, [3] Country of seed origin with less than five cultivars [1] Scale according to (Roelfs *et al.,* 1994; McIntosh *et.al.,* 1995). 0 = immune; ; = very resistant; 1 = resistant; 2 = Resistant to moderately resistant; 3 = moderately resistant to moderately susceptible; 4 = susceptible; + = larger pustules.

The ratio of resistant to susceptible populations observed in $F_2$ derived from [HKBL-1385-13 × 08-UT-86 ($\chi^2_{0.05}$ = 0.4800, p≥0.4884, df = 99)] [HKBL-1385-13 × 09-N2-19($\chi^2_{0.05}$ = 0.6405, p≥0.4235, df = 99)] [ND2649 × 09-AB-78 ($\chi^2_{0.05}$ = 1.0588, p≥0.3085, df = 48)] and [ND25882 × 09-AB-78 ($\chi^2_{0.05}$ = 3.5986, p≥0.0578, df = 48)] with observed ratios (2.6:1, 2.5:1, 3.91:1, and 1.72:1) fitted the expected Mendelian ratio (3R:1S) an indication of one gene model action (Table 4.2). However, the $F_2$ population derived from [Karne × 09-N2-19 ($\chi^2_{0.05}$= 0.0025 p≥0.9598, df = 99)], [Nguzo × 09-AB-78 ($\chi^2_{0.05}$ = 0.4292, p≥0.5124, df = 99)], [ND26249 × 09-N2-52 ($\chi^2_{0.05}$ = 2.5759, p≥0.1085, df = 108)] and [ND25882 × 09-AB-78 ($\chi^2_{0.05}$ = 0.9799, p≥0.3222, df = 48)] with observed ratios (10.3:6.3, 14:11, 10.6:9.4 and 10.6:11.2) conformed to the ratio 9:7 (resistant: susceptible) phenotypic ratio thereby demonstrating epistatic gene effect. The analysis also revealed that the following population demonstrated modifying gene effect ratio 10:6 [Karne × 09-N2-19 ($\chi^2_{0.05}$ = 1.3543 p≥0.2445, df = 99)], [Nguzo ×09-AB-78 ($\chi^2_{0.05}$ = 0.4236, p≥0.5151, df = 99)], [ND26249 × 09-N2-52 ($\chi^2_{0.05}$ = 2.5622, p≥0.1094, df = 108)] and [ND25882 × 09-AB-78 ($\chi^2_{0.05}$ = 0.9864, P≥0.3206, df = 48)].

Upon separating the seedling infection types for $F_2$ population, infection types "2" and "3" were prominent ITs for population HKBL-1385 × 09-N2-20 (Fig 4.1). HKBL-1385 × 09-N2-19, and ND25882 × 09-AB-78 exhibited infection types"2" as the prominent IT. Populations Karne × 09-N2-19, Nguzo × 09-N2-19, and Nguzo × Q21861 and ND26249 × 09-N2-52 displayed infection type "3" as the most prominent. The $F_2$ populations with "2" as the most common IT fit the monogenic ratio of 3R:1S (Figure 4.2 b and i) except population Nguzo × 09-AB-78. Moreover, population ND26249 × 09-AB-78 also fitted the monogenic ratio and exhibited "0" as the most prominent IT. However, the population exhibiting "3" as the most common IT (Figure 3.2 a, c, e, f and h) conformed to the modifying gene ratio 9R:7S

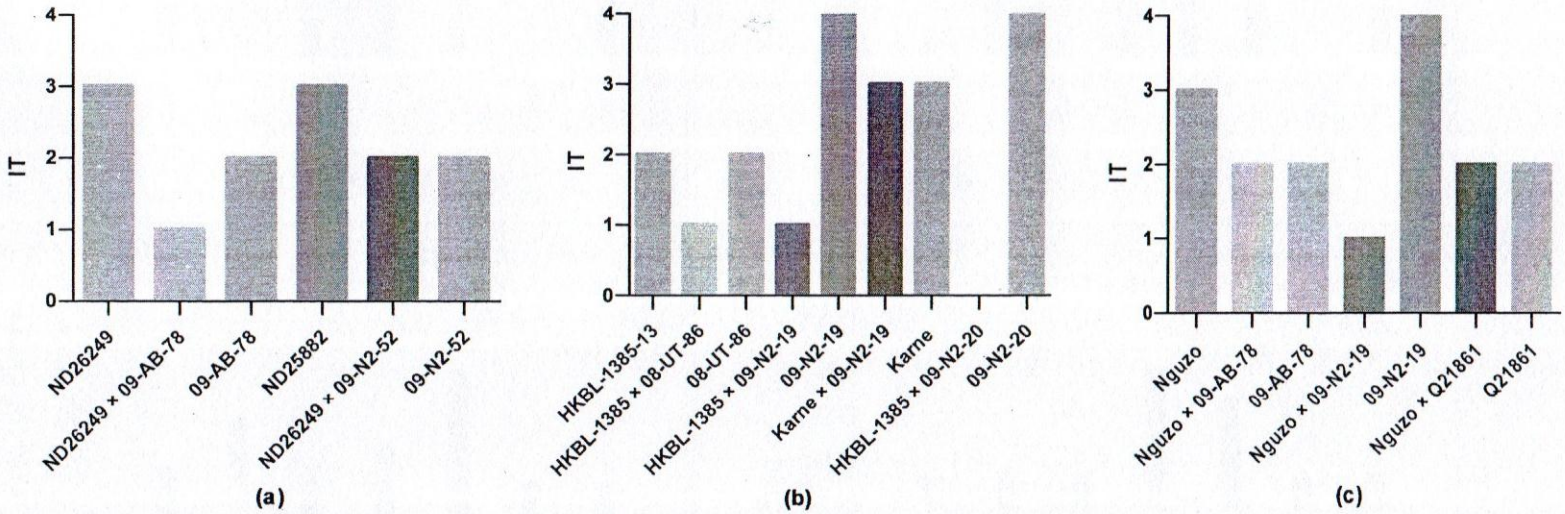



Figure 4.1. Seedling reaction of barley (*Hordeum vulgare L.*) parents and $F_1$ population to stem rust race *Ug99* in the green house. IT = Infection type according to (Roelfs *et al.,* 1994; McIntosh *et.al.,* 1995); (a) = IT of parents ND26249, 09-AB-78, ND25882, 09-N2-52 and their $F_1$ population; (b) = IT of parents HKBL-1385-13, 08-UT-86, 09-N2-19, Karne, 09-N2-20 and their $F_1$ population; (c) = IT of parents Nguzo, 09-AB-78, 09-N2-19 and Q21861 and their $F_1$ population

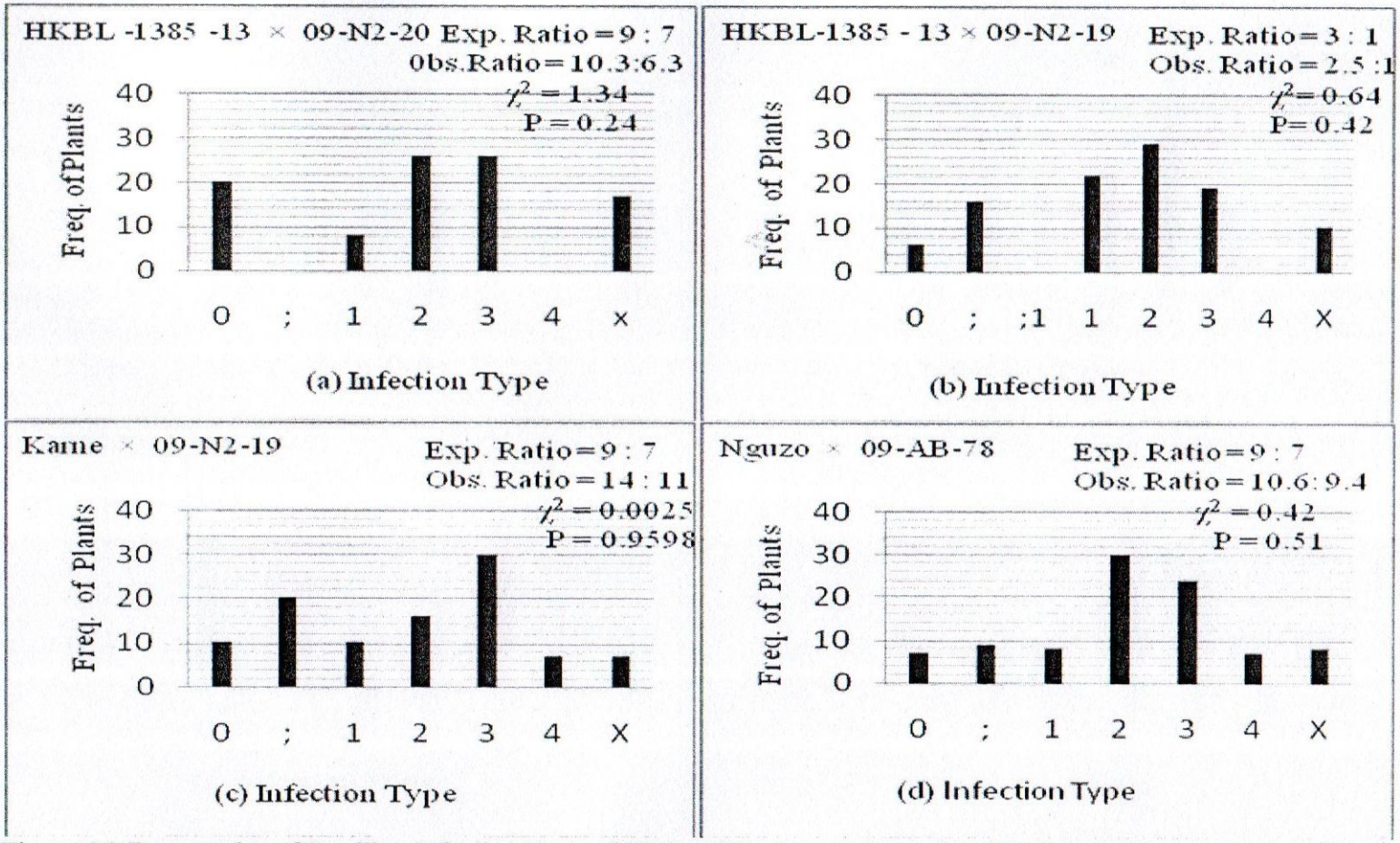



Figure 4.2 Frequencies of Seedling Infection Type of Barley (*Hordeum vulgare L.*) of $F_2$ Population to stem rust (*Puccinia graminis* f.sp. *tritici*) race *Ug99* in the green house). 0 = immune; = very resistant; 1 = resistant; 2 = Resistant to moderately resistant; 3 = moderately resistant to moderately susceptible; 4 = susceptible; X = heterogeneous reaction

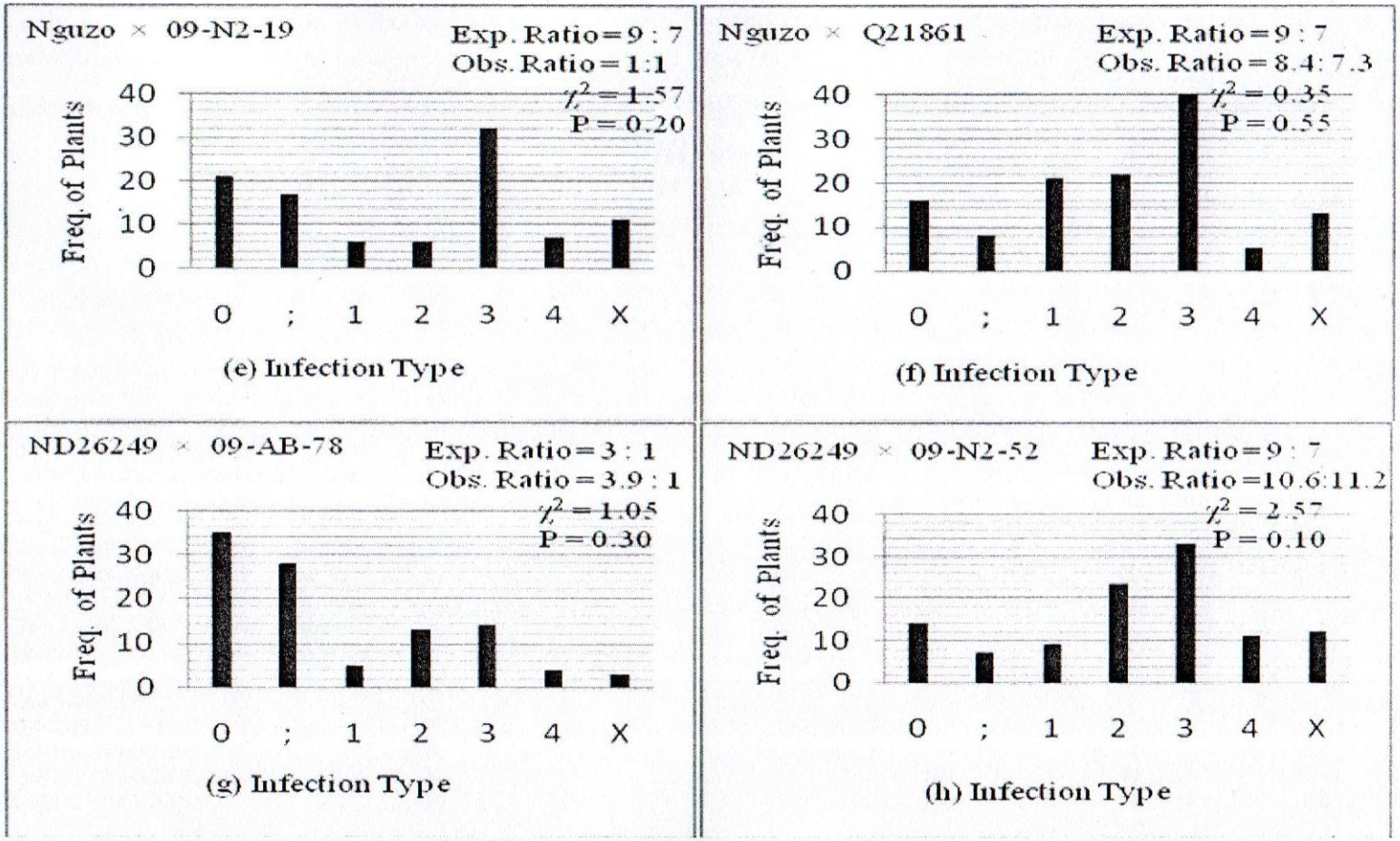



Figure 4.2 Continued: Frequencies of Seedling Infection Type of Barley (*Hordeum vulgare L.*) of $F_2$ Population to stem rust (*Puccinia graminis* f.sp. *tritici*) race *Ug99* in the green house). 0 = immune; = very resistant; 1 = resistant; 2 = Resistant to moderately resistant; 3 = moderately resistant to moderately susceptible; 4 = susceptible; X = heterogeneous reaction

Table 4.2 Seedling reaction of the barley parents, $F_1$ and $F_2$ genotypes to stem rust (*Puccinia graminis* sp. *tritici*) race *Ug99* in 2011 and 2012

| CROSS NAME | GENERATION | SEEDLING SCORE INFECTION TYPE(3LS) | | TOTAL | R | S | Ratio(R:S) Observed | Ratio(R:S) Expected | $\chi^2$ | P-Value |
|---|---|---|---|---|---|---|---|---|---|---|
| *Crosses using HKBL-1385-13, 08-UT-86, 09-N2-20 and 09-N2-19 as parents* | | | | | | | | | | |
| | P1 | 2+ | R | | | | | | | |
| HKBL-1385-13 | | | | | | | | | | |
| 08-UT-86 | P2 | 2+ | R | | | | | | | |
| 09-N2-20 | P3 | 4 | S | | | | | | | |
| 09-N2-19 | P4 | 4 | S | | | | | | | |
| HKBL-1385-13 × 08-UT-86 | $F_1$ | 1+ | R | | | | | | | |
| HKBL-1385-13 × 09-N2-20 | $F_1$ | 0 | R | | | | | | | |
| HKBL-1385-13 × 09-N2-20 | $F_2$ | | | 100 | 62 | 38 | 10.3:6.3 | 9:7 | 1.3435 | 0.2464 |
| HKBL-1385-13 × 09-N2-20 | $F_2$ | | | 100 | 62 | 38 | 10.3:6.3 | 10:6 | 1.3543 | 0.2445 |
| HKBL-1385-13 × 09-N2-19 | $F_1$ | 1+ | | | | | | | | |
| HKBL-1385-13 × 09-N2-19 | $F_2$ | | | 102 | 73 | 29 | 2.5:1 | 3:1 | 0.6405 | 0.4235 |
| *Cross using KARNE and 09-N2-19 as parents* | | | | | | | | | | |
| | P1 | 3+ | S | | | | | | | |
| KARNE | | | | | | | | | | |
| 09-N2-19 | P2 | 4 | S | | | | | | | |
| KARNE × 09-N2-19 | $F_1$ | 3 | S | | | | | | | |
| KARNE × 09-N2-19 | $F_2$ | | | 100 | 56 | 44 | 14:11 | 9:7 | 0.0025 | 0.9598 |
| KARNE × 09-N2-19 | $F_2$ | | | 100 | 56 | 44 | 14:11 | 10:6 | 0.0021 | 0.9631 |
| *Crosses using NGUZO, 09-AB-78 09-N2-19 and Q21861 as parents* | | | | | | | | | | |
| NGUZO | P1 | 3 | S | | | | | | | |
| 09-AB-78 | P2 | 2+ | R | | | | | | | |
| 09-N2-19 | P3 | 4 | S | | | | | | | |
| Q21861 | P4 | 2+ | R | | | | | | | |
| NGUZO × 09-AB-78 | $F_1$ | 2+ | R | | | | | | | |
| NGUZO × 09-AB-78 | $F_2$ | | | 100 | 53 | 47 | 10.6:9.4 | 9:7 | 0.4292 | 0.5124 |
| NGUZO × 09-AB-78 | $F_2$ | | | 100 | 53 | 47 | 10.6:9.4 | 10:6 | 0.4236 | 0.5151 |

| Table 4.2 continued | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGUZO × 09-N2-19 | $F_1$ | ; 1+ | R | | | | | | | |
| NGUZO × 09-N2-19 | $F_2$ | | | 100 | 50 | 50 | 1:1 | 9:7 | | |
| NGUZO × 09-N2-19 | $F_2$ | | | 100 | 50 | 50 | 1:1 | 10:6 | 1.5768 | 0.2092 |
| NGUZO × Q21861 | $F_1$ | 2+ | R | | | | | | | |
| NGUZO × Q21861 | $F_2$ | | | 125 | 67 | 58 | 8.4:7.3 | 9:7 | 0.3567 | 0.5503 |
| NGUZO × Q21861 | $F_2$ | | | 125 | 67 | 58 | 8.4:7.3 | 10:6 | 0.3510 | 0.5535 |
| *Crosses using ND26249, 08-UT-86 and 09-N2-52 and 09-AB-78 as parents* | | | | | | | | | | |
| ND26249 | P1 | 3 | S | | | | | | | |
| 08-UT-86 | P2 | 2+ | R | | | | | | | |
| 09-N2-52 | P3 | 2+ | R | | | | | | | |
| 09AB-78 | P4 | 2+ | S | | | | | | | |
| ND26249 × 08-UT-86 | $F_1$ | 1+ | R | | | | | | | |
| ND26249 × 09-AB-78 | $F_1$ | ; | R | | | | | | | |
| ND26249 × 09-AB-78 | $F_2$ | | | 102 | 81 | 21 | 3.9:1 | 3:1 | 1.0588 | 0.3085 |
| ND26249 × 09-N2-52 | $F_1$ | 2+ | S | | | | | | | |
| ND26249 × 09-N2-52 | $F_2$ | | | 109 | 53 | 56 | 10.6:11.2 | 9:7 | 2.5759 | 0.1085 |
| ND26249 × 09-N2-52 | $F_2$ | | | 109 | 53 | 56 | 10.6:11.2 | 10:6 | 2.5622 | 0.1094 |

0= no uredinia or flecks visible,0; = very faint hypersensitive flecks; = hypersensitive flecks,1 = small uredinia surrounded by necrosis,2 = small uredinia surrounded by chlorosis,3 = moderate size uredinia without chlorosis,+ = slightly larger uredinia than expected for the infection type,. = missing, 3LS = the plant stage at which the disease was assessed (three leaf stage)

## 4.7 Discussion

The variable infection types observed on the germplasm were due to genetic structure and origin of the germplasm. This was attributed to different genetic constitution of the germplasm. About 67% of the germplasm that were resistant are valuable sources of stem rust resistance in barley. In this study, East African barley was resistant to *Ug99*, however, this resistance could not be associated with selection pressure since some of the other germplasm from Europe, Asia, North and Central America were also resistant to stem rust. The variability was clearly manifested among 08MT-92 and 09MT-38 indicating that the genes conferring resistance to stem rust could be different. However, the identification of the specific genes among these germplasm was beyond the scope of this study. The germplasm expressing seedling resistance to stem rust race *Ug99* is speculated to contain barley stem rust resistant gene *Rpg1*. The *Rpg1* was the primary stem rust resistance gene in barley and remains the major source of resistance in almost every malting barley cultivar in the northern Great Plains region of North America (Roelfs *et al.*, 1991). This included germplasm from North America, Latin America among others. Although germplasm from Kenya, Ethiopia and Ukraine were resistant to *Ug99,* it is not evident because they had very few cultivars which were less than five (Table 4.1).

All barley evaluated from Iran, Pakistan and Tajikistan were susceptible to *Ug99*. Similarly, all existing Afghan varieties submitted by CIMMYT and ICARDA for screening in East Africa during 2009 were susceptible (Mackenzie 2008; Nazari *et al.*, 2009). The germplasm Q21861 known to carry *rpg4* resistant gene, released in Mexico was the most resistant stem rust line in this study, indicating that *rpg4* gene conferred resistance to stem rust race *Ug99*, (Jin *et al.*, 1994). Moreover, Q21861 matures early and exhibits a strong photoperiod response. Among the Switzerland germplasm was Chevron which has *RPg1* (major resistant gene) and this explains the low infection type of "0" from this region (Kleinhofs *et al.*, 2009). Germplasm from Washington USA were among the resistant germplasm despite the fact that cultivar Steptoe a susceptible check was among the germplasm. Germplasm Hietpas-5 (CIho) from Wisconsin contains *Rpg2* (Patterson *et al.*, 1957) which is an adult plant resistance gene. Hietpas-5 is resistant to stem rust race HTMJ and JCMN at seedling phenotyping. *RPg2,* derived from cultivar Heitpas- 5, is an adult and seedling resistance gene to stem rust races HTMJ and JCMN but susceptible to most stem rust races at seedling stage (Sun and Steffenson, 2005).

Reaction of the hybrids of eight crosses to stem rust suggests that dominant genes confer resistance to stem rust. It can be postulated that, the susceptibility of hybrids from Karne × 09-N2-19 cross and segregation in $F_2$ indicates that the genes conferring resistance were major but recessive. In a study on inheritance of resistance to race QCC and MCC in barley germplasm Q21861 the resistance controlled by two genes but the seedling resistance was recessively inherited (Jin *et al.,* 1994). The observed ratio of 9:7 from a population where Q21861 was used as the parent suggests that inter allelic gene interaction due to epistasis plays a role in conferring resistance to stem rust. This probably indicates that a gene with a recessive inheritance pattern for reaction to race *Ug99* was present in germplasm Nguzo. This gene and *rpg4* in Q21861 modify each other. The results of $F_2$ populations derived from HKBL-1385-13 × 09-N2-19 and ND26249 × 09-AB-78 crosses is supported by the segregation pattern of 3:1 this agree with (Jin *et al.,* 1994) where $F_2$ populations from Steptoe × Q21861 were homozygous resistant to race QCC and MCC. This suggests that a major dominant gene confers resistance to stem rust. This concurs with study on blackleg (*Leptospheria maculans*) of canola (*Brassica napus*) (Raman *et al.,* 2012). In stripe rust, the single dominant gene was confirmed by testing seedlings of the $F_1$, $BC_1$ to the two parents, and 150 $F_3$ lines from the $F_2$ plants derivered from Lemhi × PI 478214 cross, inoculated with the same race *striiformis* f. s.p.*hordei*, indicated that Lemhi has a dominant resistance gene (Vihanga *et al.,* 2004).

$F_2$ population derived from HKBL-1385-13 × 09-N2-19; Karne × 09-N2-19; Nguzo × 09-AB-78; Nguzo × Q21861 and ND26249 × 09-N2-52 expressed both modifying (10:6) and epistatic (9:7) gene effects. The effect of modifying genes expression could be due the source and genetic background of germplasm ND25882 and Karne which were used as female parents in Nguzo × 09-AB-78, Nguzo × Q21861, Karne × 09-N2-19 and ND25882 × 09-AB-78. Similarly, Kolmer (1996) noted the effect of germplasm background on the differential expression of *Lr* genes. The population [HKBL-1385-13 × 09-N2-19 and ND2649 × 09-AB-78;] conformed to ratio 3:1 (resistant: susceptible) phenotypic ratio and this is a one gene model action (Table 4.2). This clearly indicates the presence of a major gene that results from recombination among the gemplasm (Table 4.2).

## 4.8 Conclusion

The results obtained in this study showed that there are valuable major genes for stem rust resistance that could be used to improve susceptible barley varieties. The hybrids that were resistant to stem rust suggest that dominant genes confer resistance to stem rust. The action of the major genes in conferring resistance to stem rust was supported by the observed 3:1 ratio. Although major genes for resistant to stem rust were detected in this study, the result demonstrated epistatic effects on resistance. From this study germplasm Q21861, 08-UT-86, 09-AB-78, 09-WA-10, SwissHV504, 08-UT-91, 08-AB-16 and 08-UT-72 can be used to improve the susceptible germplasm because it was resistant to stem rust race *Ug99*.

## 4.9 References


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# CHAPTER FIVE

# GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

## 5.1 General Discussion

This study was set out to determine the resistance of barley genotypes from North America, Latin America, Europe, Asia and East Africa for resistance to stem rust under seedling and field conditions. After determining the resistance of the barley genotypes under field conditions, genetic studies were done to determine the mode of inheritance of resistant genes conferring resistance to race *Ug99*. The following genotypes were resistant at adult plant stage Swiss HV673, 08-AB-17, Chevron, Hietpas-5, 09-AB-78, Q21861 and 09-N2-52 with stem rust severity ranging between "0" to 10M. The genotypes Karne with stem rust severity 30S to 50S, Nguzo with stem rust severity 25S to 40S, P1347245 with stem rust severity 15MSS to 60S, P1386458 with stem rust severity TR to 70S and 17024 with stem rust severity 5M to 70S were susceptible to stem rust at adult plant stage.

The susceptible genotypes (09-WA-10, Swiss HV504, 08-UT-91, 08-AB-16, 08-UT-72, Karne, Nguzo, HKBL-1385-12 and HKBL-1385-13) were resistant at seedling stage with infection types between "0" to $2^{+}$", suggesting that major genes controls resistance. This is in agreement with Ellingboe, 1981 who found out that the susceptible genotypes mighty have only single race specific type of resistance. The high disease severity indicated lack of resistant genes to stem rust in the susceptible genotypes. According to Mackenzie 2008 all the barley evaluated from Iran, Pakistan and Tajikistan were susceptible to *Ug99*. Similarly Nazari *et al.,* 2009, found that all existing Afghan varieties screened in East Africa in 2009 were susceptible. Genotypes 08-BA-69, Q21861 and Swiss HV673 were resistant at both seedling and adult plant stage, indicating that they mighty have both major and minor genes resistant to stem rust. Roelfs in 1985 and Parlevliet in 2001 found out that adult plant resistance is under the control of minor genes while seedling resistance is under the control of major genes which provides resistance at all stages of plant growth.

The germplasm expressing seedling resistance to stem rust race *Ug99* is speculated to contain barley stem rust resistant gene *Rpg1*. According to Roelfs *et al.,* 1991, *Rpg1* was the primary stem rust resistance gene in barley and remains the major source of resistance in almost

every malting barley cultivar in the northern Great Plains region of North America. In this study, genotype Q21861 was among the resistant genotypes this agrees with Jin *et al.,* 1994 who found out that Q21861 known to carry *rpg4* resistant gene, released in Mexico was the most resistant stem rust line, indicating that *rpg4* gene conferred resistance to stem rust race *Ug99*. Moreover, Kleinhofs *et al.,* 2009 and Patterson *et al.,* 1957 found out that Chevron which has *RPg1* (major resistant gene) and Hietpas-5 (CIho) with *Rpg2* were resistant this explains the low infection type of "0" in this genotypes in this study. Hietpas-5 is resistant to stem rust race HTMJ and JCMN at seedling phenotyping. *RPg2,* derived from cultivar Heitpas- 5, is an adult and seedling resistance gene to stem rust races HTMJ and JCMN but susceptible to most stem rust races at seedling stage (Sun and Steffenson, 2005).

The $F_2$ populations were evaluated for seedling resistance to stem rust race *Ug99* in the greenhouse. The results indicated that stem rust resistant is controlled by major (3:1) and inter allelic genes interaction (9:7). The resistance reaction of the hybrids of eight crosses to stem rust suggested that dominant genes confer resistance to stem rust. Results suggests that the susceptibility of hybrids from Karne × 09-N2-19 cross and segregation in $F_2$ indicated that the genes conferring resistance were major but recessive. In a study on inheritance of resistance to race QCC and MCC in barley germplasm Q21861 conducted by Jin *et al.,* 1994 the results showed that the resistance was controlled by two genes but the seedling resistance was recessively inherited. In this study, the observed ratio of 9:7 from a population Nguzo × Q21861 where Q21861 was used as the parent suggesting that inter allelic gene interaction due to epistasis plays a role in conferring resistance to stem rust. This probably indicated that a gene with a recessive inheritance pattern for reaction to race *Ug99* was present in Nguzo. This gene in Nguzo and *rpg4* in Q21861 could have a modifying effect on each other. The seedling results of $F_2$ populations derived from HKBL-1385-13 × 09-N2-19 and ND26249 × 09-AB-78 crosses are supported by the segregation pattern of 3:1 this agreed with findings of (Jin *et al.,* 1994) where $F_2$ populations from Steptoe × Q21861 were homozygous resistant to race QCC and MCC, indicating that a major dominant gene could be conferring resistance to stem rust. The results concurred with study on blackleg (*Leptospheria maculans*) of canola (*Brassica napus*) that was done by Raman *et al.,* 2012. Similar results ported by Vihanga *et al.,* 2004 afte inoculating the $F_2$ plants derivered from Lemhi × PI 478214 cross, with the same race of *striiformis* f. s.p.*hordei*, indicated that Lemhi has a dominant resistance gene.

## 5.2 Conclusions

This study confirmed the existence of significant genetic variation among the barley germplasm for resistance to stem rust. Genotypes 08-BA-69, Q21861 and Swiss HV673 were resistant at both seedling and adult plant.

The results from the inheritance studies confirmed the control of resistance to stem rust by a single dominant gene. Apart from the single dominant gene that controls the resistance to stem rust; epistatic gene interaction was also detected to confer resistance to stem rust.

Screening barley seedling by artificial inoculation in the greenhouse permits examination of a large number of populations for resistance under uniform disease pressure. Although this was the best approach for identifying highly resistant genotypes and also major genes in genetic studies, there could be differences in seedling and adult reaction to stem rust. It is therefore advisable to screen both at seedling and adult plant stages.

## 5.3 Recommendations

Seedling resistance tends to be dominant; it helps in decelerating the epidemiological build up of the inoculums in the field. However, field evaluation provides natural environment for testing and rating of the host genotype. The $F_2$ population should therefore be selected in the field and advanced to $F_6$ and $F_7$ leading to preliminary yield trials.

The use of KARI – Njoro site to screen barley genotypes for resistance to stem rust is recommended as the site is a hot – spot for stem rust.

Genotypes 08-BA-69, Q21861 and Swiss HV673 were identified as new sources of stem rust resistance at both seedling and adult plant stages. The stem rust resistance genes in these lines should be useful in improving adapted susceptible barley genotypes.

Stem rust exists in diverse forms and differing in degree of virulence making it difficult to maintain barley lines that can withstand the new virulent isolates. Therefore screening of barley genotypes for new sources of resistance to stem rust should be a continuous process.

Further work to identify and carry out molecular mapping of stem rust resistance genes in the resistant lines is recommended. This will facilitate the development of the resistant barley lines and the pyramiding of the stem rust resistance with other traits, particularly through the use of marker-assisted selection.

# APPENDICES

**Appendix 1:** Disease reaction to *Puccinia graminis* sp. *tritici* race *Ug99* on barley lines at seedling stage in the greenhouse at Njoro in 2011

| Origin | Cultivar | Seedling screening infection type | |
|---|---|---|---|
| Alberta Canada | Diamond | 3+ | S |
| BARI | 2B03-3954 | 0 | R |
| BARI | Z173U047V | - | - |
| BARI | 6B04-0031 | 1+ | R |
| BARI | 6B05-0572 | - | - |
| BARI | 6B05-0998 | 1+ | R |
| BARI | KENP12 | ;2+ | |
| BARI | 08-BA-26 | 2+ | R |
| BARI | 08-BA-69 | ;,1+ | R |
| BARI | 08-BA-70 | 2+ | R |
| BARI | 08-BA-72 | ; | R |
| BARI | 08-BA-75 | 0 | R |
| BARI | 08-BA-77 | 2+ | R |
| BARI | 08-N2-02 | 0,; | R |
| Canada | Q21861 DHP | 0 | R |
| Canada | QSM001 | . | . |
| Canada | QSM002 | 2+ | R |
| Canada | QSM003 | . | . |
| Canada | QSM005 | 1+ | R |
| Canada | QSM008 | 0 | R |
| Canada | QSM10 | ; | R |
| Canada | QSM11 | 0 | |
| Canada | QSM13 | 0,1 | R |
| Canada | QSM14 | 2+ | R |
| Canada | QSM15 | 2+ | R |
| Canada | QSM16 | 0; | R |
| Canada | QSM17 | 0 | R |
| Canada | QSM18 | 0 | R |
| Canada | QSM19 | 0 | R |
| Canada | QSM23 | ; | R |
| Canada | QSM26 | 0,1+ | R |
| Canada | QSM029 | 1 | R |
| Canada | QSM031 | . | . |
| Canada | QSM033 | ; | R |
| Canada | QSM034 | 1 | R |
| Canada | QSM035 | 1+ | R |
| Canada | QSM036 | . | . |
| Canada | QSM037 | . | . |
| Canada | QSM038 | 0 | R |
| Canada | QSM039 | . | . |
| Canada | QSM041 | . | . |
| Canada | QSM042 | . | . |
| Canada | QSM043 | 2+ | R |
| Canada | QSM044 | . | . |
| Canada | QSM045 | ;,1+ | R |
| Canada | QSM046 | . | . |

**Appendix 1 Continued**

| Origin | Cultivar | Seedling screening infection type | |
|---|---|---|---|
| Canada | QSM047 | 1+ | R |
| Canada | QSM048 | 2+ | R |
| Canada | QSM049 | 0,1+ | R |
| Canada | QSM050 | 0,;,1+ | R |
| Canada | QSM052 | . | . |
| Canada | QSM054 | 0 | R |
| Canada | QSM055 | 3 | S |
| Canada | QSM057 | ;,2 | R |
| Canada | QSM058 | 3+ | S |
| Canada | QSM059 | 3+ | S |
| Canada | QSM060 | . | . |
| Canada | QSM061 | 0 | R |
| Canada | QSM062 | 0 | R |
| Canada | QSM063 | . | . |
| Canada | QSM065 | 2+ | R |
| Canada | QSM066 | 0 | R |
| Canada | QSM067 | 0 | R |
| Canada | QSM068 | 3 | S |
| Canada | QSM069 | 0 | R |
| Canada | QSM070 | ; | R |
| Canada | QSM074 | 0 | R |
| Canada | QSM075 | 0,; | R |
| Canada | QSM076 | . | . |
| Canada | QSM077 | 0 | R |
| Canada | QSM078 | 0 | R |
| Canada | QSM079 | . | . |
| Canada | QSM080 | . | . |
| Canada | QSM082 | . | . |
| Canada | QSM083 | . | . |
| Canada | QSM084 | . | . |
| Canada | QSM085 | 1+,3 | R |
| Canada | QSM086 | . | . |
| Canada | QSM087 | . | . |
| Canada | QSM088 | . | . |
| Canada | QSM089 | ;,1 | R |
| Canada | QSM090 | . | . |
| Canada | QSM091 | 1+ | |
| Canada | QSM093 | ; | R |
| Canada | QSM094 | 2 | R |
| Canada | QSM097 | . | . |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | PC 11 | . | . |
| CIMMYT, Mexico | PC 84a | 3 | S |
| CIMMYT, Mexico | Q21861a | 0 | R |
| CIMMYT, Mexico | Q21861* | 0 | R |
| CIMMYT, Mexico | Q21861 | ; | R |
| CIMMYT, Mexico | Q21861 | 0,1 | R |
| CIMMYT, Mexico | Q21861 | 0,; | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 0,; | R |

**Appendix 1 Continued**

| Origin | Cultivar | Seedling screening infection type | |
|---|---|---|---|
| CIMMYT, Mexico | Q21861 | . | . |
| CIMMYT, Mexico | Q21861 | ; | R |
| CIMMYT, Mexico | Q21861 | ; | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 0 | R |
| CIMMYT, Mexico | Q21861 | 1+ | R |
| CIMMYT, Mexico | Q21861 | ;,1+ | R |
| CIMMYT, Mexico | Q21861 | 0,; | R |
| England | PI 452421a | 2+ | R |
| Ethiopia | PI 382313 | . | . |
| Ethiopia | CIho 14977 | ; | R |
| Ethiopia | P1347245 | 1+ | R |
| Ethiopia | P1386458 | 2+ | R |
| Ethiopia | PI23027 | 0 | R |
| Ethiopia | PI25030 | 1+ | R |
| Kazakhstan | PI17024 | 0 | R |
| Kazakhstan | PI15517 | 0 | R |
| Kazakhstan | PI5045 | 0 | R |
| Kenya | KARNE | 3+ | . |
| Kenya | NGUZO | 3 | R |
| Kenya | HKBL-13 | 2+ | R |
| Kenya | HKBL-12 | 0 | R |
| Kyrgyzstan | PI18358 | . | . |
| Kyrgyzstan | PI18360 | . | . |
| Minnesota USA | FEG161-23 | 2+ | R |
| Minnesota USA | FEG163-48 | 1+ | R |
| Minnesota USA | FEG183-53 | 0 | R |
| Minnesota USA | FEG192-15 | X | S |
| Minnesota USA | FEG192-16 | 1+ | R |
| Minnesota USA | FEG192-17 | . | . |
| Minnesota USA | Shech/Harr079 | 0 | R |
| Minnesota USA | QSM125 | 0 | R |
| Minnesota USA | QSM126 | 1+ | R |
| Minnesota USA | QSM127 | 0 | R |
| Montana | 09-MT-16 | . | . |
| Montana | 09-MT-38 | ;,4 | S |
| Montana State University | 08-MT-28 | ;,2+ | R |
| Montana State University | 08-MT-32 | 1+ | R |
| Montana State University | 08-MT-85 | 0,1+ | R |
| Montana State University | 08-MT-86 | 3 | S |
| Montana State University | 08-MT-89 | ; | R |
| Montana State University | 08-MT-92 | . | . |
| Montana USA | Columbia-d | 2+ | R |
| North Dakota State University | ND25161 | ;1+ | R |
| North Dakota State University | Conlon | 1+,2+ | R |
| North Dakota State University | Rawson | 1+ | R |
| North Dakota State University | ND25882 | 3+ | S |
| North Dakota State University | ND25276 | 3 | S |

**Appendix 1 Continued**

| Origin | Cultivar | Seedling screening infection type | |
|---|---|---|---|
| North Dakota State University | 08-N2-22 | 0 | R |
| North Dakota State University | 08-N2-47 | 0 | R |
| North Dakota State University | 08-N2-48 | 4 | S |
| North Dakota State University | 08-N2-55 | ; | R |
| North Dakota State University | 08-N2-56 | 1+ | R |
| North Dakota State University | 08-N2-57 | 2+ | R |
| North Dakota State University | 08-N2-58 | 0 | R |
| North Dakota State University | 08-N2-87 | 0 | R |
| North Dakota State University | 08-N6-91 | 1+ | R |
| North Dakota State University | 09-N2-11 | 4 | S |
| North Dakota State University | 09-N2-19 | 4 | R |
| North Dakota State University | 09-N2-20 | 4 | S |
| North Dakota State University | 09-N2-23 | 4 | S |
| North Dakota State University | 09-N2-31 | 1+ | R |
| North Dakota State University | 09-N2-52 | 4 | S |
| North Dakota State University | 09-N2-64 | 2+ | R |
| North Dakota State University | 09-N6-08 | 0,; | R |
| Switzerland | Chevron | . | . |
| Switzerland | SwissHV501 | 0 | R |
| Switzerland | SwissHV504 | 0 | R |
| Switzerland | SwissHV508 | ; | R |
| Switzerland | SwissHV525 | . | . |
| Switzerland | SwissHV584 | . | . |
| Switzerland | SwissHV590 | . | . |
| Switzerland | SwissHV525 | . | . |
| Switzerland | SwissHV602 | . | . |
| Switzerland | SwissHV611 | 0 | R |
| Switzerland | SwissHV612 | . | . |
| Switzerland | SwissHV625 | . | . |
| Switzerland | SwissHV627 | ; | R |
| Switzerland | SwissHV631 | . | |
| Switzerland | SwissHV633 | 0 | R |
| Switzerland | SwissHV636 | 2+ | R |
| Switzerland | SwissHV644 | 2+ | R |
| Switzerland | SwissHV658 | 0 | R |
| Switzerland | SwissHV664 | 3+ | S |
| Switzerland | SwissHV665 | 2 | R |
| Switzerland | SwissHV672 | 2+ | R |
| Switzerland | SwissHV673 | 0 | R |
| Switzerland | Chevron* | 0 | R |
| Switzerland | Chevron | 1+ | R |
| Switzerland | Chevron | 0,; | R |
| Switzerland | Chevron | 0,1+ | R |
| Switzerland | Chevron | ; | R |
| Switzerland | Chevron | 0 | R |
| Switzerland | Chevron | 0 | R |
| Switzerland | Chevron | 0,; | R |
| Switzerland | Chevron | 0,2 | R |
| Switzerland | Chevron | 2+ | R |
| Switzerland | Chevron | 1 | R |
| Switzerland | Chevron | 0,1 | R |

**Appendix 1 Continued**

| Origin | Cultivar | Seedling screening infection type | |
|---|---|---|---|
| Switzerland | Chevron | 0 | R |
| Switzerland | Chevron | 1 | R |
| Switzerland | Chevron | . | . |
| Switzerland | Chevron | 0 | R |
| Switzerland | Chevron | . | . |
| Switzerland | Chevron | 0 | R |
| Tajikistan | PI14938 | ; | R |
| Tajikistan | PI14942 | 1+ | R |
| Tajikistan | PI14971 | 2+ | R |
| Tajikistan | PI21486 | X | S |
| Tajikistan | PI22482 | 4 | S |
| Tajikistan | PI24767 | 1+ | R |
| Tajikistan | PI14905 | ; | R |
| Tajikistan | PI14934 | . | . |
| Tajikistan | PI | ; | R |
| Ukraine | CI5541a | 1+ | R |
| USDA-ARS Aberdeen | 08-AB-16 | 0 | R |
| USDA-ARS Aberdeen | 08-AB-17 | 0 | R |
| USDA-ARS Aberdeen | 08-AB-28 | 0 | R |
| USDA-ARS Aberdeen | 08-AB-31 | 0 | R |
| USDA-ARS Aberdeen | 08-AB-19 | 3 | S |
| USDA-ARS Aberdeen | 08-AB-20 | 2+ | R |
| USDA-ARS Aberdeen | 08-AB-21 | 2+ | R |
| USDA-ARS Aberdeen | 08-AB-57 | 1+ | R |
| USDA-ARS Aberdeen | 08-AB-58 | 4 | S |
| USDA-ARS Aberdeen | 08-AB-66 | 2+ | R |
| USDA-ARS Aberdeen | 08-AB-78 | 1+ | R |
| USDA-ARS Aberdeen | 09-AB-79 | X | S |
| USDA-ARS Aberdeen | 09-AB-80 | 4 | S |
| USDA-ARS Aberdeen | 09-AB-82 | 3 | S |
| USDA-ARS Aberdeen | 09-AB-87 | ;1 | R |
| USDA-ARS Aberdeen | 09-AB-89 | 1+ | R |
| Utah State University | UT03B1953-64 | . | . |
| Utah State University | UT04B2041-41 | 1+ | R |
| Utah State University | 08-UT-47 | ; | R |
| Utah State University | 08-UT-72 | 0 | R |
| Utah State University | 08-UT-73 | 3 | S |
| Utah State University | 08-UT-74 | 1 | R |
| Utah State University | 08-UT-86 | 2+ | S |
| Utah State University | 08-UT-91 | 0 | R |
| Washington State University | 08-WA-01 | 0 | R |
| Washington State University | 05WA-328.8 | 0,2 | R |
| Washington State University | 04WA-122.9 | 2+ | R |
| Washington State University | 06WA-408.18 | . | . |
| Washington State University | 06WA-406.27 | 4 | S |
| Washington State University | 06WA-466.6 | 4 | S |
| Washington State University | 06WA-437.14 | X | S |
| Washington State University | 06WA-427.12 | 4 | S |
| Washington State University | 06WA-421.6 | 3 | S |
| Washington State University | X02035-DH2 | . | . |

**Appendix 1 Continued**

| Origin | Cultivar | Seedling screening infection type | |
|---|---|---|---|
| Washington State University | 07MB-405 | 1+ | R |
| Washington State University | 07B-362 | . | . |
| Washington State University | 08-MN-49 | ;,2+ | R |
| Washington State University | 08WA-42 | 0 | R |
| Washington State University | 08WA-64 | . | . |
| Washington State University | 09WA-07 | 0 | R |
| Washington State University | 09WA-08 | 0 | R |
| Washington State University | 09WA-09 | 1+ | R |
| Washington State University | 09WA-10 | 0 | R |
| Washington State University | 09WA-20 | 2+ | R |
| Washington State University | 09WA-35 | . | . |
| Washington State University | 09WA-36 | . | . |
| Washington State University | 09WA-62 | 1+ | R |
| Washington State University | 09WA-63 | 0 | R |
| Washington State University | 09WA-80 | . | . |
| Washington State University | 09WA-92 | 1+ | R |
| Washington USA | Steptoe* | 2 | R |
| Washington USA | Steptoe | . | . |
| Washington USA | Steptoe | 3 | R |
| Washington USA | Steptoe | . | . |
| Washington USA | Steptoe | . | . |
| Washington USA | Steptoe | 0 | R |
| Washington USA | Steptoe | . | . |
| Washington USA | Steptoe | . | . |
| Washington USA | Steptoe | 1+,2+ | R |
| Washington USA | Steptoe | 1+ | R |
| Washington USA | Steptoe | 0 | R |
| Washington USA | Steptoe | 2+ | R |
| Washington USA | Steptoe | 0 | R |
| Washington USA | Steptoe | 0 | R |
| Washington USA | Steptoe | . | . |
| Washington USA | Steptoe | 0 | R |
| Washington USA | Steptoe | 0 | R |
| Washington USA | Steptoe | 3 | R |
| Washington USA | Steptoe | 4 | S |
| Washington USA | Hietpas 5 | 2+ | R |

Infection type scale

0= no uredinia or flecks visible, 0; = very faint hypersentive flecks ; = hypersentive flecks 1 = small uredinia surrounded by necrosis 2 = small uredinia surrounded by chlorosis 3 = moderate size uredinia without chlorosis 4 = large uredinia without chlorosis + = slightly larger uredinia than expected for the infection type - = slightly smaller uredinia than expected for the infection type, . = missing * = repeated genotypes

Appendix2: Means of agronomic traits for different barley (*Hordeum vulgare*) lines for season one at Njoro in 2010

| Cultivar | MEAN SCORE | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikes/ear | Biomass $m^2$(g) | Grain yield$m^2$(g) | 1000KW(kg) | AUDPC | Final Score | Disease |
| Diamond | 265.0 | 140.0 | 270.5 | 248.0 | 157.5 | 59.0 | 198.5 | 180.5 | |
| Q21861DH | 42.0 | 86.5 | 32.5 | 52.0 | 121.0 | 197.0 | 23.0 | 33.5 | |
| Q001 | 59.0 | 204.0 | 132.0 | 51.0 | 49.5 | 152.0 | 186.5 | 180.5 | |
| Q002 | 15.5 | 184.0 | 189.0 | 270.0 | 116.5 | 68.0 | 33.0 | 55.5 | |
| QSM003 | - | 63.5 | - | - | - | - | 119.5 | 128.0 | |
| QSM005 | 15.5 | 128.0 | 35.5 | 190.0 | 136.5 | 60.0 | 98.0 | 128.0 | |
| QSM008 | 27.5 | 52.5 | 75.5 | 257.0 | 95.5 | 83.0 | 98.0 | 33.5 | |
| QSM010 | 15.5 | 67.0 | 50.0 | 29.0 | 58.5 | 119.0 | 62.0 | 65.0 | |
| QSM011 | 171.5 | 115.0 | 160.0 | 194.5 | 271.0 | 130.0 | 202.0 | 128.0 | |
| QSM013 | 59.0 | 93.5 | 95.5 | 168.0 | 136.5 | 122.0 | 202.0 | 128.0 | |
| QSM014 | 219.5 | 35.5 | 99.5 | 181.5 | 176.5 | 151.0 | 163.0 | 128.0 | |
| QSM015 | 252.5 | 237.5 | 95.5 | 208.5 | 153.0 | 201.0 | 98.0 | 128.0 | |
| QSM016 | 15.5 | 232.5 | 20.0 | 177.0 | 41.5 | 66.0 | 62.0 | 65.0 | |
| QSM017 | 15.5 | 93.5 | 44.0 | 110.0 | 10.5 | 124.0 | 186.5 | 180.5 | |
| QSM018 | 124.5 | 103.5 | 67.0 | 24.0 | 46.0 | 105.0 | 62.0 | 65.0 | |
| QSM019 | 171.5 | 67.0 | 28.0 | 36.0 | 196.0 | 165.0 | 74.5 | 85.0 | |
| QSM023 | 15.5 | 13.5 | 75.5 | 196.0 | 131.5 | 53.5 | 232.0 | 221.5 | |
| QSM026 | 33.5 | 115.0 | 138.5 | 137.5 | 38.5 | 42.0 | 74.5 | 85.0 | |
| QSM029 | 15.5 | 158.0 | 9.0 | 141.0 | 38.5 | 11.0 | 98.0 | 128.0 | |
| QSM031 | 77.0 | 90.0 | 84.5 | 66.0 | 157.5 | 166.0 | 186.5 | 180.5 | |
| QSM033 | 7.5 | 173.5 | 15.5 | 97.0 | 1.0 | 276.0 | 87.0 | 85.0 | |
| QSM034 | 42.0 | 211.0 | 4.0 | 156.0 | 105.5 | 137.0 | 232.0 | 221.5 | |
| QSM036 | 193.0 | 153.5 | 187.0 | 158.0 | 200.5 | 172.5 | 218.0 | 221.5 | |
| QSM037 | 84.4 | 259.0 | 113.5 | 83.0 | 116.5 | 160.0 | 119.5 | 128.0 | |
| QSM038 | 171.5 | 27.5 | 154.0 | 80.0 | 85.0 | 135.0 | 228.0 | 242.0 | |
| QSM039 | - | 128.0 | 148.5 | 255.0 | 243.5 | 198.5 | 8.0 | 7.5 | |
| QSM041 | 59.0 | 227.0 | 105.0 | 55.0 | 116.5 | 203.0 | 8.0 | 7.5 | |
| QSM042 | 33.5 | 247.5 | 166.5 | 65.0 | 74.5 | 277.0 | 163.0 | 128.0 | |
| QSM043 | 59.0 | 123.0 | 163.0 | 210.0 | 116.5 | 110.0 | 186.5 | 180.5 | |
| QSM044 | 38.0 | 239.5 | 120.0 | 16.5 | 95.5 | 155.0 | 74.5 | 85.0 | |
| QSM045 | 15.5 | 146.5 | 90.0 | 167.0 | 213.5 | 74.0 | 186.5 | 180.5 | |
| QSM046 | 5.0 | 188.0 | 105.0 | 48.0 | 64.0 | 25.0 | 255.5 | 253.5 | |
| QSM047 | 252.5 | 182.0 | 61.5 | 132.0 | 196.0 | 206.0 | 239.0 | 180.5 | |
| QSM048 | 33.0 | 162.0 | 55.0 | 247.0 | 79.5 | 176.5 | 119.5 | 128.0 | |

Appendix2 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikes/ear | Biomass $m^2$(g) | Grain yield$m^2$(g) | 1000KW(kg) | AUDPC | Final Disease Score |
| QSM049 | 124.5 | 0 | 142.5 | 272.5 | 25.5 | 44.5 | 119.5 | 128.0 |
| QSM050 | 124.5 | 103.5 | 142.5 | 272.5 | 25.5 | 44.5 | 119.5 | 128.0 |
| QSM052 | 33.0 | 123.0 | 120.0 | 174.0 | 176.5 | 72.5 | 74.5 | 85.5 |
| QSM054 | 33.0 | 167.5 | 120.0 | 174.0 | 176.5 | 72.5 | 33.0 | 55.5 |
| QSM055 | 15.5 | 90.0 | 105.5 | 84.0 | 54.0 | 23.0 | 23.0 | 33.5 |
| QSM057 | 79.5 | 120.0 | 110.0 | 227.0 | 58.5 | 135.0 | 33.0 | 55.5 |
| QSM058 | 219.5 | 128.0 | 44.0 | 198.0 | 233.0 | 208.0 | 202.0 | 128.0 |
| QSM059 | 219.5 | 201.5 | 44.0 | 198.0 | 233.0 | 208.0 | 264.0 | 269.0 |
| QSM060 | 46.5 | 220.5 | 58.5 | 73.0 | 71.0 | 121.0 | 150.5 | 180.5 |
| QSM061 | 171.5 | 32.5 | 163.0 | 95.0 | 143.5 | 120.0 | 255.5 | 253.5 |
| QSM062 | 59.0 | 201.5 | 55.0 | 27.0 | 54.0 | 117.0 | 210.0 | 221.5 |
| QSM063 | 59.0 | 74.5 | 20.0 | 28.0 | 31.0 | 109.0 | 62.0 | 65.0 |
| QSM065 | 5.0 | 171.0 | 202.0 | 8.0 | 6.0 | 14.0 | 46.5 | 33.5 |
| QSM066 | 59.0 | 178.0 | 163.0 | 131.0 | 176.5 | 187.0 | 119.5 | 128.0 |
| QSM067 | 59.0 | 215.0 | 50.0 | 63.5 | 79.5 | 138.0 | 87.0 | 85.0 |
| QSM068 | 74.0 | 162.0 | 132.0 | 116.0 | 54.0 | 239.0 | 33.0 | 55.5 |
| QSM069 | 124.5 | 79.5 | 127.0 | 12.0 | 15.0 | 227.0 | 87.0 | 85.0 |
| QSM070 | 124.5 | 74.5 | 101.0 | 97.0 | 136.5 | 107.0 | 67.5 | 65.0 |
| QSM074 | 33.0 | 220.5 | 197.0 | 92.0 | 88.5 | 79.0 | 172.0 | 221.5 |
| QSM075 | 15.5 | 146.5 | 138.0 | 164.0 | 237.0 | 75.0 | 210.0 | 221.5 |
| QSM076 | 5.0 | 43.5 | 2.5 | 4.0 | 3.5 | 6.0 | 210.0 | 180.5 |
| QSM077 | 71.5 | 134.5 | 98.5 | 220.0 | 246.0 | 106.0 | 222.5 | 180.5 |
| QSM078 | 124.5 | 98.0 | 84.5 | 75.0 | 126.0 | 95.0 | 163.0 | 128.0 |
| QSM079 | 124.5 | 250.0 | 179.0 | 191.0 | 187.5 | 229.5 | 247.5 | 253.5 |
| QSM080 | 148.0 | 83.0 | 80.5 | 239.0 | 95.5 | 229.5 | 232.0 | 221.5 |
| QSM083 | 59.0 | 38.0 | 113.5 | 91.0 | 74.5 | 171.0 | 210.0 | 221.5 |
| QSM084 | 24.5 | 227.0 | 12.5 | 32.0 | 20.5 | 148.0 | 8.0 | 85.0 |
| QSM085 | 252.5 | 237.5 | 39.5 | 252.0 | 255.5 | 262.0 | 74.5 | 180.5 |
| QSM086 | 124.5 | 252.0 | 170.0 | 265.0 | 172.0 | 131.0 | 222.5 | 128.0 |
| QSM087 | 59.0 | 27.5 | 113.5 | 71.0 | 25.5 | 52.0 | 119.5 | 33.5 |
| QSM088 | 29.5 | 56.0 | 142.5 | 140.0 | 153.0 | 192.0 | 23.0 | 221.5 |
| QSM089 | 124.5 | 110.5 | 157.5 | 264.0 | 264.5 | 193.0 | 210.0 | 128.0 |
| QSM090 | 2.0 | 35.5 | 15.5 | 43.5 | 2.0 | 76.0 | 98.0 | 180.5 |
| QSM091 | 15.5 | 115.0 | 148.5 | 15.0 | 18.5 | 272.0 | 150.5 | 221.5 |

Appendix2 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikes/ear | Biomass $m^2$(g) | Grain yield$m^2$(g) | 1000KW(kg) | AUDPC | Final Disease Score |
| QSM049 | 124.5 | 0 | 142.5 | 272.5 | 25.5 | 44.5 | 119.5 | 128.0 |
| QSM050 | 124.5 | 103.5 | 142.5 | 272.5 | 25.5 | 44.5 | 119.5 | 128.0 |
| QSM052 | 33.0 | 123.0 | 120.0 | 174.0 | 176.5 | 72.5 | 74.5 | 85.5 |
| QSM054 | 33.0 | 167.5 | 120.0 | 174.0 | 176.5 | 72.5 | 33.0 | 55.5 |
| QSM055 | 15.5 | 90.0 | 105.5 | 84.0 | 54.0 | 23.0 | 23.0 | 33.5 |
| QSM057 | 79.5 | 120.0 | 110.0 | 227.0 | 58.5 | 135.0 | 33.0 | 55.5 |
| QSM058 | 219.5 | 128.0 | 44.0 | 198.0 | 233.0 | 208.0 | 202.0 | 128.0 |
| QSM059 | 219.5 | 201.5 | 44.0 | 198.0 | 233.0 | 208.0 | 264.0 | 269.0 |
| QSM060 | 46.5 | 220.5 | 58.5 | 73.0 | 71.0 | 121.0 | 150.5 | 180.5 |
| QSM061 | 171.5 | 32.5 | 163.0 | 95.0 | 143.5 | 120.0 | 255.5 | 253.5 |
| QSM062 | 59.0 | 201.5 | 55.0 | 27.0 | 54.0 | 117.0 | 210.0 | 221.5 |
| QSM063 | 59.0 | 74.5 | 20.0 | 28.0 | 31.0 | 109.0 | 62.0 | 65.0 |
| QSM065 | 5.0 | 171.0 | 202.0 | 8.0 | 6.0 | 14.0 | 46.5 | 33.5 |
| QSM066 | 59.0 | 178.0 | 163.0 | 131.0 | 176.5 | 187.0 | 119.5 | 128.0 |
| QSM067 | 59.0 | 215.0 | 50.0 | 63.5 | 79.5 | 138.0 | 87.0 | 85.0 |
| QSM068 | 74.0 | 162.0 | 132.0 | 116.0 | 54.0 | 239.0 | 33.0 | 55.5 |
| QSM069 | 124.5 | 79.5 | 127.0 | 12.0 | 15.0 | 227.0 | 87.0 | 85.0 |
| QSM070 | 124.5 | 74.5 | 101.0 | 97.0 | 136.5 | 107.0 | 67.5 | 65.0 |
| QSM074 | 33.0 | 220.5 | 197.0 | 92.0 | 88.5 | 79.0 | 172.0 | 221.5 |
| QSM075 | 15.5 | 146.5 | 138.0 | 164.0 | 237.0 | 75.0 | 210.0 | 221.5 |
| QSM076 | 5.0 | 43.5 | 2.5 | 4.0 | 3.5 | 6.0 | 210.0 | 180.5 |
| QSM077 | 71.5 | 134.5 | 98.5 | 220.0 | 246.0 | 106.0 | 222.5 | 180.5 |
| QSM078 | 124.5 | 98.0 | 84.5 | 75.0 | 126.0 | 95.0 | 163.0 | 128.0 |
| QSM079 | 124.5 | 250.0 | 179.0 | 191.0 | 187.5 | 229.5 | 247.5 | 253.5 |
| QSM080 | 148.0 | 83.0 | 80.5 | 239.0 | 95.5 | 229.5 | 232.0 | 221.5 |
| QSM083 | 59.0 | 38.0 | 113.5 | 91.0 | 74.5 | 171.0 | 210.0 | 221.5 |
| QSM084 | 24.5 | 227.0 | 12.5 | 32.0 | 20.5 | 148.0 | 8.0 | 85.0 |
| QSM085 | 252.5 | 237.5 | 39.5 | 252.0 | 255.5 | 262.0 | 74.5 | 180.5 |
| QSM086 | 124.5 | 252.0 | 170.0 | 265.0 | 172.0 | 131.0 | 222.5 | 128.0 |
| QSM087 | 59.0 | 27.5 | 113.5 | 71.0 | 25.5 | 52.0 | 119.5 | 33.5 |
| QSM088 | 29.5 | 56.0 | 142.5 | 140.0 | 153.0 | 192.0 | 23.0 | 221.5 |
| QSM089 | 124.5 | 110.5 | 157.5 | 264.0 | 264.5 | 193.0 | 210.0 | 128.0 |
| QSM090 | 2.0 | 35.5 | 15.5 | 43.5 | 2.0 | 76.0 | 98.0 | 180.5 |
| QSM091 | 15.5 | 115.0 | 148.5 | 15.0 | 18.5 | 272.0 | 150.5 | 221.5 |

Appendix2 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikes/ear | Biomass $m^2$(g) | Grain yield$m^2$(g) | 1000KW(kg) | AUDPC | Final Disease Score |
| FEG16123 | 99.5 | 8.0 | 174.5 | 123.0 | 163.0 | 48.0 | 222.5 | 180.5 |
| FEG16348 | 219.5 | 46.5 | 223.0 | 53.0 | 46.0 | 168.0 | 222.5 | 253.5 |
| FEG18353 | 193.0 | 153.5 | 270.5 | 30.0 | 95.5 | 63.0 | 186.5 | 180.5 |
| FEG19215 | 219.5 | 201.5 | 274.5 | 125.5 | 259.5 | 108.0 | 243.5 | 221.5 |
| FEG19216 | 193.0 | 4.0 | 225.5 | 153.0 | 190.5 | 57.0 | 186.5 | 180.5 |
| FEG19217 | 252.5 | 440.0 | 255.0 | 148.0 | 217.0 | 91.5 | 186.5 | 180.5 |
| Shech/Ha | 84.0 | 198.5 | 197.0 | 76.0 | 41.5 | 114.0 | 46.5 | 33.5 |
| Q125 | 2.0 | 115.0 | 7.0 | 3.0 | 64.0 | 22.0 | 8.0 | 7.5 |
| QSM126 | 236.5 | 1.0 | 218.9 | 253.0 | 163.0 | 81.0 | 202.0 | 128.0 |
| QSM127 | 124.5 | 31.0 | 20.9 | 63.5 | 126.0 | 191.0 | 261.0 | 263.0 |
| 09MT16 | 24.5 | 173.5 | 90.0 | 23.0 | 12.5 | 182.0 | 119.5 | 180.5 |
| 09MT38 | 219.5 | 128.0 | 44.0 | 198.0 | 233.0 | 208.0 | 186.5 | 180.5 |
| 09MT28 | 236.5 | 18.0 | 157.5 | 204.0 | 266.0 | 146.0 | 198.5 | 85.0 |
| 09MT32 | 74.0 | 79.5 | 120.0 | 20.5 | 95.5 | 153.0 | 23.0 | 33.5 |
| 09MT85 | 148.0 | 21.5 | 154.0 | 161.0 | 193.0 | 4.5 | 23.0 | 33.5 |
| 09MT86 | 182.0 | 247.5 | 44.0 | 225.5 | 259.5 | 2.0 | 46.5 | 65.0 |
| 09MT89 | 219.5 | 207.0 | 50.0 | 187.0 | 230.5 | 242.0 | 67.5 | 128.0 |
| 09MT92 | 219.5 | 260.0 | 23.0 | 245.5 | 220.0 | 264.0 | 163.0 | 65.0 |
| Columbia | 46.5 | 19.5 | 216.0 | 62.0 | 121.0 | 7.0 | 46.5 | 33.5 |
| ND25161 | 24.5 | 6.5 | 190.5 | 1.0 | 20.5 | 27.0 | 247.5 | 253.5 |
| Conlon | 7.5 | 17.0 | 2.5 | 7.0 | 18.5 | 18.0 | 119.5 | 128.0 |
| Rawson | 99.5 | 43.5 | 64.5 | 50.0 | 200.5 | 188.0 | 210.0 | 221.5 |
| ND25882 | 193.0 | 194.0 | 276.0 | 178.0 | 262.5 | 84.0 | 269.5 | 274.0 |
| ND26249 | 124.5 | 60.5 | 268.0 | 179.5 | 239.0 | 61.0 | 275.0 | 277.0 |
| 2ND25276 | 84.0 | 153.5 | 132.0 | 59.0 | 143.5 | 159.0 | 269.5 | 274.0 |
| 08N222 | 219.5 | 103.5 | 196.0 | 183.5 | 187.5 | 237.0 | 46.5 | 128.0 |
| 08N247 | 142.5 | 93.5 | 113.5 | 97.0 | 146.5 | 127.0 | 119.5 | 85.0 |
| 08N248 | 59.0 | 27.5 | 15.5 | 145.5 | 116.5 | 156.0 | 87.0 | 65.0 |
| 08N255 | 33.0 | 115.0 | 44.0 | 70.0 | 46.0 | 41.0 | 138.5 | 128.0 |
| 08N256 | 84.0 | 146.5 | 30.5 | 124.0 | 182.0 | 145.0 | 119.5 | 180.5 |
| 08N257 | 84.0 | 140.0 | 35.5 | 129.0 | 79.5 | 163.0 | 186.5 | 85.0 |
| 08N258 | 59.0 | 188.0 | 61.5 | 244.0 | 182.0 | 147.0 | 143.5 | 55.5 |
| 08N287 | 107.5 | 86.5 | 64.5 | 234.0 | 182.0 | 112.0 | 23.0 | 128.0 |
| 08N691 | 59.0 | 235.0 | 10.0 | 58.0 | 31.0 | 179.0 | 23.0 | 180.5 |

Appendix2 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikes/ear | Biomass $m^2$(g) | Grain yield$m^2$(g) | 1000KW(kg) | AUDPC | Final Disease Score |
| 09N220 | 99.5 | 209.0 | 55.5 | 160.0 | 46.5 | 250.0 | 119.5 | 128.0 |
| 09N223 | 219.5 | 146.5 | 132.0 | 262.0 | 237.0 | 265.0 | 119.5 | 65.0 |
| 09N231 | 124.5 | 205.0 | 24.5 | 242.0 | 193.0 | 218.0 | 119.5 | 55.56 |
| 09N252 | 99.5 | 194.0 | 132.0 | 174.0 | 140.5 | 253.0 | 67.5 | 55.5 |
| 09N264 | 171.5 | 108.0 | 188.0 | 259.0 | 213.5 | 180.0 | 58.0 | 253.5 |
| 09N608 | 171.5 | 13.5 | 242.0 | 229.0 | 126.0 | 88.0 | 216.0 | 128.0 |
| 08AB16 | 124.5 | 69.5 | 190.5 | 218.0 | 202.5 | 125.0 | 163.0 | 128.0 |
| 08AB17 | 59.0 | 177.0 | 95.5 | 120.0 | 85.0 | 194.5 | 119.5 | 33.5 |
| 08AB28 | 91.0 | 146.5 | 1.0 | 128.0 | 111.0 | 190.0 | 46.5 | 33.5 |
| 08AB31 | 77.0 | 128.0 | 157.5 | 165.0 | 168.5 | 98.5 | 46.5 | 33.5 |
| 09AB19 | 193.0 | 237.0 | 185.5 | 143.0 | 163.0 | 251.0 | 163.0 | 128.0 |
| 09AB20 | 171.5 | 241.5 | 179.0 | 151.0 | 207.5 | 220.0 | 98.0 | 180.5 |
| 09AB21 | 219.5 | 254.5 | 174.5 | 268.0 | 241.5 | 223.0 | 186.5 | 128.0 |
| 09AB57 | 265.0 | 247.5 | 183.5 | 224.0 | 222.5 | 245.0 | 202.0 | 180.5 |
| 09AB58 | 193.0 | 173.5 | 174.5 | 254.0 | 249.5 | 247.0 | 157.0 | 128.0 |
| 09AB66 | 124.5 | 188.0 | 120.0 | 11.0 | 196.0 | 174.0 | 119.5 | 128.0 |
| 09AB78 | 124.5 | 257.5 | 193.0 | 267.0 | 246.0 | 254.0 | 119.5 | 180.5 |
| 09AB79 | 203.0 | 263.0 | 157.5 | 251.0 | 101.5 | 238.0 | 186.5 | 85.5 |
| 09AB80 | 155.0 | 79.5 | 30.5 | 243.0 | 79.5 | 89.0 | 87.0 | 221.5 |
| 09AB82 | 59.0 | 220.5 | 50.0 | 263.0 | 207.5 | 219.0 | 210.0 | 33.5 |
| 09AB87 | 59.0 | 254.5 | 127.0 | 240.5 | 131.5 | 94.0 | 46.5 | 33.5 |
| 09AB89 | 142.5 | 170.5 | 174.5 | 249.0 | 227.0 | 228.0 | 46.5 | 65.5 |
| UT03B195 | 268.5 | 33.0 | 265.0 | 217.0 | 254.0 | 217.0 | 150.5 | 180.5 |
| UT04B20 | 270.0 | 27.5 | 261.0 | 233.0 | 251.0 | 28.5 | 176.0 | 128.0 |
| 08UT47 | 59.0 | 35.5 | 28.0 | 89.0 | 182.0 | 231.0 | 23.0 | 65.5 |
| 08UT72 | 59.0 | 103.5 | 24.5 | 14.0 | 64.0 | 225.0 | 23.0 | 242.0 |
| 08UT73 | 219.5 | 167.5 | 61.5 | 238.0 | 241.5 | 270.0 | 251.0 | 221.5 |
| 08UT74 | 171.5 | 239.6 | 110.0 | 109.0 | 163.0 | 278.0 | 243.5 | 269.0 |
| 08UT86 | 124.5 | 15.5 | 163.0 | 13.0 | 41.5 | 263.0 | 268.0 | 180.5 |
| 08UT91 | 124.5 | 182.0 | 270.5 | 208.5 | 207.5 | 21.0 | 222.5 | 221.5 |
| 05WA328 | 261.5 | 71.0 | 270.5 | 114.0 | 246.0 | 113.0 | 218.0 | 221.5 |
| 05WA316 | 193.0 | 146.5 | 132.0 | 100.0 | 153.0 | 214.0 | 119.5 | 128.0 |
| 05WA408 | 219.5 | 185.0 | 132.0 | 115.0 | 176.5 | 50.0 | 119.5 | 128.0 |
| 05WA406 | 84.0 | 120.0 | 110.0 | 18.0 | 79.5 | 194.5 | 87.0 | 85.5 |

Appendix2 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikes/ear | Biomass $m^2$(g) | Grain yield$m^2$(g) | 1000KW(kg) | AUDPC | Final Disease Score |
| 05WA427 | 171.5 | 12.0 | 95.5 | 231.0 | 259.5 | 221.0 | 46.5 | 33.5 |
| X02035DH | 124.5 | 74.5 | 105.0 | 35.5 | 79.5 | 185.0 | 87.0 | 85.0 |
| 07B405 | 171.5 | 146.5 | 105.0 | 135.5 | 172.0 | 184.0 | 87.0 | 85.5 |
| 07B362 | 124.5 | 153.5 | 142.5 | 25.5 | 25.5 | 53.5 | 46.5 | 33.5 |
| 08WA01 | 193.0 | 220.5 | 170.0 | 94.0 | 88.5 | 87.0 | 119.5 | 180.5 |
| 08WA42 | 142.5 | 194.0 | 55.0 | 55.0 | 193.0 | 249.0 | 23.0 | 85.5 |
| 08WA64 | 219.5 | 134.5 | 247.5 | 266.0 | 270.0 | 96.0 | 23.0 | 128.0 |
| 09WA07 | 107.5 | 224.0 | 8.0 | 194.5 | 64.0 | 266.0 | 138.5 | 221.5 |
| 09WA08 | 99.5 | 257.0 | 148.5 | 187.0 | 168.5 | 4.5 | 232.0 | 128.0 |
| 09WA09 | 193.0 | 162.0 | 26.0 | 150.0 | 222.5 | 252.0 | 210.0 | 128.8 |
| 09WA10 | 203.0 | 218.0 | 154.0 | 155.0 | 105.5 | 90.0 | 163.0 | 221.5 |
| 09WA20 | 124.5 | 188.0 | 138.0 | 235.0 | 259.5 | 244.0 | 172.0 | 33.5 |
| 09WA35 | 193.0 | 177.0 | 28.0 | 211.5 | 207.5 | 233.0 | 46.5 | 128.0 |
| 09WA36 | 99.5 | 83.0 | 105.0 | 112.5 | 182.0 | 170.0 | 163.0 | 128.0 |
| 09WA62 | 219.5 | 52.5 | 11.0 | 159.0 | 207.5 | 183.0 | 163.0 | 128.0 |
| 09WA63 | 15.5 | 56.0 | 99.5 | 77.0 | 168.5 | 211.0 | 119.5 | 180.5 |
| 09WA80 | 2.0 | 67.0 | 44.0 | 39.0 | 5.0 | 142.0 | 186.5 | 33.5 |
| 09WA92 | 74.0 | 256.0 | 125.0 | 213.5 | 116.5 | 167.0 | 23.0 | 128.0 |
| Steptoe | 194.1 | 59.1 | 211.5 | 163.9 | 148.3 | 99.0 | 140.7 | 249.4 |
| Hietpas5 | 171.5 | 194.0 | 228.5 | 87.5 | 54.0 | 43.0 | 87.0 | 85.0 |
| B033954 | 155.0 | 215.0 | 120.0 | 40.0 | 64.0 | 144.0 | 119.5 | 128.0 |
| Z173U047 | 142.5 | 167.5 | 185.5 | 61.0 | 111.0 | 128.5 | 74.5 | 85.0 |
| 6B040031 | 155.0 | 128.0 | 84.5 | 60.0 | 157.5 | 215.0 | 210.0 | 221.5 |
| 6B050572 | 252.5 | 146.5 | 263.5 | 187.0 | 267.0 | 115.0 | 222.5 | 180.5 |
| 6B050998 | 252.5 | 49.0 | 258.0 | 104.5 | 207.5 | 37.5 | 150.5 | 180.5 |
| KENP12 | 219.5 | 93.5 | 249.0 | 120.0 | 262.5 | 111.0 | 236.5 | 253.5 |
| 08BA26 | 88.5 | 188.0 | 69.5 | 189.0 | 273.0 | 260.0 | 23.0 | 128.0 |
| 08BA69 | 24.5 | 230.0 | 20.0 | 99.0 | 15.0 | 189.0 | 23.0 | 85.0 |
| 08BA70 | 99.5 | 229.0 | 177.0 | 222.0 | 217.0 | 154.0 | 87.0 | 242.0 |
| 08BA72 | 268.5 | 207.0 | 181.5 | 228.0 | 227.0 | 269.0 | 259.5 | 204.5 |
| 08BA75 | 193.0 | 247.5 | 80.5 | 215.0 | 264.5 | 257.0 | 227.0 | 180.5 |
| 08BA77 | 265.0 | 215.0 | 170.0 | 232.0 | 268.0 | 216.0 | 150.5 | 85.0 |
| 08N202 | 124.5 | 3.0 | 120.0 | 16.5 | 3.5 | 273.0 | 87.0 | 180.0 |
| PII5517 | 219.5 | 123.0 | 221.0 | 135.5 | 163.0 | 46.0 | 150.5 | 180.5 |

N = 1 except Chevron = 19; Steptoe = 19; Q21861 = 19; Swiss HV6 = 10; - = missing AUDPC = Area under disease progress curve.

Appendix 3: Means of agronomic traits for barley (*Hordeum vulgare L.*) lines for Season two at Njoro in 2010 and 2011

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikelets ear$^{-1}$ | Biomass(Kg) | Actual weight(Kg) | 1000KW(Kg) | AUDPC | Final Disease Score |
| Diamond | 20.5 | 24.0 | 196.5 | 68.0 | 155.5 | 65.0 | 46.5 | 50.5 |
| Q21861DH | 165.0 | 185.0 | 143.5 | 215.0 | 240.5 | 225.0 | 12.5 | 50.5 |
| Q001 | 11.0 | 159.0 | - | - | - | - | 33.5 | 98.0 |
| Q002 | 36.0 | 170.0 | 143.5 | 169.0 | 160.0 | 41.0 | 233.0 | 216.0 |
| QSM005 | 46.5 | 48.5 | 126.5 | 76.5 | 181.0 | 99.0 | 9.5 | 19.5 |
| QSM008 | 46.5 | 31.0 | 161.5 | 166.0 | 215.0 | 44.0 | 12.5 | 50.5 |
| QSM010 | 2.0 | 48.5 | 65.0 | 9.0 | 18.5 | 59.5 | 73.5 | 158.0 |
| QSM011 | 59.5 | 165.5 | 140.0 | 12.5 | 29.5 | 265.0 | 28.5 | 50.5 |
| QSM013 | 46.5 | 194.0 | 101.0 | 15.5 | 44.0 | 6.0 | 83.0 | 98.0 |
| QSM014 | 121.5 | 165.5 | 101.0 | 18.0 | 58.0 | 54.0 | 225.0 | 216.0 |
| QSM015 | 59.5 | 87.5 | 78.5 | 11.0 | 177.0 | 30.0 | 61.5 | 98.0 |
| QSM016 | 256.0 | 262.0 | 101.0 | 152.0 | 181.0 | 141.0 | 33.5 | 98.0 |
| QSM017 | 147.0 | 265.0 | 175.0 | 15.5 | 38.5 | 157.0 | 248.0 | 253.0 |
| QSM018 | 99.0 | 244.0 | 95.0 | 127.0 | 198.5 | 80.0 | 169.5 | 216.0 |
| QSM019 | 59.5 | 71.0 | 101.0 | 57.0 | 175.0 | 84.0 | 225.0 | 216.0 |
| QSM023 | 28.0 | 207.0 | 146.5 | 21.0 | 66.0 | 51.0 | 195.0 | 158.0 |
| QSM026 | 147.0 | 63.0 | 95.0 | 19.0 | 119.0 | 201.0 | 99.5 | 158.0 |
| QSM029 | 72.5 | 219.5 | 170.5 | 100.0 | 264.0 | 63.0 | 237.5 | 216.0 |
| QSM033 | 59.5 | 145.0 | 172.5 | 94.5 | 205.0 | 45.0 | 67.5 | 98.0 |
| QSM034 | 266.0 | 230.0 | 166.5 | 12.5 | 41.5 | 52.0 | 177.5 | 158.0 |
| QSM035 | 15.5 | 125.0 | 0 | 38.0 | 61.5 | 55.0 | 150.5 | 158.0 |
| QSM036 | 11.0 | 207.0 | 10.0 | 73.0 | 27.0 | 26.0 | 255.5 | 253.0 |
| QSM037 | 85.0 | 125.0 | 143.5 | 249.0 | 186.5 | 122.0 | 237.5 | 216.0 |
| QSM038 | 28.0 | 133.0 | 75.0 | 30.0 | 18.5 | 18.0 | 173.5 | 216.0 |
| QSM039 | 59.5 | 92.0 | 88.5 | 61.0 | 189.0 | 89.0 | 9.5 | 19.5 |
| QSM042 | 147.0 | 169.0 | 91.5 | 190.0 | 211.0 | 197.0 | 240.0 | 216.0 |
| QSM043 | 46.5 | 236.0 | 126.5 | 7.5 | 18.5 | 237.0 | 253.0 | 253.0 |
| QSM044 | 46.5 | 78.5 | 71.0 | 25.0 | 46.5 | 15.0 | 233.0 | 216.0 |
| QSM045 | 218.0 | 234.0 | 137.5 | 76.5 | 13.5 | 178.0 | 16.5 | 19.5 |
| QSM047 | 36.0 | 117.0 | 45.0 | 28.0 | 83.0 | 62.0 | 73.5 | 158.0 |
| QSM048 | 72.5 | 165.5 | 75.0 | 213.0 | 128.0 | 95.0 | 102.5 | 158.0 |
| QSM049 | 147.0 | 216.0 | 49.5 | 250.0 | 162.0 | 210.0 | 80.0 | 158.0 |

Appendix 3: Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikelets ear$^{-1}$ | Biomass(Kg) | Actual weight(Kg) | 1000KW(Kg) | AUDPC | Final Disease Score |
| QSM057 | 28.0 | 133.0 | 140.0 | 197.0 | 169.5 | 33.0 | 173.5 | 216.0 |
| QSM058 | 46.5 | 130.0 | 53.5 | 97.0 | 132.0 | 58.0 | 195.0 | 158.0 |
| QSM059 | 46.5 | 223.0 | 131.5 | 153.0 | 152.0 | 83.0 | 215.5 | 216.0 |
| QSM061 | 147.0 | 139.5 | 88.5 | 181.0 | 147.0 | 130.0 | 233.0 | 216.0 |
| QSM062 | - | - | - | - | - | - | 169.5 | 216.0 |
| QSM065 | 72.5 | 50.0 | 116.0 | 93.0 | 66.0 | 26.0 | 207.0 | 216.0 |
| QSM066 | 226.5 | 255.0 | 146.5 | 53.0 | 29.5 | 150.0 | 195.0 | 158.0 |
| QSM067 | 194.5 | 257.0 | 183.0 | 162.0 | 105.5 | 118.5 | 97.5 | 98.0 |
| QSM068 | 85.0 | 143.0 | 136.0 | 82.0 | 10.0 | 250.0 | 209.0 | 158.0 |
| QSM069 | 59.5 | 45.0 | 7.0 | 126.0 | 32.0 | 78.5 | 195.0 | 158.0 |
| QSM070 | 46.5 | 13.0 | 40.5 | 196.0 | 244.5 | 61.0 | 75.0 | 98.0 |
| QSM074 | 121.5 | 251.5 | 178.0 | 56.0 | 61.5 | 26.0 | 240.0 | 216.0 |
| QSM075 | 99.0 | 125.0 | 65.0 | 112.0 | 128.0 | 72.0 | 223.0 | 216.0 |
| QSM077 | 15.5 | 152.5 | 120.5 | 7.5 | 23.5 | 11.0 | 215.5 | 216.0 |
| QSM078 | 7.5 | 11.0 | 1.0 | 14.0 | 2.0 | 44.0 | 172.0 | 192.5 |
| QSM079 | 248.5 | 251.5 | 179.0 | 178.0 | 157.0 | 137.0 | 266.5 | 266.5 |
| QSM082 | 46.5 | 121.0 | 101.0 | 5.5 | 32.0 | 78.5 | - | - |
| QSM084 | - | - | - | - | - | - | 215.5 | 216.0 |
| QSM085 | 147.0 | 207.0 | 131.5 | 51.0 | 61.5 | 212.0 | 263.5 | 253.0 |
| QSM086 | 165.0 | 249.0 | 150.0 | 253.0 | 247.0 | 158.0 | 28.5 | 50.5 |
| QSM087 | 36.0 | 103.0 | 56.0 | 98.0 | 71.5 | 76.0 | 124.0 | 158.0 |
| QSM089 | 147.0 | 152.5 | 126.5 | 227.5 | 242.0 | 188.5 | 61.5 | 98.0 |
| QSM091 | 20.5 | 194.0 | 120.5 | 22.0 | 18.5 | 1.0 | 248.0 | 253.0 |
| QSM093 | 121.5 | 133.0 | 60.5 | 263.0 | 224.5 | 112.0 | 15.0 | 50.5 |
| QSM094 | 46.5 | 207.0 | 109.0 | 4.0 | 6.5 | 128.0 | 150.5 | 158.0 |
| QSM097 | 4.5 | 28.0 | 78.5 | 158.0 | 169.5 | 219.0 | 107.0 | 216.0 |
| FEG16123 | 194.5 | 26.0 | 209.0 | 143.0 | 23.5 | 46.0 | 215.5 | 216.0 |
| FEG16348 | 121.5 | 39.5 | 200.0 | 101.0 | 44.0 | 87.0 | 228.0 | 216.0 |
| FEG18353 | 28.0 | 16.5 | 185.0 | 17.0 | 184.0 | 19.0 | 195.0 | 158.0 |
| FEG19215 | 99.0 | 178.0 | 227.5 | 32.0 | 34.5 | 96.0 | 184.0 | 158.0 |
| FEG19216 | 121.5 | 5.0 | 65.0 | 55.0 | 13.5 | 193.0 | 195.0 | 158.0 |
| Shech/Ha | 85.0 | 259.0 | 23.5 | 204.0 | 203.5 | 172.0 | 114.0 | 98.0 |
| QSM127 | 218.0 | 87.5 | 195.0 | 235.0 | 223.0 | 216.0 | 215.5 | 216.0 |
| 09MT16 | 265.0 | 229.0 | 131.5 | 182.0 | 249.0 | 153.0 | 71.5 | 50.5 |
| 09MT38 | 165.0 | 211.5 | 75.0 | 125.0 | 246.0 | 245.0 | 150.5 | 158.0 |

Appendix 3: Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikelets ear$^{-1}$ | Biomass(Kg) | Actual weight(Kg) | 1000KW(Kg) | AUDPC | Final Disease Score |
| 08MT28 | 179.5 | 190.5 | 170.5 | 72.0 | 119.0 | 135.0 | 150.5 | 158.0 |
| 08MT32 | 179.5 | 165.5 | 112.0 | 167.0 | 66.0 | 155.0 | 150.5 | 98.0 |
| 08MT85 | 121.5 | 238.5 | 95.0 | 243.0 | 105.5 | 223.0 | 51.5 | 195.5 |
| 08MT86 | 207.5 | 188.0 | 164.0 | 220.0 | 90.5 | 241.0 | 18.0 | 6.0 |
| 08MT89 | 194.5 | 197.0 | 181.0 | 155.0 | 215.0 | 151.0 | 37.5 | 19.5 |
| 08MT92 | 207.5 | 247.5 | 78.5 | 257.0 | 210.0 | 205.0 | 90.5 | 50.5 |
| Columbia | 46.5 | 37.0 | 15.5 | 5.5 | 51.5 | 149.0 | 46.5 | 50.5 |
| ND25161 | 72.5 | 119.0 | 65.0 | 133.0 | 164.5 | 98.0 | 227.0 | 216.0 |
| Conlon | 72.5 | 161.0 | 32.0 | 63.5 | 124.5 | 186.0 | 46.5 | 50.5 |
| Rawson | 194.5 | 71.0 | 261.0 | 136.0 | 169.5 | 248.0 | 67.5 | 98.0 |
| ND25882 | 121.5 | 152.5 | 230.0 | 210.5 | 139.5 | 32.0 | 261.0 | 253.0 |
| ND26249 | 46.5 | 59.0 | 131.5 | 116.0 | 54.5 | 23.0 | 263.5 | 253.0 |
| 2ND25276 | 234.0 | 214.5 | 246.0 | 122.0 | 92.5 | 47.0 | 240.0 | 216.0 |
| 08N222 | 194.5 | 2.0 | 2.0 | 222.0 | 166.5 | 116.0 | 124.0 | 158.0 |
| 08N247 | 121.5 | 6.5 | 6.0 | 199.0 | 105.5 | 133.0 | 150.5 | 98.0 |
| 08N248 | 147.0 | 9.0 | 5.0 | 149.0 | 76.5 | 43.0 | 150.5 | 98.0 |
| 08N255 | 194.5 | 173.0 | 11.5 | 208.0 | 58.0 | 100.0 | 150.5 | 98.0 |
| 08N256 | 165.0 | 22.0 | 3.0 | 218.0 | 90.5 | 57.0 | 195.0 | 158.0 |
| 08N257 | 121.5 | 42.0 | 15.5 | 117.0 | 54.5 | 154.0 | 67.0 | 50.5 |
| 08N258 | 121.5 | 33.5 | 21.0 | 173.0 | 124.5 | 126.0 | 57.5 | 19.5 |
| 08N287 | 165.0 | 143.0 | 11.5 | 233.0 | 154.0 | 188.5 | 90.5 | 158.0 |
| 08N691 | 165.0 | 25.0 | 214.5 | 3.0 | 48.5 | 22.0 | 171.0 | 158.0 |
| 09N211 | 121.5 | 161.0 | 60.5 | 174.0 | 205.5 | 244.0 | 150.5 | 158.0 |
| 09N219 | 218.0 | 113.0 | 116.0 | 255.0 | 193.5 | 170.0 | 90.5 | 50.5 |
| 09N220 | 179.5 | 139.5 | 6.0 | 244.0 | 198.5 | 233.0 | 57.5 | 50.5 |
| 09N223 | 121.5 | 244.0 | 101.0 | 223.0 | 224.5 | 254.0 | 90.5 | 98.0 |
| 09N231 | 59.5 | 125.0 | 106.0 | 212.0 | 243.0 | 243.0 | 150.5 | 98.0 |
| 09N252 | 179.5 | 125.0 | 123.5 | 187.0 | 228.0 | 160.0 | 80.0 | 98.0 |
| 09N264 | 121.5 | 226.0 | 116.0 | 242.0 | 234.5 | 101.0 | 150.5 | 158.0 |
| 09N608 | 72.5 | 78.5 | 254.5 | 240.0 | 256.0 | 104.0 | 51.5 | 50.5 |
| 08AB16 | 72.5 | 113.0 | 168.0 | 110.0 | 238.5 | 162.5 | 124.0 | 158.0 |
| 08AB17 | 147.0 | 147.0 | 154.5 | 206.0 | 34.5 | 234.0 | 25.5 | 6.0 |
| 08AB28 | 147.0 | 158.0 | 101.0 | 113.0 | 148.0 | 230.0 | 25.5 | 6.0 |
| 08AB31 | 121.5 | 137.0 | 174.0 | 138.0 | 108.5 | 235.0 | 57.5 | 50.5 |
| 09AB19 | 99.0 | 261.0 | 184.0 | 34.0 | 163.0 | 120.0 | 195.0 | 216.0 |

Appendix 3 continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikelets ear$^{-1}$ | Biomass(Kg) | Actual weight(Kg) | 1000KW(Kg) | AUDPC | Final Disease Score |
| 09AB20 | 218.0 | 178.0 | 159.5 | 245.0 | 178.5 | 206.0 | 90.5 | 50.5 |
| 09AB21 | 218.0 | 244.0 | 177.0 | 189.0 | 230.0 | 209.0 | 129.5 | 98.0 |
| 09AB57 | 99.0 | 247.5 | 150.0 | 107.0 | 81.5 | 123.0 | 102.5 | 98.0 |
| 09AB58 | 85.0 | 219.5 | 28.5 | 261.0 | 234.0 | 226.0 | 150.5 | 98.0 |
| 09AB66 | 147.0 | 152.5 | 83.5 | 188.0 | 112.5 | 94.0 | 119.5 | 71.0 |
| 09AB78 | 234.0 | 71.0 | 180.0 | 192.5 | 221.0 | 255.0 | 124.0 | 158.0 |
| 09AB79 | 234.0 | 219.5 | 83.5 | 202.0 | 191.0 | 258.0 | 37.5 | 50.5 |
| 09AB80 | 240.5 | 232.0 | 56.0 | 192.0 | 18.5 | 242.0 | 150.5 | 98.0 |
| 09AB82 | 179.5 | 100.5 | 88.5 | 265.0 | 226.5 | 152.0 | 90.5 | 98.0 |
| 09AB87 | 99.0 | 178.0 | 56.0 | 148.0 | 178.5 | 136.0 | 25.5 | 6.0 |
| 09AB89 | 121.5 | 190.5 | 243.5 | 96.0 | 190.0 | 229.0 | 90.5 | 98.0 |
| UT03B195 | 226.5 | 42.0 | 245.0 | 147.0 | 231.5 | 179.0 | 182.5 | 216.0 |
| UT04B204 | 121.5 | 55.0 | 232.5 | 151.0 | 135.5 | 211.0 | 97.5 | 98.0 |
| 0UT47 | 207.5 | 47.0 | 69.0 | 195.0 | 212.0 | 256.0 | 57.5 | 50.5 |
| 08UT72 | 165.0 | 87.5 | 28.5 | 129.0 | 172.5 | 260.0 | 90.5 | 98.0 |
| 08UT73 | 179.5 | 98.5 | 116.0 | 200.0 | 195.0 | 257.0 | 129.5 | 98.0 |
| 08UT74 | 147.0 | 76.0 | 49.5 | 69.0 | 92.5 | 259.0 | 150.5 | 158.0 |
| 08UT86 | 207.5 | 71.0 | 238.5 | 224.0 | 255.0 | 145.5 | 177.5 | 216.0 |
| 08UT91 | 240.5 | 93.0 | 226.0 | 232.0 | 219.0 | 108.0 | 150.5 | 216.0 |
| Steptoe | 168.8 | 70.1 | 216.7 | 158.0 | 223.5 | 141.1 | - | - |
| 05WA328 | 147.0 | 125.0 | 91.5 | 66.0 | 48.5 | 21.0 | 114.0 | 98.0 |
| 05WA316 | 121.5 | 161.0 | 49.5 | 124.0 | 101.5 | 64.0 | 119.5 | 158.0 |
| 04WA122 | 147.0 | 95.0 | 35.5 | 118.0 | 139.5 | 148.0 | - | - |
| 05WA406 | 99.0 | 87.5 | 60.5 | 205.0 | 71.5 | 102.0 | 150.5 | 158.0 |
| 05WA466 | 207.5 | 113.0 | 13.0 | 115.0 | 175.0 | 164.0 | 105.0 | 98.0 |
| 05WA437 | 85.0 | 16.5 | 49.5 | 203.0 | 98.0 | 175.0 | 114.0 | 98.0 |
| 05WA427 | 46.5 | 100.5 | 140.0 | 43.0 | 94.5 | 56.0 | 114.0 | 98.0 |
| 06WA421 | 207.5 | 87.5 | 23.5 | 229.0 | 108.5 | 159.0 | - | - |
| X02035DH | 256.0 | 3.0 | 135.0 | 225.0 | 88.5 | 218.0 | 21.5 | 28.5 |
| 07B405 | 194.5 | 234.0 | 182.0 | 214.0 | 251.0 | 249.0 | 129.5 | 158.0 |
| 08N49 | 194.9 | 139.5 | 236.5 | 237.0 | 252.0 | 143.0 | - | - |
| 08WA01 | 85.0 | 113.0 | 105.0 | 150.0 | 200.5 | 185.0 | 177.5 | 158.0 |
| 08WA42 | 28.0 | 199.5 | 131.5 | 10.0 | 192.0 | 161.0 | 150.5 | 158.0 |
| 08WA64 | 36.0 | 211.5 | 137.5 | 36.0 | 263.0 | 145.5 | 16.5 | 158.0 |

Appendix 3 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikelets ear$^{-1}$ | Biomass(Kg) | Actual weight(Kg) | 1000KW(Kg) | AUDPC | Final Disease Score |
| 09WA08 | 179.5 | 178.0 | 150.0 | 264.0 | 265.0 | 246.0 | 195.0 | 158.0 |
| 09WA09 | 147.0 | 242.0 | 159.5 | 75.0 | 51.5 | 129.0 | 150.5 | 98.0 |
| 09WA10 | 36.0 | 42.0 | 35.5 | 33.0 | 3.5 | 147.0 | 108.0 | 50.5 |
| 09WA20 | 256.0 | 263.0 | 176.0 | 262.0 | 229.0 | 236.0 | 150.5 | 158.0 |
| 09WA35 | 121.5 | 52.5 | 53.5 | 134.0 | 79.5 | 77.0 | 150.5 | 98.0 |
| 09WA36 | 179.5 | 129.0 | 65.0 | 175.0 | 85.5 | 36.0 | 195.0 | 158.0 |
| 09WA63 | 72.5 | 87.5 | 164.0 | 154.0 | 96.0 | 103.0 | 90.5 | 98.0 |
| 09WA80 | 226.5 | 194.0 | 161.5 | 194.0 | 240.5 | 194.0 | 25.5 | 6.0 |
| 09WA92 | 121.5 | 52.5 | 31.0 | 236.0 | 175.0 | 187.0 | 150.5 | 158.0 |
| Hietpas5 | 207.5 | 33.5 | 251.5 | 141.5 | 200.5 | 180.0 | 114.0 | 98.0 |
| B033954 | 179.5 | 264.0 | 169.0 | 65.0 | 98.0 | 165.0 | 185.0 | 216.0 |
| Z173U047 | 4.5 | 4.0 | 73.0 | 63.5 | 85.5 | 105.5 | 46.5 | 50.5 |
| 6B040031 | 20.5 | 20.0 | 8.0 | 4.0 | 6.5 | 231.0 | 19.0 | 50.5 |
| 6B050572 | 179.5 | 36.0 | 190.5 | 146.0 | 13.5 | 134.0 | 124.0 | 158.0 |
| 6B050998 | 85.0 | 39.5 | 187.0 | 157.0 | 71.5 | 131.0 | 114.0 | 98.0 |
| KENP12 | 99.0 | 266.0 | 192.0 | 121.0 | 32.0 | 50.0 | 215.5 | 216.0 |
| 08BA26 | 72.5 | 185.0 | 154.5 | 83.0 | 51.5 | 208.0 | 99.5 | 50.5 |
| 08BA69 | 59.5 | 226.0 | 154.5 | 84.5 | 143.5 | 91.0 | 81.0 | 158.0 |
| 08BA70 | 85.0 | 203.0 | 109.0 | 71.0 | 81.5 | 118.5 | 150.5 | 158.0 |
| 08BA72 | 179.5 | 171.0 | 164.0 | 183.0 | 122.0 | 139.0 | 195.0 | 216.0 |
| 08BA75 | 36.0 | 238.5 | 116.0 | 67.0 | 128.0 | 190.5 | 150.5 | 158.0 |
| 08BA77 | 147.0 | 152.5 | 172.5 | 42.0 | 46.5 | 196.0 | 63.5 | 19.5 |
| 08N202 | 207.5 | 30.0 | 4.0 | 47.0 | 88.5 | 251.0 | 129.5 | 158.0 |
| PII7024 | 248.5 | 103.0 | 199.0 | 254.0 | 101.5 | 82.0 | 258.5 | 253.0 |
| PII5517 | 259.0 | 152.5 | 220.0 | 104.0 | 38.5 | 5.0 | 67.5 | 98.0 |
| PII5045 | 261.0 | 226.0 | 251.5 | 170.0 | 217.0 | 124.0 | 150.5 | 158.0 |
| PI18358 | 165.0 | 178.0 | 40.5 | 88.0 | 41.5 | 28.5 | - | - |
| PI18360 | 165.0 | 143.0 | 236.5 | 145.0 | 160.0 | 113.0 | - | - |
| PII4938 | 262.0 | 199.5 | 235.0 | 163.0 | 197.0 | 171.0 | 207.0 | 158.0 |
| PII4942 | 248.5 | 133.0 | 243.0 | 246.0 | 164.5 | 111.0 | 266.5 | 266.5 |
| PII4971 | 240.5 | 119.0 | 259.0 | 258.0 | 160.0 | 127.0 | 266.5 | 266.5 |
| PI21486 | 234.0 | 146.0 | 241.0 | 226.0 | 158.0 | 105.5 | 53.0 | 98.0 |
| PI22482 | 99.0 | 16.5 | 186.0 | 105.0 | 117.0 | 132.0 | 150.5 | 158.0 |
| PI24767 | 121.5 | 119.0 | 264.0 | 251.0 | 233.0 | 203.0 | 233.0 | 216.0 |
| PII4905 | 99.0 | 260.0 | 126.5 | 108.0 | 188.0 | 222.0 | 182.5 | 216.0 |

Appendix 3 Continued

| Cultivar | MEAN SCORE | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean height(cm) | Spikelet length(cm) | No. of spikelets ear$^{-1}$ | Biomass(Kg) | Actual weight(Kg) | 1000KW(Kg) | AUDPC | Final Disease Score |
| PII4934 | 165.0 | 251.5 | 204.0 | 231.0 | 222.0 | 81.0 | 114.0 | 98.0 |
| PI21481 | 99.0 | 188.0 | 258.0 | 210.5 | 207.0 | 173.0 | 233.0 | 216.0 |
| Q21861 | 73.3 | 90.2 | 88.6 | 74.1 | 103.2 | 170.2 | 73.9 | 67.3 |
| PC84a | 121.5 | 10.0 | 217.5 | 52.0 | 18.5 | 67.0 | 177.5 | 158.0 |
| Q21861a | 194.5 | 28.0 | 189.0 | 230.0 | 237.0 | 156.0 | 40.5 | 50.5 |
| PI452421 | 165.0 | 199.5 | 35.5 | 70.0 | 150.0 | 213.0 | 215.5 | 216.0 |
| Chevron | 183.7 | 157.3 | 191.3 | 137.1 | 114.0 | 50.5 | 106.0 | 98.1 |
| SwiSSHV5 | 11.0 | 113.0 | 71.0 | 48.0 | 66.0 | 181.0 | 40.5 | 50.5 |
| SwissHV5 | 127.1 | 171.5 | 96.5 | 144.6 | 88.0 | 165.5 | 30.1 | 40.1 |
| SwissHV6 | 187.3 | 206.0 | 114.2 | 134.5 | 117.8 | 150.2 | 66.3 | 73.3 |
| SwissHV1 | 179.5 | 258.0 | 131.5 | 20.0 | 23.5 | 198.0 | 114.0 | 98.0 |
| CI5541a | 147.0 | 98.5 | 238.5 | 59.0 | 76.5 | 66.0 | 205.0 | 158.0 |
| PI382313 | 179.5 | 78.5 | 254.5 | 130.0 | 213.0 | 88.0 | 46.5 | 50.5 |
| CIho1497 | 194.5 | 152.5 | 196.5 | 86.0 | 231.5 | 117.0 | 258.5 | 253.0 |
| P1347245 | 147.0 | 152.5 | 83.5 | 89.0 | 166.5 | 200.0 | 225.0 | 216.0 |
| P1386458 | 240.5 | 238.5 | 109.0 | 74.0 | 135.5 | 42.0 | 233.0 | 216.0 |
| PI23027 | 248.5 | 106.5 | 201.5 | 227.5 | 10.0 | 228.0 | - | - |
| PI25030 | 256.0 | 194.0 | 260.0 | 219.0 | 10.0 | 140.0 | - | - |
| KARNE | 72.5 | 19.0 | 223.5 | 238.5 | 261.5 | 216.0 | - | - |
| NGUZO | 121.5 | 185.0 | 248.0 | 164.0 | 122.0 | 16.5 | - | - |
| HKBL13 | 59.5 | 87.5 | 23.5 | 79.5 | 112.5 | 74.5 | - | - |
| HKBL12 | 99.0 | 71.0 | 154.5 | 84.5 | 143.5 | 91.0 | - | - |

N=1 except Chevron = 19; Steptoe = 19; Q21861 = 19; Swiss HV5 = 3 and Swiss HV6=10; - = missing; AUDPC = Area Under disease progress curve

**Appendix4 SAS Procedure for $\chi^2$ and Nparlway analysis**

```
(a)Title 'name of the cross';
Data ……;
Input type $ count;
Cards;
R …
S …;
Proc freq;
Tables type/ test p= (0.75, 0.25);
Tables type/ test p= (0.93, 0.07);
Tables type/ test p= (0.5625, 0.4375);
Tables type/ test p= (0.562,0.4375);
Tables type/ test p= (0.92857,0.07142);
Tables type/ test p= (0.5625,0.25,0.1875);
Tables type/ test p= (0.5625,0.375,0.0625);
Tables type/ test p= (0.75,0.1875,0.0625);
Weight count;
Run;


(b)Title 'Field Screening';
Data Stem rust;
Input Origin $ Cultivar $ Season AUDPC FDS PH SP NOF BM AW TKW;
Cards;

;
Proc sort; by Origin;
Proc Univariate; by Origin;
Var season AUDPC FDS PH SP NOF BM AW TKW;
Proc sort; by Season;
Proc Univariate; by Season;
PROC MEANS; BY SEASON;
Proc Nparlway Wilcoxon; by Origin;
Proc Nparlway Wilcoxon; by Season;
Class cultivar;
PROC RANK;
Var season AUDPC FDS PH SP NOF BM AW TKW;
RANKS;
Proc print;
Run;
```

Means and standard error for each datum were also computed using the above procedure.



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