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RESEARCH ARTICLE

SCREENING AND EVALUATION OF BREAD WHEAT (*TRITICUMAESTIVUM L.*) GENOTYPES RESISTANCE TO STRIPE RUST

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ABSTRACT

Stripe (yellow) rust caused by *Pucciniastriiformisf.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 green house 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 Merao 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). Seventy two genotypes (36%) showed resistant reaction at both locations in field condition for adult plant stage (CI < 20).

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INTRODUCTION

Wheat is the most widely grown cereal crop globally and feeds 4.5 billion people in 95 developing countries (Braun *et al*., 2010). It is also one of the major cereal crops in Ethiopia that is central to achieve food and nutrition security. It is the 4th most important cereal crop after teff (Eragrostistef), maize (Zea mays) and sorghum (Sorghum bicolor) in area coverage and 3rd in total production in Ethiopia (Teklay *et al*., 2013). Meanwhile biotic and biotic stresses as hamper the productivity of this crop leading to great economic losses. Among the most important 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 (Ayele*et al.,* 1990, 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).

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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 Dashenwere 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 spores stages. New races continually surfaced-out due to rust ability to mutate and sexually recombine. Understanding wheat rust severity and coefficient of infection and 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.

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. and mean annual rainfall of 820 mm with maximum temperature of 22.8 ^{0}C and minimum temperatures of 10.5^{0}C. Meraro represents extreme highland and cold area. It is located at an altitude of 2990 m.a.s.l. The mean annual rainfall of the site is 1196mm and maximum temperature is 18.10C while the minimum temperature is 5.70C.

Experimental materials: A total of 192 elite spring bread wheat genotypes and 8 checks Pastor-2, Qimma-12, Attila-7, Kabowsh-1, SIDS-1, Debira, Goumria-3 and Hiddabwere tested (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 univarsal 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 a 7cm x7cm x 7cm 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 isolates urediospores suspended in mineral oil using an atomizer. Inoculated plants were allowed to dry for 5 minutes and 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^{0}C for 24 hours in a dew chamber with relative humidity close to 100%. Seedlings were transferred to a greenhouse with mean temperature of about 18^{0}C at the Ethiopian Institute of Agricultural research, Kulumsa Agricultural Research Center (KARC), greenhouse lab. Disease assessment was carried out on the 15th days 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 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) in 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 50cm 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 Knabsak 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 siringe. 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 percentage of 0 to 100 scale (Roelf *et al*., 1992).

Thus, Yellow rust scores 10 MRMS 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 *et al*. (1986), the field severity data was converted to Coefficient of Infection (CI) by multiplying with constant values of response. Genotypes with coefficient of infections ranging 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. After the last disease score when the disease progress ceased, according to Stubbs *et al*. (1986), the disease severity data and host reaction response were combined to calculate the coefficient of infection (CI) following Pathan and Park (2006), by multiplying severity value with constant values of 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 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 Madden, 1990).The formula is:

$$AUDPC = \Sigma_{i=1}^{n-1} [(t_{i+1} - t_i)(y_i + y_{i+1})/2],$$

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 observedat 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 & 2 and Appendix Table 2. 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.

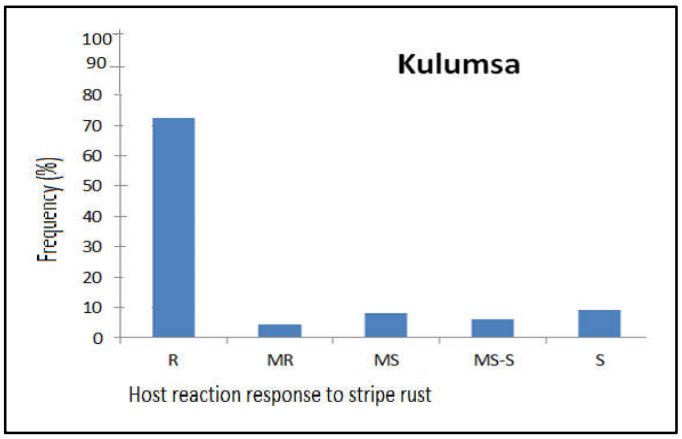

Figure 1. Frequency (%) of elite spring bread wheat genotypes under different severity classes at Kulumsa during 2015 cropping season

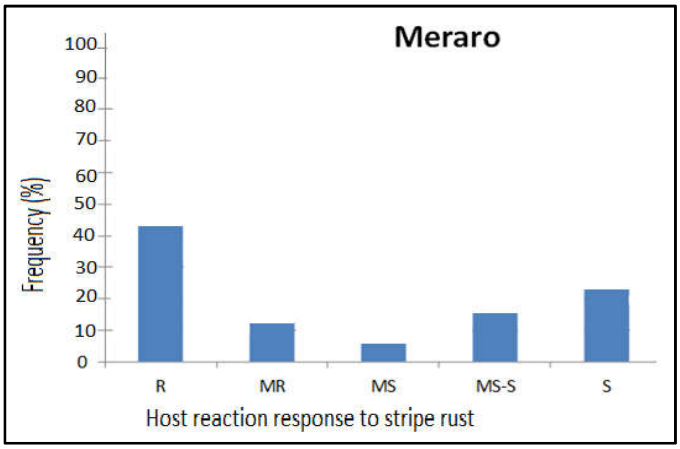

Figure 2. Frequency (%) of elite bread wheat genotypes under different severity classes tested at Meraroduring 2015 cropping season

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 rustisolates were used for their virulence and a virulence against the 200 elite spring bread wheat genotypes including the 8 checks at seedling stage. Among them, mixed stripe rust isolates were the more virulent than Kubsa isolates. Out of the 200 spring bread wheat genotypes tested in the greenhouse, 53% of the genotypes showed susceptible reaction (IT=3-4) for the mixed stripe rust isolates and 43 % of the genotypes showed susceptible reaction (IT=3-4) for Kubsaisolates. Reaction of elite spring bread 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% were resistance for kubsa isolate. Out of 192 bread wheat genotypes tested in the greenhouse sixty two (31%) exhibited common resistance reaction response for both (Kubsa and mixed) stripe rust isolate.

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 bread 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 cause substantial yield loss in higher elevation (>2400 masl), however, in 2010, the disease was wide spread 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 Badebo, 2002). This study was undertaken with the objectives of screening 192 elite spring bread wheat genotypes from ICARDA along with eight checks under field (adult plant stage) and greenhouse (seedling stage) conditions for resistance against Ethiopian path types of stripe rust. Results of these testing in 2015 revealed that many of the elite spring bread wheat genotypes (72.5% at Kulumsa, 43% at Meraro), 47% for mixed isolates and 31% for kubsa isolates) showed resistance reaction responses to stripe rust disease based on coefficient of infection (CI). Seventy two genotypes (36%) showed resistant reaction at both locations in field condition for adult plant stage (CI < 20). Thirteen genotypes (6.5%) were immune to the disease at both locations (CI=0). In general higher disease severity level was observed at Meraro as compared to that at Kulumsa (mean CI of 36.1 vs 18.9). 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. Chen (2005) reported that high humidity with cool environment and low temperature promotes stripe rust disease by favoring spore germination. 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 Pavon-76 which has been grown in Ethiopia for the last many decades remained effective under high stripe rust pressure. Pavon-76 contains three to four genes for APR that are different from Yr18. Two QTLs in Pavon-76 have been designated as Yr29 (chromosome 1BL) and Yr30 (chromosome 3BS). Host plant resistance 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 resistance for both isolates (Kubsa and Mixed) (appendix table2). There were more susceptible genotypes in the mixed isolate than Kubsa isolate, these mostly true the mixed races would attack more genotypes than one single race; due to more genes would be attack by more race than single race.

Summary

In search for 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 stag 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.

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Appendix Table2. Stripe rust terminal disease scores, coefficient of infection (CI), Area under Disease Progress Curve (AUDPC) and seedling test of elite spring bread wheat genotypes based at Kulumsa and Meraro during 2014/15

No	Designation	Kulumsa			Meraro			Isolates	
		Dis. Score	CI	AUDPC	Dis. Score	CI	AUDPC	Mixed	Kubsa
1	genotype1	5M	3	81.6	15S	15	420	3	0
2	genotype2	5MS	4	43.2	10S	10	246	3	3
3	genotype3	5MS	4	24	60S	60	468	3	0
4	genotype4	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 12	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	Genotype16	tMR	0.4	24	10S	10	180	3	3
17	Genotype17	60S	60	1020	60S	60	726	3	3+
18	Genotype18	10M	6	1089	50S	50	486	3	3
19	Genotype19	5MS	4	45.6	20S	20	300	2	3
20	Genotype20	10M	6	144	15S	15	336	1	1
21	Genotype21	tM	0.6	13.2	30S	30	318	3	2
22	Genotype22	35MS	28	918	30S	30	690	0	4
23	Genotype23	tMR	0.4	2.4	15MS	15	93.6	3	2
24	Genotype24	15M	9	204	40S	40	546	2	-
25	PASTOR-2	10MS	8	106.8	60S	60	60	2	4
26	Genotype26	100S	100	2046	60S	60	966	2	2
27	Genotype27	10M	0;6	67.2	40SMS	40	394.8	0	3+
28	Genotype28	10M	6	204	10S	10	60	2	0
29	Genotype29	tMR	0.4	24	5SMS	4.5	91	3	2
30	Genotype30	5MR	2	32.4	60S	60	492	3	3
31	Genotype31	40S	40	810	30S	30	486	2	2
32	Genotype32	15M	9	336	10MS	10	96	0	0
33	Genotype33	10MS	8	156	60S	60	780	3	0
34	Genotype34	20MS	16	381	30MSS	27	330	0	3
35	Genotype35	tMR	0.4	2.4	0	0	0	2	0
36	genotype36	tMR	0.4	2.4	40S	40	264	3	0
37	Genotype37	80S	80	1434	85S	85	1596	3	0
38	Genotype38	20MS	16	474	40S	40	786	3	3
39	Genotype39	0	0	0	0	0	0	0	0
40	Genotype40	20SMS	18	378	30MS	24	250.8	0	0
41	Genotype41	20M	12	456	20SMS	18	408	0	3
42	Genotype42	5M	3	66	15SMS	13.5	204.6	0	1
43	Genotype43	5M	3	75.6	20MSS	18	408	3	3+
44	Genotype44	5M	3	126	15SMS	13.5	243	3	2
45	Genotype45	20M	12	336	70S	70	846	3	0
46	Genotype46	10M	6	180	20SMS	18	310.8	3	4
47	Genotype47	20MS	16	204	40S	40	666	3	3+
48	Genotype48	80S	80	1410	Tms	0.8	26.4	1	3+
49	Genotype49	5M	3	141	70S	70	1266	0	2
50	QIMMA-12	40MS	32	831	70S	70	960	3	2
51	Genotype51	15M	9	354	60S	60	1086	2	1
52	Genotype52	5M	3	120	60S	60	606	3	4
53	Genotype53	5SMS	4.5	87	30S	30	459.6	0	3
54	Genotype54	tM	0.6	20	0	0	0	0	3+
55	Genotype55	tMR	0.4	2.4	tM	0.6	14.4	0	0
56	Genotype56	80S	80	1170	80s	80	1470	3	4
57	Genotype57	100S	100	2190	85S	85	1590	3	2
58	Genotype58	20MS	16	372	50S	50	846	3	2
59	Genotype59	10M	6	282	70S	70	672	3	3+
60	Genotype60	60SMS	60	966	80S	80	1446	3	3

……Continue

61	Genotype61	5M	3	120	tMS	0	26.4	3	2
62	Genotype62	40SMS	36	624	95S	95	1836	3	3
63	Genotype63	30MS	24	444	90S	90	1290	4	3
64	Genotype64	10MS	8	156	80S	80	1194	3	3
65	Genotype65	40MS	32	708	70S	70	1290	3	2
66	Genotype66	tMR	0.4	20.4	30S	30	405.6	2	3
67	Genotype67	tMR	0.4	22.8	5MS	4	126	3	2
68	Genotype68	5M	3	108	15MS	12	303	2	0
69	Genotype69	0	0	0	tMR	0.4	8.4	3	0
70	Genotype70	0	0	0	0	0	0	4	0
71	Genotype71	5M	0.4	126	80s	4	1260	2	3+
72	Genotype72	80S	80	1500	80S	80	1686	2	0
73	Genotype73	5M	3	114	5SMS	4.5	99	0	2
74	Genotype74	30MS	24	522	90S	90	930	0	2
75	Atilla-7	50S	50	930	90S	90	1146	3	3+
76	Genotype76	5M	3	141	tMS	0.8	14.4	3	0
77	Genotype77	0	0	0	5SMS	4.5	90.6	2	0
78	Genotype78	0	0	0	0	0	6	0	1
79	Genotype79	5SMS	45	675	90S	90	1956	3	0
80	Genotype80	30SMS	27	492	70S	70	1146	3	3
81	Genotype81	tMR	0.4	24	5MS	4	81.6	3	3
82	Genotype82	60S	60	1092	20S	20	426	2	3^+
83	Genotype83	0	0	0	0	0	0	3	0
84	Genotype84	20SMS	18	165.6	45S	45	900	2	3
85	Genotype85	50SMS	45	732	40S	40	1080	4	0
86	Genotype86	10MSS	9	117.6	30S	30	480	3	0
87	Genotype87	10M	6	186	90S	90	1500	3	3
88	Genotype88	50S	50	756	60S	60	588	0	1
89	Genotype89	20MS	16	324.6	50S	50	930	3	3^+
90	Genotype90	tMR	0.4	3.6	10MSS	9	216	2	3^+
91	Genotype91	5MR	2	114	15MSS	13.5	255	3	2
92	Genotype92	5SMS	4.5	36.6	5SMS	4.5	90.6	3	0
93	Genotype93	5M	3	43.2	10SMS	9	172.8	3	0
94	Genotype94	10M	6	210	30S	30	480	4	0
95	Genotype95	10M	6	58.8	70S	70	726	0	0
96	Genotype96	10M	8	123.6	70S	70	846	3	0
97	Genotype97	10M	6	186	60S	60	906	0	0
98	genotype 98	5M	3	38.4	40S	40	480	4	0
99	Genotype99	10SMS	9	102	70S	70	636	4	0
100	KABOWSH-1	20MS	16	276	60S	60	630	4	0
101	Genotype101	tMR	0.4	12	tM	0.6	13.2	2	0
102	Genotype102	20M	12	177.6	60S	60	1026	4	0
103	Genotype103	0	0	19.2	30S	30	666	2	0
104	Genotype104	10MSS	9	76.8	80S	80	720	2	0
105	Genotype105	5MS	4	48	30S	30	396	3	0
106	Genotype106	10M	6	99.6	50S	50	606	1	0
107	Genotype107	10M	6	55.2	30S	30	462	0	0
108	Genotype108	30S	30	238.8	10MS	8	294	1	0
109	Genotype109	20M	12	474	10S	10	246	3	0
110	Genotype110	20M	12	234	25S	25	366	3	0
111	Genotype111	10M	6	138	20S	20	342	3	0
112	Genotype112	10MR	4	174	20S	20	279.6	3	3
113	Genotype113	5MR	2	144	10MSS	9	222	1	3^+
114	Genotype113	25M	15	486	40S	40	846	3	1
115	Genotype115	10M	4	228	10SMS	9	117.6	3	0
116	Genotype116	5MS	6	36	5MSS	4.5	99	2	2
117	Genotype117	5M	3	81.6	tMS	0.8	30	3	3
118	Genotype118	40MS	32	732	25S	25	501	2	3^+
119	Genotype119	tMR	0.4	24	5MS	4	45.6	1	2
120	Genotype120	tMR	0.4	24	tMS	0.8	15.2	2	0
121	Genotype121	40MS	32	546	25S	25	540	0	0
122	Genotype122	5MR	2	108	10MS	0.8	156	3	3
123	Genotype123	20MS	16	220.8	30S	30	330	1	0
124	Genotype124	100S	100	1890	80S	80	1650	2	0
125	Sids-1	100S	100	2010	50S	50	846	3	0
126	Genotype126	50S	50	960	60S	60	906	0	0

……continue

127	Genotype127	100S	100	2490	95S	95	1890	0	0
128	Genotype128	100S	100	1230	90S	90	1740	1	0
129	Genotype129	80S	80	1230	70S	70	906	4	4
130	Genotype130	5MR	2	72	15MS	12	177.6	3	0
131	Genotype131	tMR	0.4	2.4	0	0	0	0	2
132	Genotype132	tMR	0.4	12	0	0	0	0	1
133	Genotype133	5M	3	42	60S	60	900	0	3^{+}
134	Genotype134	40MS	32	510	80s	80	1326	0	4
135	Genotype135	5MR	2	70.8	10MR	4	105.6	2	3
136	Genotype136	0	0	96	5S	5	150	3	3
137	Genotype137	40MS	32	624	70S	70	1350	3	0
138	Genotype138	0	0	19.2	15S	15	282	2	0
139	Genotype139	20MS	16	198	80S	80	900	3	3
140	Genotype140	10MS	8	156	40S	40	552	3	4
141	Genotype141	5MR	2	108	15S	15	222	0	0
142	Genotype142	60S	60	966	70S	70	966	0	2
143	Genotype143	40MS	32	702	75S	75	1056	2	0
144	Genotype144	100S	100	2280	65S	65	1236	0	1
145	Genotype145	tMR	0.4	27.6	tMS	0.8	26.4	2	0
146	Genotype146	80S	80	942	70S	70	870	3	0
147	Genotype147	10MS	8	156	80S	80	906	2	0
148	Genotype148	40S	40	498	85S	85	840	2	0
149	Genotype149	10M	0.6	192	60S	60	612	3	4
150	Debira	40M	24	414	60S	60	1110	3	0
151	Genotype151	40M	24	780	70S	70	1050	2	2
152	Genotype152	0	0	21.6	0	0	0	1	3
153	Genotype153	tMR	0.4	12	5M	3	66	0	3
154	Genotype154	0	0	0	0	0	0	2	0
155	Genotype155	tMR	0.4	27.6	0	0	0	0	0
156	Genotype156	50MS	40	1230	70S	70	1266	3	2
157	Genotype157	0	0	0	10S	10	192	0	3
158	Genotype158	100S	100	1350	80S	80	1626	0	2
159	Genotype159	30SMS	27	594	65S	65	1350	2	0
160	Genotype160	10MR	4	246	60S	60	786	3	2
161	Genotype161	10M	6	61.2	40SMS	36	492	1	2
162	Genotype162	10M	6	98.4	30MS	24	342	2	2
163	Genotype163	20SMS	18	258	25MSS	22.5	411	2	3
164	Genotype164	tR	0.2	1.2	tMS	0.8	16.4	3	1
165	Genotype165	5M	3	43.2	10MS	8	159.6	0	4
166	Genotype166	30SMS	27	408	40S	40	480	4	3
167	Genotype167	tR	0.2	1.2	tMS	0.8	20.4	3	3^{+}
168	Genotype168	100S	100	1530	30S	30	1890	4	3^{+}
169	Genotype169	0	0	0	tMR	0.4	16.8	4	3
170	Genotype170	0	0	0	tM	0.6	20.2	3	3
171	Genotype171	tR	0.2	1.2	0	0	0	1	1
172	Genotype172	tM	0.6	3.6	15SMS	13.5	297	3	3^{+}
173	Genotype173	tMR	0.4	24	0	0	0	3	3
174	Genotype174	60S	60	1146	70S	70	1020	3	3
175	GOUMRIA-3	100S	100	1770	80S	80	1830	3	3^{+}
176	Genotype176	0	0	0	0	0	0	2	2
177	Genotype177	5M	3	43.2	5MS	4	87.6	0	3
178	Genotype178	20MS	16	366	80S	80	1230	3	3^{+}
179	Genotype179	10MR	4	174	60S	60	978	4	3^{+}
180	Genotype180	0	0	0	0	0	0	0	2
181	Genotype181	15SMS	0	138.6	70S	70	1050	3	3
182	Genotype182	5MR	2	114	15SMS	13.5	303	0	2
183	Genotype183	10MR	4	168	45SMS	40.5	789	0	3
184	Genotype184	tMR	0.4	27.6	0	0	0	0	2
185	Genotype185	40MS	32	672	25S	25	411	4	3
186	Genotype186	tMR	0.4	24	15SMS	13.5	309	3	3
187	Genotype187	40S	90	1446	85S	85	1740	3	3
188	Genotype188	30M	18	528	40S	40	660	0	0
189	Genotype189	tMR	0.4	12	5M	3	63.6	3	4
190	Genotype190	5MR	2	138	tMR	0.4	12	0	3
191	Genotype191	40MS	32	558	25SMS	22.5	465	0	3
192	Genotype192	10MS	8	69.6	50S	50	447.6	3	3
193	Genotype193	0	0	0	tM	0.6	10.8	3	3
194	Genotype194	10MR	4	174	5MS	4	87.6	2	3^{+}
195	Genotype195	tMR	0.4	27.6	tMS	0.8	30	4	4
196	Genotype196	10MR	4	198	15SMS	13.5	297	3+	2
197	Genotype197	20M	12	360	60S	60	1146	3	0
198	Genotype198	10M	6	93.6	70S	70	906	0	4
199	Genotype199	5MR	2	66	25S	25	459	4	0
200	HIDDAB	80S	80	1320	60S	60	1110	4	4

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