Screening and evaluation of bread wheat (*Triticum aestivum* L.) genotypes resistance to stripe rust

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Stripe (yellow) rust caused by *Puccinia striiformis* f.sp. *tritici*, is one of the major diseases of wheat in the world. Development and use of resistant wheat cultivars is the most economical and environmentally friendly solution in combating wheat stripe rust. Field experiments were carried out at two sites in Ethiopia (Kulumsa and Meraro) and seedling tests were conducted at KARC greenhouse during the 2015 cropping season to evaluate the response 192 elite spring bread wheat genotypes and eight checks to the prevailing races of stripe rust at adult plant stage and seedling stage. About 72.5 and 42.5% of the lines exhibited resistance to stripe rust during the field screening at Kulumsa and Meraro, respectively. Disease was more severe at the cooler site Meraro than Kulumsa. Eighteen genotypes at Kulumsa and 16 genotypes at Meraro were almost immune to the disease (severity and AUDPC of zero). Seventy-two genotypes (36%) showed resistant reaction at both locations in field condition for adult plant stage (CI < 20). For seedling, 47% for mixed isolates and 31% for kubsa isolates showed resistance reaction responses to stripe rust disease based on coefficient of infection (CI).

Key words: *Puccinia striiformis*, resistance, susceptible, *Triticum aestivum*, genotypes.

INTRODUCTION

Wheat is one of the world’s leading and widely grown cereal crop serving as a staple food for more than 1/3 of the global population. With the rising global population and decreasing arable land, wheat production and yield improvement became crucial. Therefore, to fulfill the food demands of ever-growing population, the food produced in developing countries has to be enhanced by 70% till 2050 (Semenov et al., 2014).

Ethiopia is the largest wheat producer in Sub-Saharan Africa (FAOSTAT, 2018) and wheat is central to achieving food and nutrition security. About 5 million Ethiopian farmers produce 5.3 million tons of wheat across 1.8 million hectares of land under rain-fed conditions (CSA, 2020). Its popularity comes from the versatility of its use in the production of a wide range of food products, such as injera, breads, cakes, pastas, etc. Wheat ranks third in area coverage and total production after teff and maize. Although the productivity of wheat has increased in the last few years in Ethiopia, it is still low as compared to other wheat producing countries. The national average productivity is estimated to be 2.97 t ha\(^{-1}\) (CSA, 2020), which is by far below experimental yields of over 5 tons ha\(^{-1}\) (Mengistu et al., 2018). So, for national productivity reduction, there are different constraints from

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those with plant diseases among the major factors affecting the yield of wheat.

Among these plant diseases in wheat that significantly reduce wheat production are those caused by the rusts (yellow, stem and leaf) (Khan et al., 2013). Stripe (yellow) rust disease caused by *Puccinia striiformis f.sp. tritici* is one of the major diseases of wheat in the cool environments including in Ethiopia (Singh et al., 2000). Infection can occur anytime from the one-leaf stage to plant maturity, provided plants are still green (Chen, 2005). Damage of stripe rust depends on susceptibility of the variety, how early epidemic begins, the amount of stripe rust that develops and temperature during grain filling (Uauy et al., 2005). So, breeding for resistant cultivars is considered the most effective, economic and environmentally friendly approach to control stripe rust. Race-specific resistance with single resistance gene is often short lived. Gene pyramiding strategies deploying race-specific and non-race specific resistance genes is required to achieve durable resistance. However, detailed knowledge of resistance genes present in wheat cultivars is a prerequisite in resistance breeding (Reema et al., 2019).

In Ethiopia, major stripe rust epidemics occurred in 1970’s, 1980, 1988, 2000 and 2010 (Teklay et al., 2013). In 2010, more than 400,000 ha of wheat were affected which led to serious yield losses, though difficult to quantify. Most popular commercial bread wheat cultivars; Kubsa and Dashen were susceptible to stripe rust (Nazari, 2011) and it causes yield loss of 70-100% in Ethiopia. This has been clear in the breakdown of stripe rust resistance genes Yr9 in cultivars derived from "Veery" in 1980’s and Yr27 in 2000 and 2010 in widely grown cultivars derived from “Attila” cross such as PBW343 (India), Inquilab-91 (Pakistan), Kubsa (Ethiopia) and others in almost all CWANA (Central and West Asia and North African) countries (Solh et al., 2012). Hence, continuous search for new sources of resistance ahead of changing pathogen and pyramiding of more resistance genes in single cultivars is important to control stripe rust and to avoid the ‘boom and bust cycle’ of cultivar performance.

Field and seedling evaluation of the level of resistance of various genotypes and multi-locational disease testing of germplasm is used to obtain data to support breeding strategies aimed at broadening the genetic base (Khan et al., 2013). Stripe rust like the other rusts have complex life cycle that involve alternate hosts and several sporophores stages. New races continually surfaced-out due to rust ability to mutate and sexually recombine. Understanding wheat rust severity and coefficient of infection, along with identifying of effective genes and characterizing them would help to design future breeding schemes. Hence, the objective of this study was to screen and identify elite spring bread wheat genotypes for resistance to stripe rust for adult plant and seedling resistance.

Although these Yr genes have been identified in diverse wheat accessions, the race specificity of seedling resistance genes limits their efficacy against pathotypes (Kankwatsa et al., 2017). In contrast, APR is generally considered to be durable, but APR genes represent a minority of known resistance genes (Kankwatsa et al., 2017; Yuan et al., 2018). Therefore, enhancing the resistance of adult plants to cope with evolving races of *Pst* is the preferred strategy to breeding for resistance. The objectives of this study were to evaluate 192 ICARDA, wheat genotypes with 8 checks for stripe rust resistance at adult plant and seedling stage conditions and therefore, the resistance genotypes can be used for further manipulation in the wheat breeding program by incorporation into adapted cultivars to assess the variability to yellow rust resistance.

**MATERIALS AND METHODS**

**Description of experimental locations**

The field experiment was conducted at two locations in Arsi zone, Ethiopia; namely, Kulumsa and Meraro. These locations are hot spot for wheat stripe rust in Ethiopia. Kulumsa represents highland areas with an altitude of 2200 m a.s.l., mean annual rainfall of 820 mm with maximum temperature of 22.8°C and minimum temperature of 10.5°C. Meraro represents extreme highland and cold area and is located at an altitude of 2990 m a.s.l. The mean annual rainfall of the site is 1196 mm, maximum temperature is 18.1°C while the minimum temperature is 5.7°C.

**Experimental materials**

A total of 192 elite spring bread wheat genotypes and 8 checks (Pastor-2, Gimma-12, Attila-7, Kabowsh-1, SIDS-1, Debira, Goumria-3 and Hiddab were tested using alpha lattice design with two replications (Appendix Table 1). The checks were used to compare the resistance of these genotypes to stripe rust. The stripe rust spore was harvested and maintained from the field during the previous growing season (September-October 2014) and multiplied in the greenhouse using universal susceptible wheat cultivars (Morocco and Kubsa) during (July-September, 2014/15) and used for inoculating 192 elite spring bread wheat genotypes and the eight checks.

**Seedling test**

Four to five seeds of each genotype were planted in 7 cm x 7 cm x 7 cm plastic pots. Each pot was filled with a potting mix which consists of soil, sand and compost at a ratio of 2:1:1 (v/v/v). After one week of planting, when the first leaves were fully expanded, the seedlings were inoculated by spraying the most virulent and dominant varieties Kubsa/Attila and mixed isolatesurediospores suspended in mineral oil using an atomizer. Inoculated plants were allowed to dry for 5 min, were fine-misted with water and placed in a wet plastic cage with a small amount of water at the bottom. The inoculated seedlings were incubated at 10°C for 24 h in a dew chamber with relative humidity close to 100%. Seedlings were transferred to a greenhouse with mean temperature of about 18°C at the Ethiopian Institute of Agricultural Research, Kulumsa.
Agricultural Research Center (KARC), Greenhouse Lab. Disease assessment was carried out on the 15th day after inoculation using 0–4 scale (McIntosh et al., 1995) based on the infection types. Low infection types (LITs = 0–2) were considered resistant, and infection type = 2+ as intermediate while high infection types (HITs = 3–4) were rated susceptible.

**Field test**

One hundred and ninety-two genotypes and 8 checks in this study were planted using an alpha lattice design in two replications in a plot size of 1 m length, planted in two rows with 0.2 m spacing between rows at Kulumsa and Meraro. The eight bread wheat cultivars that were used as checks were planted within intervals of twenty-four entries. Field managements and agronomic practices were carried out as recommended for each location. Spreader rows were planted as mixtures of universal susceptible bread wheat cultivars and the dominant varieties (Morocco and Kubsa) adjacent to the 192 elite genotypes and 8 checks on both sides of each block, bordering the trials to ensure production of sufficient inoculum to provide uniform stripe rust infection. The inoculation of spreader row was carried out during tillering stage by spraying method and during stem elongation stage by injection methods at 50 cm interval. Spraying of stripe rust on spreader row during tillering stage was done by mixing fresh stripe rust spore with water and then sprayed to spreader row using Knapsack sprayer. Stripe rust injection to spreader row was conducted by mixing stripe rust spore with pure water and was applied to the spreader row by injecting stem at stem elongation stage using injection syringe.

Disease severity was assessed according to the modified Cobb’s scale (Peterson et al., 1948). The genotype’s reaction response to the infection in the field was scored four times at 12 days interval starting from mid-September when disease symptom commenced up to the time when disease development progress ceased as “R” or resistant (small uredinia surrounded by chlorosis or necrosis); “MR” or moderately resistant (medium sized uredinia surrounded by chlorosis or necrosis); “MS” or moderately susceptible (medium large compatible uredinia without chlorosis and necrosis); and “S” or susceptible (large, compatible uredinia without chlorosis and necrosis) while the disease severity was scored in the 0 to 100-percent scale (Roelf et al., 1992). Thus, Yellow rust scores 10 MRMSS means 10% severity of moderate resistant-to-moderately susceptible response while the 20MSS score indicates 20% severity of moderately susceptible-to-susceptible response and yellow rust score 60S suggests, 60% severity of susceptible type response. Finally, after the last disease score when the disease progress ceased, according to Stubbs (1986), the field severity data was converted to Coefficient of Infection (CI) by multiplying with constant values of response. After the last disease score when the disease progress ceased, according to Stubbs (1986), the disease severity data and host reaction score were combined to calculate the coefficient of infection (CI) following Pathan and Park (2006), by multiplying severity value with constant values of 0.0, 0.2, 0.4, 0.6, 0.8, or 1.0 for host response ratings of immune (I), resistant (R), moderately resistant (MR), intermediate (M), moderately susceptible (MS), or susceptible (S), respectively. Genotypes with coefficient of infections ranging from 0 to 20 were considered as resistant while 20 to 30, 30 to 40, 40 to 60 and 60 to 100 were moderately resistance, moderately susceptible, moderately susceptible to susceptible, and susceptible, respectively based on the reaction of check cultivars.

Area under Disease Progress Curve (AUDPC) was calculated in order to compare the genotypes’ susceptibility and resistance. The AUDPC was calculated using the midpoint rule method (Campbell and Maddren, 1990). The formula is:

\[
\text{AUDPC} = \sum_{i=1}^{n} \left[ (t_i - t) (y_i + y_{i+1}) / 2 \right],
\]

Where “t” is time in days of each reading, “y” is the percentage of affected foliage at each reading and “n” is the number of readings. AUDPC was calculated by considering each disease severity score and the coefficient of infection that was taken four times.

**RESULTS**

Response of genotypes in field condition

Phenotypic variation for stripe rust was observed at both environments for infection types and level of severity for the 192 ICARDA elite spring bread wheat genotypes and eight susceptible checks. Terminal score ranged from 0 (immune) to 100 S (highly susceptible). Reaction response to stripe rust for these genotypes at Kulumsa and Meraro locations are summarized in Figures 1 and 2 and Appendix Table 1. More disease severity/pressure was observed at Meraro than at Kulumsa. The checks showed variable reaction responses from moderately resistant to susceptible and a severity level ranging from 10 to 100%. Some of the checks such as Attila-7 (Kubsa), Sids-1, Goumaria-3 and Hiddab exhibited high terminal severity (>50) at both sites while Pastor-2, Qimma-12, Kabowsh-1 and Debira showed lower terminal severity at Kulumsa and high terminal severity at Meraro. Five of the eight checks showed higher stripe rust severity level at Meraro than at Kulumsa (Appendix Table 2). The frequency of these elite spring bread wheat genotypes, and the checks under different severity classes at Kulumsa and Meraro is presented on Figures 1 and 2, respectively, according to the coefficient of infection (CI) score. At Kulumsa, of the total 192 elite spring bread wheat genotypes and eight checks evaluated, 145 (72.5%) including 2 checks (Pastor-2 and Kabowsh-1) exhibited resistance reaction response (CI = 0 to 20); nine genotypes including one check (Debira) (4.5%) were moderately resistant (CI = 20 to 30); sixteen (8%) with one check (Qimma-12) were moderately susceptible (CIs = 30 to 40), twelve (6%) genotypes with Attila-7 were moderately susceptible to susceptible (CI = 40 to 60) and 18 (9%) including the remaining three checks were susceptible (CI= 60 to 100).

At Meraro, 86 (43%) elite genotypes exhibited resistance reaction response (CI = 0 to 20); 24 (12%) moderately resistance (CI = 20 to 30), 12 (6%) moderately susceptible (CI = 30 to 40), 30 (15%) including the five checks (Pastor-2, Kabowsh-1, Sids-1, Debira and Hiddab) were moderately susceptible to susceptible (CI = 40 to 60) and 48 (24%) were found to be susceptible (CI = 60 to 100).

After the final score, 74 genotypes (37%) out of the 200 spring bread wheat genotypes showed similar reaction response at both environments, they were resistant to stripe rust (CI from 0 to 20); 27 of these genotypes had
CI less than 2 at both locations and were almost resistance to the disease. Disease severity development was increased gradually through time from 0 to 100% depending upon differences in stripe rust reaction response of the genotypes. AUDPC computed for each genotype varied from 0 to 2490 and from 0 to 1956 for Kulumsa and Meraro, respectively. The stripe rust disease development intensity through time and AUDPC at both locations are given in Appendix Table 2. Thirteen genotypes (6.5%) were susceptible to stripe rust (CI > 60) at both locations.

Generally, the AUDPC showed that the disease severity development at Meraro was higher than at Kulumsa, which indicated the availability of more virulent races, high disease pressure and/or suitable environment at Meraro than at Kulumsa.

**Seedling stage screening in greenhouse**

Kubsa and one mixed stripe rust isolates were used for their virulence and avirulence against the 192 elite spring
broad wheat genotypes and 8 checks at seedling stage. Among them, mixed stripe rust isolates were the more virulent than Kubsa isolates. Out of the 192 spring broad wheat genotypes and 8 checks tested in the greenhouse, 53% of the genotypes showed susceptible reaction (infection type (IT)=3-4) for the mixed stripe rust isolates and 43% of the genotypes showed susceptible reaction (infection type (IT)=3-4) for Kubsa isolates. Reaction of elite spring broad wheat genotypes and checks against Kubsa and mixed isolated at seedling stage is shown in Appendix Table 2. Nearly 47% of the genotypes exhibited resistance reaction response (IT=0-2), only one genotypes showed intermediate reaction (2') for mixed stripe rust isolates and 57% showed resistance for Kubsa isolate. Out of 192 broad wheat genotypes tested in the greenhouse, sixty-two (31%) exhibited common resistance reaction response for both (Kubsa and mixed) stripe rust isolates.

DISCUSSION

Knowledge of the genetic basis of stripe rust resistance is very essential because it will facilitate the incorporation of resistance genes into high yielding and locally adapted broad wheat cultivars and release new stripe rust resistant varieties for large scale production by end users/farmers. According to Chen et al. (2002), considerable numbers of virulent races of the stripe rust have appeared through somatic recombination or mutation.

Somatic recombination plays a major role in variation of stripe rust populations and formation of new races with combinations of previously existing virulence. Ayele et al. (1990) also reported that stripe rust isolates with virulence factors on Yr8 and Yr9 were detected in Ethiopia. In Ethiopia, stripe rust often causes substantial yield loss in higher elevation (>2400 masl); however, in 2010, the disease was widespread reaching even to the lower elevations as a result of virulence to Yr27 present in the most widely grown cultivar, ‘Kubsa’. The country previously experienced yellow rust epidemics resulting in significant yield losses to farmers (Ayele, 2002). Chen (2005) reported that high humidity with cool environment and low temperature promotes stripe rust disease by favoring spore germination.

The AUDPC result also confirmed the availability of more disease severity/pressure and suitable environment for stripe rust development at Meraro than at Kulumsa (mean AUDPC of 567.9 vs 371.4). This may be attributed to variation of environmental conditions that favor the incidence, level of disease expressions and presence of more stripe rust races and greater rust pressure at Meraro. In fact, Meraro’s environment is very cool with high humidity that is suitable for stripe rust spore germination and multiplication. Several sources of durable stripe rust resistance have been reported in wheat lines from Europe, Northwest USA, and China and in cultivars released from CIMMYT. Wang et al. (2002) indicated that field resistance in the CIMMYT wheat genotypes like Pavon-76 which has been grown in Ethiopia for the last many decades remained effective under high stripe rust pressure because Pavon-76 is adult plant resistant (APR) varieties which contain three to four genes. So, developing durable/adult plant resistance varieties like Pavon-76 is key and primary goal for breeders and is the most economically effective option to manage stripe rust in developing countries. According to Tadesse et al. (2014), most of the spring bread wheat genotypes introduced to Ethiopia from CIMMYT and ICARDA possess adult plant resistance to stripe and leaf rust based on several genes with minor effects, there is significant diversity for genes that have minor to intermediate additive effects on stripe rust resistance. In the case of seedling stage test, sixty-two (31%) of the tested genotypes were resistant for both isolates (Kubsa and Mixed) (Appendix Table 2). There were more susceptible genotypes in the mixed isolate than Kubsa isolate, mostly since the mixed races would attack more genotypes than one single race; and also due to more genes being attacked by more race than single race.

Conclusion

In search of resistance to wheat stripe rust, 192 elite spring bread wheat genotypes along with eight checks were tested at two locations in Ethiopia to identify those with resistance to the local pathotypes of stripe rust races and in greenhouse for seedling stage test. The identified resistant genotypes can be released to end users after testing for other traits in multi-environment trials or used as parental lines for crosses with potential and adapted wheat cultivars to develop resistant varieties.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Table 1. List of elite bread wheat genotypes including check cultivars evaluated against the prevailing stripe rust Pedigree

| S.N | Genotype                                                                                   |
|-----|-------------------------------------------------------------------------------------------|
| 1   | ATTILA*2/PBW65/PFAU/MILAN                                                                  |
| 2   | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN                                                      |
| 3   | QAFZAH-21/ICARDA-SRRL-9                                                                     |
| 4   | KAUZ*S'/SERI/3/KAUZ/KAUZ/STAR                                                              |
| 5   | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN                                                      |
| 6   | ATTILA*2/PBW65/PFAU/MILAN                                                                  |
| 7   | CROC1/AY.SQUARROSSA(205)/KAUZ/3/ATTILA/4/FLAG-1                                            |
| 8   | BACANORA T 88/SHIHAB-8                                                                     |
| 9   | KAUZ*S'/BOCRO-3/KAUZ*2/OPATA//KAUZ                                                       |
| 10  | GOUBARA-1/ANGI-1                                                                          |
| 11  | ATTILA 50Y/ATTILA/BCN/3/PFAU/MILAN                                                        |
| 12  | HUBARA-5/ANGI-1                                                                           |
| 13  | SERI.1B/KAUZ/HEVO/3/AMAD/4/KAUZ/FLORKWA-1                                                |
| 14  | KAUZ*S'/SERI/3/KAUZ/KAUZ/STAR                                                             |
| 15  | GIRWILL-13/2/PASTOR                                                                       |
| 16  | CHILERO-1/4/VEE'S'/3/HORK/4MH//KAL-BB/5/PFAU/MILAN                                         |
| 17  | HIDDAB/CHAM-8                                                                             |
| 18  | CROC1/AY.SQUARROSSA(205)/KAUZ/3/ATTILA/4/FLAG-1                                            |
| 19  | SERI 82/SHUHA'S'/GRU90-204782/4/PASTOR/3/KAUZ*2/OPATA//KAUZ                              |
| 20  | ZEMAMRA-1/2/SOMAMA-3                                                                       |
| 21  | ZOLOTARA//SHA3/SERI/3/KAUZ*2/STAR                                                          |
| 22  | ATTILA/VEE#5/DOBUC'S/3/QADANFER-9                                                          |
| 23  | ATTILA/VEE#5/DOBUC'S/3/QADANFER-9                                                          |
| 24  | ESDA/SHWA//BCN/3/MILAN/PASTOR                                                             |
| 25  | PASTOR-2 (CHECK-1)                                                                        |
| 26  | HUBARA-13/4/TRAP#1/BOW//PFAU/3/MILAN                                                       |
| 27  | HUBARA-5/5/CHEN/AEGILOPSSQUARROSA (TAUS)/BCN/3/VEE#7/BOW/4/PASTOR                        |
| 28  | IZAZ-1/KATILA-1//GOUMRIA-3                                                                  |
| 29  | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN                                                      |
| 30  | BOUSHODA-1/5/CHEN/AEGILOPSSQUARROSA (TAUS)/BCN/3/VEE#7/BOW/4/PASTOR                      |
| 31  | ANGI-2/HUBARA-3                                                                           |
| 32  | QIMMA-12/PASTOR-6/QIMMA-12                                                                 |
| 33  | SOMAMA-9/ICARDA-SRRL-2                                                                     |
| 34  | VEE/PJN//2*KAUZ/3/SHUHA-4/FOW-2                                                            |
| 35  | QAFZAH-2/FERROUG-2/ZEMAMRA-8                                                               |
| 36  | SOMAMA-9/NEJMAH-1                                                                         |
| 37  | KAUZ*S'/SERI/3/KAUZ/KAUZ/STAR                                                             |
| 38  | HUBARA-5/5/CHEN/AEGILOPSSQUARROSA (TAUS)/BCN/3/VEE#7/BOW/4/PASTOR                        |
| 39  | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN                                                      |
| 40  | QAFZAH-35/AMIR-2                                                                          |
| 41  | KAUZ//ALTAR 84/AOS/3/MILAN/DUCULA                                                          |
| 42  | QAFZAH-16/ICARDA-SRRL-5                                                                    |
| 43  | ESDA/SHWA//BCN/3/MILAN/PASTOR                                                             |
| 44  | KAUZ//ALTAR 84/AOS/3/MILAN/DUCULA                                                          |
| 45  | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-2                                                      |
| 46  | HUBARA-5/PASTOR-2                                                                         |
| 47  | GIRWILL-13/2/PASTOR-2                                                                      |
| 48  | HUBARA-7/4/PASTOR/3/KAUZ*2/OPATA//KAUZ                                                    |
| 49  | HIDDAB/CHAM-8                                                                             |
| 50  | QIMMA-12 (CHECK-2)                                                                        |
### Table 1. Contd.

|   |   |
|---|---|
| 51 | ANGI-2/HUBARA-3 |
| 52 | ESDA/SHWA/BCN/3/MILAN/PASTOR |
| 53 | SOMAMA-9/ICARDA-SRRL-2 |
| 54 | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN |
| 55 | ATTILA/VEE#5/DOBUC'S'/3/QADANFER-9 |
| 56 | HIDDAB/CHAM-8 |
| 57 | DEBEIRA/ANGI-2 |
| 58 | QAFZAH-2/FERROUG-2/ZEMAMRA-8 |
| 59 | KAUZ/MON/CROW'S'/3/VEE/PJN//2*KAUZ |
| 60 | KAUZ'S'/SERI/3/KAUZ//KAUZ/STAR |
| 61 | ANGI-5/ZEMAMRA-8 |
| 62 | KAUZ'S'/FLORKWA-1//GOUFORMIA-3 |
| 63 | YMI #6/GEN//TIA.1//VEE#5//DOVE/BUC//MILAN/PASTOR |
| 64 | SERI 82/SHUHA'S'/GRU90-204782/3/MUNIA/CHTO//MILAN |
| 65 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-1 |
| 66 | HUBARA-5/PASTOR-2 |
| 67 | HUBARA-15/CATBIRD//PASTOR-2 |
| 68 | QAFZAH-23/SOMAMA-3//GOUFORMIA-3 |
| 69 | ATTILA*2/PBW65/PFAU/MILAN |
| 70 | PASTOR-2/HUBARA-5 |
| 71 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/KAUZ/FLORKWA-1 |
| 72 | KAUZ'S'/FLORKWA-1//GOUFORMIA-3 |
| 73 | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN |
| 74 | HAAMA-17/ANGI-2 |
| 75 | ATTILA-7 (CHECK-3) |
| 76 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-2 |
| 77 | ATTILA*2/PBW65/PFAU/MILAN |
| 78 | ATTILA/VEE#5/DOBUC'S'/3/QADANFER-9 |
| 79 | KAUZ/MON/CROW'S'/3/KAUZ//KAUZ/STAR/5//SHAMIEKH-7 |
| 80 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-1 |
| 81 | SERI.1B/KAUZ/HEVO/3/AMAD/4/PFAU/MILAN |
| 82 | GOUFORMIA-15/ANGI-2 |
| 83 | HUBARA-16/4/PASTOR/3/KAUZ*2/OPATA//KAUZ |
| 84 | SERI 82/SHUHA'S//'GRU90-204782/3/MUNIA/CHTO//MILAN |
| 85 | HIDDAB/CHAM-8 |
| 86 | SOMAMA-9/ICARDA-SRRL-2 |
| 87 | KAUZ'S'/SERI/3/KAUZ//KAUZ/STAR |
| 88 | VEE/PJN//2*KAUZ//SHUHA-4/FOW-2 |
| 89 | VEE/PJN//2*KAUZ//SHUHA-4/FOW-2 |
| 90 | ATTILA*2/PBW65/PFAU/MILAN |
| 91 | SERI 82/SHUHA'S//'GRU90-204782/4/PASTOR/3/KAUZ*2/OPATA//KAUZ |
| 92 | ATTILA/VEE#5/DOBUC'S'/3/QADANFER-9 |
| 93 | QAFZAH-33*2/SALSAL-2 |
| 94 | ATTILA/VEE#5/DOBUC'S'/3/QADANFER-9 |
| 95 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-1 |
| 96 | BOUSHODA-1-5/CHEN/AEGILOPSQUARROSA (TAUS)//BCN/3/VEE#7/BOW//4/PASTOR |
| 97 | PASTOR-2/HUBARA-5 |
| 98 | SERI 82/SHUHA'S//'GRU90-204782/3/MUNIA/CHTO//MILAN |
| 99 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-2 |
| 100 | KABOWSH-1 (CHECK-4) |
| 101 | QAFZAH-35/AMIR-2 |
| 102 | LAKTA-1/QAFZAH-21 |
| 103 | SOMAMA-9 |
Table 1. Contd.

| No. | Variety Details |
|-----|-----------------|
| 104 | SERI.1B//KAUZ/HEVO/3/AMAD/4/ATTILA/PSN/BOW/3/ATTILA/5/KAUZ’S'/SHUHA-15 |
| 105 | VEE7/KAUZ//PFAU/MILAN/3/MILAN/PASTOR |
| 106 | MUNIA/ALTAR 84//AMSEL |
| 107 | ATTILA/VEE#5/DOBUC’S'/3/PYN/BAU//MILAN/4/ZEMAMRA-8 |
| 108 | ATTILA-7//MILAN/PASTOR/3/HXL8088/DUCULA |
| 109 | VEE7/KAUZ//PFAU/MILAN/3/MILAN/PASTOR |
| 110 | URES/BOW//OPATA/3/HDL206/HORK’S’ |
| 111 | SERI.1B//KAUZ/HEVO/3/AMAD/4/ATTILA/PSN/BOW/3/ATTILA/5/KAUZ’S'/SHUHA-15 |
| 112 | SHIHAB-16 |
| 113 | VEE7/KAUZ//PFAU/MILAN/3/MILAN/PASTOR |
| 114 | KAUZ’S//SERI/3/KAUZ//KAUZ/STAR |
| 115 | MILAN/DUCULA |
| 116 | MILAN/DUCULA//AL-ZEHRAA-1 |
| 117 | QADANFER-11/REBWAH-11 |
| 118 | SERI.1B//KAUZ/HEVO/3/AMAD/4/ATTILA/PSN/BOW/3/ATTILA/5/KAUZ’S'/SH |
| 119 | P1.861/RDWG//PBW343/3/MUNIA/ALTAR 84//AMSEL |
| 120 | KAUZ//ALTAR 84/OS 3/KAUZ/3/SHUHA-4//NS732/HER/4/QAFZAH-33 |
| 121 | P1.861/RDWG//PBW343/3/MUNIA/ALTAR 84//AMSEL |
| 122 | OPATA/RAYON//KAUZ/3/2*MILAN/DUCULA |
| 123 | KAUZ’S//SHUHA-15 |
| 124 | VEE/PJN//2*TUI/3/WH576/4/AL-ZEHRAA-5 |
| 125 | Sids-1 (CHECK-5) |
| 126 | ANGI-2 |
| 127 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-1/5/KABOWSH-1 |
| 128 | MILAN/DUCULA//AL-ZEHRAA-1 |
| 129 | BOW/PRL//BUC/3/WH576 |
| 130 | CHEN/AEGILOPS SQUARROSA (TAUS)//FCT/3/2*WEAVER/4/IPA-95 |
| 131 | QADANFER-11 |
| 132 | QADANFER-11/REBWAH-11 |
| 133 | PASTOR/3/KAUZ*2/OPATA//KAUZ |
| 134 | P1.861/RDWG//VEE/PJN//2*KAUZ/4/CMPH82A.1294/2*KAUZ//MUNIA/CHTO/3/MILAN |
| 135 | VEE7/KAUZ//3/KAUZ//MON/CROWS’/4/QAFZAH-33 |
| 136 | MILAN//PSN/BOW |
| 137 | KAUZ//MON/CROWS’/3/SOMAMA-3/4/MILAN/DUCULA |
| 138 | GOUBARA-1/ANGI-1//QAFZAH-21 |
| 139 | ATTILA 50Y//ATTILA/BCN/3/KAUZ//MON/CROWS’/4/MILAN/PASTOR |
| 140 | VEE7/KAUZ//PFAU/MILAN/3/MILAN/PASTOR |
| 141 | VEE7/KAUZ//PFAU/MILAN/3/MILAN/PASTOR |
| 142 | QADANFER-11/REBWAH-11 |
| 143 | P1.861/RDWG//VEE/PJN//2*KAUZ/4/CMPH82A.1294/2*KAUZ//MUNIA/CHTO/3/MILAN |
| 144 | SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-1/5/KABOWSH-1 |
| 145 | ZEMAMRA-1 |
| 146 | VEE/PJN//2*TUI/3/WH576 |
| 147 | CHEN/AEGILOPS SQUARROSA (TAUS)//FCT/3/2*WEAVER |
| 148 | P1.861/RDWG//DAJAJ-10/3/MILAN/PASTOR |
| 149 | PASTOR-6 |
| 150 | Debira (CHECK-6) |
| 151 | QAMAR-6 |
| 152 | KAUZ//ALTAR 84/AOS//3/TNNU/MILAN//PSN/BOW |
| 153 | PFAU/MILAN |
| 154 | KAUZ//ALTAR 84/AOS//3/TNNU/MILAN//PSN/BOW |
| 155 | KASYON/GENARO 81//TEVEE-1//3/2/QADANFER-11 |
| 156 | VEE/PJN//2*KAUZ |
### Table 1. Contd.

| 157 | SERI.1B//KAUZ/HEVO/3/AMAD/4/ATTILA//PSN/BOW/3/ATTILA/5/KAUZ’S//SH |
| 158 | OPATA/RAYON//KAUZ/3/CHAM-6/FLORKWA-2/5/SHAMIEKH-7 |
| 159 | P1.861/RDWG//PBW343/3/MUNIA/ALTER 84//AMSEL |
| 160 | WEAVER/WL 3928//SW 89.3064/3/SOMAMA-3//BOW/PRL//BUC//3/WH576 |
| 161 | FLAG-1 |
| 162 | KAUZ’S//FLORKWA-1 |
| 163 | QAFZAH-35 |
| 164 | ZEMAMRA-8 |
| 165 | ATTILA//VEE#5//DOBUC’S//3/PYN/BAU//MILAN//4/ZEMAMRA-8 |
| 166 | QAFZAH-33 |
| 167 | KAUZ//ALTER 84/AOS//3/KAUZ//ATTILA 50Y//ATTILA//BCN//4//PASTOR-6 |
| 168 | VEE//PNJ//2//TUJ//3//WH576//4//AL-ZEHRRAA-5 |
| 169 | P1.861/RDWG//DAJAJ-10//3//MILAN//PASTOR |
| 170 | ATTILA 50Y//ATTILA//BCN//3//KAUZ//MON//CROW’S//4//MILAN//PASTOR |
| 171 | OPATA/RAYON//KAUZ//3//2*MILAN//DUCULA |
| 172 | QADANFER-11//REBWAH-11 |
| 173 | SHAMISS-3 |
| 174 | SERI.1B//KAUZ/HEVO/3/AMAD/4//ATTILA//PSN//BOW//3//ATTILA//5//KAUZ’S//SH |
| 175 | GOUMRIA-3 (CHECK-7) |
| 176 | OPATA/RAYON//KAUZ//3//2*MILAN//DUCULA |
| 177 | QADANFER-11//REBWAH-11 |
| 178 | KATILA-8//SKAUZ//BAV92//3//CROC-1//AE.SQUARROSA (224) //OPATA//5//MUNIA//ALTER 84//MILAN |
| 179 | FAYEO-1 |
| 180 | RABIH-7 |
| 181 | ATTILA-7//MILAN//PASTOR//3//ICARDA-SRRL-2 |
| 182 | QADANFER-11//REBWAH-11 |
| 183 | QADANFER-9 |
| 184 | KASYON//GENARO 81//TEVEE-1//3//2*QADANFER-11 |
| 185 | KAUZ//ALTER 84/AOS//3//KAUZ//3//SHUHA-4//NS732//HER//4//QAFZAH-33 |
| 186 | SERI.1B//2//3//KAUZ//3//BOW//3//KAUZ//GYS////KAUZ//5//MUNIA//ALTER 84//MILAN |
| 187 | VEE//PNJ//2//TUJ//3//WH576//4//AL-ZEHRRAA-5 |
| 188 | HAAMA-17//QIMMA-12 |
| 189 | KAUZ//MON//CROW’S//3//SHUHA-4//NS732//HER//4//MILAN//PASTOR |
| 190 | QADANFER-11//REBWAH-11 |
| 191 | SERI.1B//KAUZ/HEVO/3//AMAD/4//ATTILA//PSN//BOW//3//ATTILA//5//KAUZ’S//SH |
| 192 | KAUZ’S//SERI//STAR’S//FLORKWA-2//3//FLAG-1 |
| 193 | MILAN//PASTOR |
| 194 | ANGI-1 |
| 195 | SAMIRA-9 |
| 196 | MILAN//DUCULA//AL-ZEHRRAA-1 |
| 197 | KAUZ//MON//CROW’S//3//KAUZ//5//SHAMIEKH-7 |
| 198 | SHIHAB-19 |
| 199 | VEE7//KAUZ//3//KAUZ//MON//CROW’S//4//QAFZAH-33 |
| 200 | HIDDAB (CHECK-8) |
| No. | Designation | Kulumsa | Meraro | Isolate |
|-----|-------------|---------|--------|---------|
|     |             | Disease Score | CI | AUDPC | Disease Score | CI | AUDPC | Mixed | Kubsa |
| 1   | Genotype 1  | 5M       | 3  | 81.6 | 15S       | 15 | 420   | 3    | 0    |
| 2   | Genotype 2  | 5MS      | 4  | 43.2 | 10S       | 10 | 246   | 3    | 3    |
| 3   | Genotype 3  | 5MS      | 4  | 24   | 60S       | 60 | 468   | 3    | 0    |
| 4   | Genotype 4  | 0        | 0  | 0    | 60S       | 60 | 1146  | 3    | 3+   |
| 5   | Genotype 5  | 40SMS    | 36 | 624  | 30S       | 30 | 312   | 4    | 3+   |
| 6   | Genotype 6  | 20MSS    | 18 | 384  | 25S       | 25 | 456   | 0    | 0    |
| 7   | Genotype 7  | tMR      | 0.4| 12   | 5SMS      | 4.5| 81    | 4    | 3    |
| 8   | Genotype 8  | 10SMS    | 9  | 126  | 80S       | 80 | 786   | 3    | 0    |
| 9   | Genotype 9  | 40MSS    | 36 | 747  | 70S       | 70 | 966   | 3    | 0    |
| 10  | Genotype 10 | 60S      | 60 | 1146 | 80S       | 80 | 906   | 3    | 3+   |
| 11  | Genotype 11 | tMS      | 0.8| 4.8  | 5S        | 5   | 54    | 3    | 3+   |
| 12  | Genotype 12 | 40SMS    | 36 | 462  | 5MS       | 4   | 88.8  | 1    | 3    |
| 13  | Genotype 13 | 0        | 0.8| 4.8  | 5MS       | 4   | 88.8  | 0    | 2    |
| 14  | Genotype 14 | 60S      | 60 | 1089 | 60S       | 60 | 1326  | 3    | 3    |
| 15  | Genotype 15 | 20MS     | 16 | 330  | 20S       | 20 | 366   | 4    | 3+   |
| 16  | Genotype 16 | tMR      | 0.4| 24   | 10S       | 10 | 180   | 3    | 3    |
| 17  | Genotype 17 | 60S      | 60 | 1020 | 60S       | 60 | 726   | 3    | 3+   |
| 18  | Genotype 18 | 10M      | 6  | 1089 | 50S       | 50 | 486   | 3    | 3    |
| 19  | Genotype 19 | 5MS      | 4  | 45.6 | 20S       | 20 | 300   | 2    | 3    |
| 20  | Genotype 20 | 10M      | 6  | 144  | 15S       | 15 | 336   | 1    | 1    |
| 21  | Genotype 21 | tM       | 0.6| 13.2 | 30S       | 30 | 318   | 3    | 2    |
| 22  | Genotype 22 | 35MS     | 28 | 918  | 30S       | 30 | 690   | 0    | 4    |
| 23  | Genotype 23 | tMR      | 0.4| 2.4  | 15MS      | 15 | 93.6  | 3    | 2    |
| 24  | Genotype 24 | 15M      | 9  | 204  | 40S       | 40 | 546   | 2    | -    |
| 25  | Pastor-2    | 10MS     | 8  | 106.8| 60S       | 60 | 60    | 2    | 4    |
| 26  | Genotype 26 | 100S     | 100| 2046 | 60S       | 60 | 966   | 2    | 2    |
| 27  | Genotype 27 | 10M      | 0.6| 67.2 | 40SMS     | 40 | 394.8 | 0    | 3+   |
| 28  | Genotype 28 | 10M      | 6  | 204  | 10S       | 10 | 60    | 2    | 0    |
| 29  | Genotype 29 | tMR      | 0.4| 24   | 5SMS      | 4.5| 91    | 3    | 2    |
| 30  | Genotype 30 | 5MR      | 2  | 32.4 | 60S       | 60 | 492   | 3    | 3    |
| 31  | Genotype 31 | 40S      | 40 | 810  | 30S       | 30 | 486   | 2    | 2    |
| 32  | Genotype 32 | 15M      | 9  | 336  | 10MS      | 10 | 96    | 0    | 0    |
| 33  | Genotype 33 | 10MS     | 8  | 156  | 60S       | 60 | 780   | 3    | 0    |
| 34  | Genotype 34 | 20MS     | 16 | 381  | 30MSS     | 27 | 330   | 0    | 3    |
| 35  | Genotype 35 | tMR      | 0.4| 2.4  | 0         | 0   | 0     | 2    | 0    |
| 36  | Genotype 36 | tMR      | 0.4| 2.4  | 40S       | 40 | 264   | 3    | 0    |
| 37  | Genotype 37 | 80S      | 80 | 1434 | 85S       | 85 | 1596  | 3    | 0    |
| 38  | Genotype 38 | 20MS     | 16 | 474  | 40S       | 40 | 786   | 3    | 3    |
| 39  | Genotype 39 | 0        | 0  | 0    | 0         | 0   | 0     | 0    | 0    |
| 40  | Genotype 40 | 20SMS    | 18 | 378  | 30MS      | 24 | 250.8 | 0    | 0    |
| 41  | Genotype 41 | 20M      | 12 | 456  | 20SMS     | 18 | 408   | 0    | 3    |
| 42  | Genotype 42 | 5M       | 3  | 66   | 15SMS     | 13.5| 204.6| 0    | 1    |
| 43  | Genotype 43 | 5M       | 3  | 75.6 | 20MS      | 18 | 408   | 3    | 3+   |
| 44  | Genotype 44 | 5M       | 3  | 126  | 15SMS     | 13.5| 243  | 3    | 2    |
| 45  | Genotype 45 | 20M      | 12 | 336  | 70S       | 70  | 846   | 3    | 0    |
| 46  | Genotype 46 | 10M      | 6  | 180  | 20MS      | 18  | 310.8| 3    | 4    |
| 47  | Genotype 47 | 20MS     | 16 | 204  | 40S       | 40  | 666   | 3    | 3+   |
| 48  | Genotype 48 | 80S      | 80 | 1410 | Tms       | 0.8 | 26.4  | 1    | 3+   |
| Genotype | 5M | 5MR | 5MS | 5SMS | 70S | 70S | 80S | 80S | 5S | 5S | 85S | 85S | 8S | 8S | 30S | 30S | 50S | 50S | 60S | 60S | 70S | 70S | 80S | 80S |
|----------|----|-----|-----|------|-----|-----|-----|-----|-----|-----|------|------|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 49       | 5M | 3   | 141 | 70S  | 70  | 1266| 0   | 2   |
| 50       | QIMMA-12 | 40MS | 32  | 831  | 70S  | 70  | 960 | 3   |
| 51       | 15M | 9   | 354 | 60S  | 60  | 1086| 2   | 1   |
| 52       | 5M  | 3   | 120 | 60S  | 60  | 606 | 3   | 4   |
| 53       | 5SMS | 3   | 87  | 30S  | 30  | 459.6| 0   | 3   |
| 54       | tM  | 0.6 | 20  | 0    | 0   | 14.4| 0   | 0   |
| 55       | tMR | 0.4 | 2.4 | tM   | 0.6 | 14.4| 0   | 3+  |
| 56       | 80S | 80  | 1170| 80s  | 80  | 1470| 3   | 4   |
| 57       | 100S | 100 | 2190| 85S  | 85  | 1590| 3   | 2   |
| 58       | 20MS | 16  | 372 | 50S  | 50  | 846 | 3   |
| 59       | 10M  | 6   | 282 | 70S  | 70  | 672 | 3   |
| 60       | 60SMS | 60  | 966 | 80S  | 80  | 1446| 3   |
| 61       | 5M  | 3   | 120 | tMS  | 0   | 26.4| 3   |
| 62       | 40SMS | 36  | 624 | 95S  | 95  | 1836| 3   |
| 63       | 30MS | 24  | 444 | 90S  | 90  | 1290| 4   |
| 64       | 10MS | 8   | 156 | 80S  | 80  | 1194| 3   |
| 65       | 40MS | 32  | 708 | 70S  | 70  | 1290| 3   |
| 66       | tMR | 0.4 | 20.4| 30S  | 30  | 405.6| 2   |
| 67       | tMR | 0.4 | 22.8| 5MS  | 4   | 126 | 3   |
| 68       | 5M  | 3   | 108 | 15MS | 12  | 303 | 2   |
| 69       | 0   | 0   | 0   | tMR  | 0.4 | 8.4 | 3   |
| 70       | 0   | 0   | 0   | 0    | 0   | 4   |
| 71       | 5M  | 0.4 | 126 | 80s  | 4   | 1260| 2   |
| 72       | 5M  | 0   | 1500| 80S  | 80  | 1686| 2   |
| 73       | 5M  | 3   | 114 | 5SMS | 4.5 | 99  |
| 74       | 30MS | 24  | 522 | 90S  | 90  | 930 | 0   |
| 75       | 5S  | 50  | 930 | 90S  | 90  | 1146| 3   |
| 76       | 5M  | 3   | 141 | tMS  | 0.8 | 14.4| 3   |
| 77       | 0   | 0   | 0   | 5SMS | 4.5 | 90.6| 2   |
| 78       | 0   | 0   | 0   | 0    | 0   | 6   |
| 79       | 5SMS | 45  | 675 | 90S  | 90  | 1956| 3   |
| 80       | 30SMS | 27  | 492 | 70S  | 70  | 1146| 3   |
| 81       | tMR | 0.4 | 24  | 5MS  | 4   | 81.6| 3   |
| 82       | 60S | 60  | 1092| 20S  | 20  | 426 |
| 83       | 0   | 0   | 0   | 0    | 0   | 3   |
| 84       | 20S | 18  | 165.6| 45S | 45  | 900 | 2   |
| 85       | 50S | 45  | 732 | 40S  | 40  | 1080| 4   |
| 86       | 10MSS | 9   | 117.6| 30S | 30  | 480 |
| 87       | 10M | 6   | 186 | 90S  | 90  | 1500| 3   |
| 88       | 50S | 50  | 756 | 60S  | 60  | 588 |
| 89       | 20MS | 16  | 324.6| 50S | 50  | 930 | 3   |
| 90       | tMR | 0.4 | 3.6 | 10MSS | 9  | 216 | 2   |
| 91       | 5MR | 2   | 114 | 15MSS | 13.5| 255 | 3   |
| 92       | 5SMS | 4.5 | 36.6| 5SMS | 4.5 | 90.6| 3   |
| 93       | 5M  | 3   | 43.2| 10MSS | 9  | 172.8| 3  |
| 94       | 10M | 6   | 210 | 30S  | 30  | 480 |
| 95       | 10M | 6   | 58.8| 70S  | 70  | 726 |
| 96       | 10M | 8   | 123.6| 70S | 70  | 846 |
| 97       | 10M | 6   | 186 | 60S  | 60  | 906 |
| 98       | genotype 98 | 5M | 3   | 38.4| 40S | 40  |
| 99       | genotype 99 | 10SMS | 9   | 102 | 70S | 70  | 636 | 4   | 0|

**Table 2.**
Table 2. Contd.

| Genotype     | Type | Genotype     | Type | Genotype     | Type | Genotype     | Type |
|--------------|------|--------------|------|--------------|------|--------------|------|
| Genotype 101 | 20M  | Genotype 102 | 20M  | Genotype 103 | 0    | Genotype 104 | 20MS |
| Genotype 105 | 5MS  | Genotype 106 | 6    | Genotype 107 | 10M  | Genotype 108 | 30S  |
| Genotype 111 | 10M  | Genotype 112 | 4    | Genotype 113 | 5MR  | Genotype 114 | 25M  |
| Genotype 115 | 10M  | Genotype 116 | 6    | Genotype 117 | 5M   | Genotype 118 | 40MS |
| Genotype 119 | 0.4  | Genotype 120 | 0.4  | Genotype 121 | 40MS | Genotype 122 | 5MR  |
| Genotype 123 | 20S  | Genotype 124 | 100S | Genotype 125 | 100S | Genotype 126 | 50S  |
| Genotype 127 | 100S | Genotype 128 | 100S | Genotype 129 | 80S  | Genotype 130 | 5MR  |
| Genotype 131 | 0.4  | Genotype 132 | 0.4  | Genotype 133 | 5M   | Genotype 134 | 40MS |
| Genotype 135 | 5MR  | Genotype 136 | 0    | Genotype 137 | 40MS | Genotype 138 | 0    |
| Genotype 139 | 20MS | Genotype 140 | 8    | Genotype 141 | 5MR  | Genotype 142 | 60S  |
| Genotype 143 | 40MS | Genotype 144 | 100S | Genotype 145 | 0.4  | Genotype 146 | 80S  |
| Genotype 147 | 10MS | Genotype 148 | 40S  | Genotype 149 | 10M  | Genotype 150 | Debira |
Table 2. Contd.

|   | Genotype       | 40M  | 50MS  | 60S  | 70S  | 70 | 1050  | 2  | 2 |
|---|----------------|------|-------|------|------|----|--------|---|---|
| 151| Genotype151    | 24   | 780   | 70S  | 70   | 1050 | 2  | 2  |
| 152| Genotype152    | 0    | 21.6  | 0    | 0    | 0   | 1     | 3 |
| 153| Genotype153    | 0.4  | 12    | 5M   | 3    | 66  | 0     | 3 |
| 154| Genotype154    | 0    | 0     | 0    | 0    | 0   | 2     | 0 |
| 155| Genotype155    | 0.4  | 27.6  | 0    | 0    | 0   | 0     | 0 |
| 156| Genotype156    | 40   | 1230  | 70S  | 70   | 1266 | 3   | 2 |
| 157| Genotype157    | 0    | 0     | 10S  | 10   | 192 | 0     | 3 |
| 158| Genotype158    | 100  | 1350  | 80S  | 80   | 1626| 0     | 2 |
| 159| Genotype159    | 27   | 594   | 65S  | 65   | 1350| 2     | 0 |
| 160| Genotype160    | 10MR | 4     | 246  | 60S  | 60  | 786   | 3 |
| 161| Genotype161    | 10M  | 6     | 61.2 | 40SMS| 36  | 492   | 1 |
| 162| Genotype162    | 10M  | 6     | 98.4 | 30MS | 24  | 342   | 2 |
| 163| Genotype163    | 20S  | 18    | 258  | 25MSS| 22.5| 411   | 2 |
| 164| Genotype164    | 0.2  | 1.2   | tMS  | 0.8  | 16.4| 3     | 1 |
| 165| Genotype165    | 5M   | 3     | 43.2 | 10MS | 8   | 159.6 | 0 |
| 166| Genotype166    | 30S  | 27    | 408  | 40S  | 40  | 480   | 4 |
| 167| Genotype167    | 0.2  | 1.2   | tMS  | 0.8  | 20.4| 3     | 3 |
| 168| Genotype168    | 100S | 1530  | 30S  | 30   | 1890 | 4   | 3 |
| 169| Genotype169    | 0    | 0     | 0    | tMR  | 0.4 | 16.8  | 4 |
| 170| Genotype170    | 0    | 0     | 0    | tM   | 0.6 | 20.2  | 3 |
| 171| Genotype171    | 0    | 0     | 0    | 0    | 0   | 1     | 1 |
| 172| Genotype172    | 0.6  | 3.6   | 15SMS| 13.5 | 297 | 3     | 3 |
| 173| Genotype173    | 0.4  | 24    | 0    | 0    | 0   | 3     | 3 |
| 174| Genotype174    | 60S  | 60    | 1146 | 70S  | 70  | 1020  | 3 |
| 175| GOUUMRIA-3     | 100S | 1770  | 80S  | 80   | 1830| 3     | 3 |
| 176| Genotype176    | 0    | 0     | 0    | 0    | 0   | 2     | 2 |
| 177| Genotype177    | 5M   | 3     | 43.2 | 5MS  | 4   | 87.6  | 0 |
| 178| Genotype178    | 20S  | 16    | 366  | 80S  | 80  | 1230  | 3 |
| 179| Genotype179    | 10MR | 4     | 174  | 60S  | 60  | 978   | 4 |
| 180| Genotype180    | 0    | 0     | 0    | 0    | 0   | 0     | 2 |
| 181| Genotype181    | 15SMS| 0     | 138.6| 70S  | 70  | 1050  | 3 |
| 182| Genotype182    | 5MR  | 2     | 114  | 15SMS| 13.5| 303   | 0 |
| 183| Genotype183    | 4MR  | 4     | 168  | 45MS | 40.5| 789   | 0 |
| 184| Genotype184    | 4.0  | 27.6  | 0    | 0    | 0   | 0     | 2 |
| 185| Genotype185    | 40MS | 32    | 672  | 25S  | 25  | 411   | 4 |
| 186| Genotype186    | 0.4  | 24    | 15SMS| 13.5 | 309 | 3     | 3 |
| 187| Genotype187    | 40S  | 90    | 1446 | 85S  | 85  | 1740  | 3 |
| 188| Genotype188    | 30M  | 18    | 528  | 40S  | 40  | 660   | 0 |
| 189| Genotype189    | 0.4  | 12    | 5M   | 3    | 63.6| 3     | 4 |
| 190| Genotype190    | 5MR  | 2     | 138  | tMR  | 0.4 | 12    | 0 |
| 191| Genotype191    | 40MS | 32    | 558  | 25S  | 22.5| 465   | 0 |
| 192| Genotype192    | 10MS | 8     | 69.6 | 50S  | 50  | 447.6 | 3 |
| 193| Genotype193    | 0    | 0     | 0    | tM   | 0.6 | 10.8  | 3 |
| 194| Genotype194    | 10MR | 4     | 174  | 5MS  | 4   | 87.6  | 2 |
| 195| Genotype195    | 0.4  | 27.6  | tMS  | 0.8  | 30  | 4     | 4 |
| 196| Genotype196    | 10MR | 4     | 198  | 15SMS| 13.5| 297   | 3 |
| 197| Genotype197    | 20M  | 12    | 360  | 60S  | 60  | 1146  | 3 |
| 198| Genotype198    | 10M  | 6     | 93.6 | 70S  | 70  | 906   | 0 |
| 199| Genotype199    | 5MR  | 2     | 66   | 25S  | 25  | 459   | 4 |
| 200| HIDDAB         | 80S  | 80    | 1320 | 60S  | 60  | 1110  | 4 |