

1 **Resistance levels to the cassava green mite, *Mononychellus***
2 ***tanajoa*, in cassava germplasm (*Manihot esculenta*)**

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11

12 **Abstract**

13 The cassava green mite (CGM), *Mononychellus tanajoa* (Acari: Tetranychidae), is one of the
14 main pests of cassava, causing direct damage by sucking the plant's sap. Although the mite
15 has a wide distribution in Latin America and Africa and a high potential to expand to Asia,
16 limited information is available on *M. tanajoa* biology and life history parameters on its
17 primary host. In this study, we quantified the levels of resistance of 10 cassava genotypes
18 (i.e., NAT-31, ALT-12, ALT-6, COL-1505, ECU-72, ECU-160, PER-182, PER-335, 60444,
19 CMC-40) based on the mite's oviposition preference and development time in no-choice and
20 choice bioassays. The genotype NAT-31 significantly differed from other genotypes for *M.*
21 *tanajoa* development time and oviposition rate: each stage of the CGM life cycle appeared to
22 be delayed in NAT-31, suggesting that NAT-31 resistance is mediated through a general
23 reduction of CGM fitness on this genotype. Resistance in the remaining genotypes was
24 variable in comparison to a susceptible (control) genotype. ECU-72, a parental line of NAT-
25 31, present a difference related to oviposition preference, development time and sex ratio.
26 These parameters allow the identification of different levels of resistance (antixenotic and
27 antibiosis) when compared to the susceptible genotype. CGM displayed significantly different
28 oviposition preference from the susceptible genotypes. Identification and characterization of
29 resistance to CGM in cassava germplasm might be key to further advance knowledge about
30 natural resistance mechanisms and develop strategies to introgress resistance to CGM in
31 farmer- and industry-preferred cassava varieties.

32

33 **Key words:** CGM, cassava green mite, cassava, resistance, pest, oviposition

34

35 **Introduction**

36 Cassava (*Manihot esculenta* Crantz, Euphorbiaceae) is a woody perennial shrub originating
37 from South America (Olsen and Schaal, 1999). With a total world production of over 280
38 million tons in 2012, it constitutes an essential source of carbohydrates for about 800 million
39 people in tropical countries (FAO, 2012; FAOSTAT, 2009; Lebot, 2009). In addition to its
40 use in human diets, cassava is widely used as a raw material in processed products as well as
41 for the animal feed, ethanol and starch industries (Anggraini *et al.*, 2009; Balagopalan 2002).

42 Approximately 200 species of arthropod pests are associated with cassava (Bellotti *et*
43 *al.*, 2002, 2010, 2012). Green mites [cassava green mite (CGM), *Mononychellus tanajoa*
44 (Bondar), and *Mononychellus caribbeanae* (McGregor)], whiteflies (*Aleurotrachelus socialis*,
45 *Bemisia tabaci* and *Aleurothrixus aepim*) and mealybugs (*Phenacoccus manihoti*) are among
46 the most important arthropod pests infecting cassava (Parsa *et al.*, 2015; Bellotti, 2002). These
47 pest species, almost all native from the Neotropics, have adapted in various forms to the
48 physical and biochemical defences of the plant, including its leaf pubescence and its
49 laticiferous and cyanogenic compounds (Bellotti and Riis, 1994). Green mites and mealybugs
50 negatively impact cassava yield by feeding on the terminal parts of the plants triggering cell
51 death and reduced photosynthesis (Gomez *et al.*, 2001). Field research has indicated that
52 extended attacks (i.e., between 3 and 6 months) of *M. tanajoa* can cause up to 80% losses in
53 root yields (Bellotti *et al.*, 2012). *Mononychellus tanajoa* attacks are favoured by dry
54 conditions, in unfertile plants, inadequate fertilisation and the presence of weeds (Bellotti *et al.*,
55 2012). Whereas *M. tanajoa* presently affects several of the world's prime cassava-growing
56 areas, climate change and continued global spread have been predicted to further exacerbate
57 mite pest problems in the African rift valley, the Mato Grosso in Brazil, northern South
58 America and Southeast Asia (Herrera *et al.*, 2011). The vast majority of cassava farmers tend
59 to use insecticides to control CGM (CIAT, 2006; Arias, 1995). However, efficacy of spraying
60 against this mite is usually limited, and multiple applications are required to keep CGM
61 populations under control, making the crop economically unsustainable in regions where
62 green mites are endemic (Panda and Khush, 1995). Biological control relying on the use of
63 naturally occurring predators and entomopathogens as well as the deployment of mite-
64 resistant cassava varieties are effective and complementary methods that may be used to
65 manage *M. tanajoa* (Bellotti *et al.*, 2012).

66 Wild relatives of cassava constitute important sources of genes for resistance against
67 cassava arthropod pests (Vargas *et al.*, 2002; Burbano *et al.*, 2007; Carabali *et al.*, 2010a, b;

68 Parsa *et al.*, 2015). Moderate to high levels of resistance to green mites, whiteflies and
69 mealybugs were identified in inter-specific hybrids of *M. esculenta* subsp. (CIAT, 2006;
70 Carabalí *et al.* 2010a, 2013). Furthermore, resistance to CGM was transferred to F₁ inter-
71 specific hybrids, suggesting a simple inheritance of this trait (A. Bellotti and M. Fregene,
72 pers. comm.). However, the long reproductive cycle and lengthy time required to develop new
73 cassava varieties (8-10 years) often discourages the use of wild species in conventional
74 cassava breeding programs (Rudy *et al.*, 2010; Legg *et al.*, 2006). A preliminary assessment
75 by Parsa *et al.* (2015) reported 33 potential sources of resistance to *M. tanajoa* in the cassava
76 germplasm. Robust assessment of resistance levels to CGM in the cassava germplasm as well
77 as identification of different types of resistance are urgently needed to develop and deploy
78 sustainable management of CGM resistance in the field. Characterization of the CGM
79 resistance is also essential to help understanding the associated physiological and phenotypic
80 traits. In the present study we report on the assessment of resistance levels to CGM of selected
81 cassava breeding lines. We used bioassays and measured biological parameters such as
82 oviposition preference, development time and sex ratio to estimate the resistance level and to
83 characterize the impact of resistant cassava host on CGM.

84

85 **MATERIALS AND METHODS**

86 *Plants and mites*

87 The study was conducted in 2012 in glasshouse facilities at the Universidad del Valle
88 (Univalle) in Cali, Colombia ($28 \pm 2^\circ\text{C}$, $70 \pm 5\%$ relative humidity [RH]). Ten genotypes of
89 *M. esculenta* (i.e., NAT-31, ALT-12, ALT-6, COL-1505, ECU-72, ECU-160, PER-182, PER-
90 335, 60444, and CMC-40) were obtained from the CIAT germplasm bank. Genotypes were
91 selected based on their potential or known levels of arthropod resistance/susceptibility (Table
92 1). CMC-40 accession was used as a susceptible control and was also used as host plant for
93 CGM colony maintenance (Bellotti, 2002, Bellotti *et al.*, 2010, 2012). All the genotypes were
94 established *in vitro* and then planted in sterile soil in plastic pots and kept in a glasshouse at
95 $30 \pm 2^\circ\text{C}$ and $70 \pm 5\%$ RH. Plants were irrigated 3× per week and the plants did not receive
96 pesticide or fertilizer applications. Six-month-old plants were used for the bioassays. A stock
97 colony of *M. tanajoa*, isolated in the cassava fields at CIAT (Cali, Colombia), was established
98 and reared on CMC-40 plants under controlled conditions ($28 \pm 2^\circ\text{C}$, $70 \pm 5\%$ RH and
99 L12:D12 photoperiod) for the bioassays. Cassava green mites were placed on fresh cassava
100 plants every 20 days. Hybrid vigor was guaranteed bringing mites from the field every 2
101 months.

102

103 ***Bioassays***

104 Mite performance on the selected genotypes was evaluated using the following biological
105 parameters: host plant selection, oviposition preference, development time and offspring sex
106 ratio. First, in a preliminary trial, the 10 genotypes were screened, followed by a second trial
107 using the five genotypes that were tolerant to CGM attack in the first trial. Due to reduced
108 establishment rate using stem propagation for ALT-6, this genotype was not included in the
109 second screening assay. In all cases, two sets of bioassays (choice and no-choice) were
110 conducted.

111 Oviposition preference assays were based on choice and no-choice tests. The choice
112 assay consisted of facing susceptible CMC-40 (control) genotype with the other nine
113 genotypes in a Petri dish (200 × 15 mm). Lobes of each genotype were placed on top in a
114 circle on foam moistened with water. In the choice assay, the position of the materials in the
115 Petri dish was rotated clockwise, in order to guarantee independence and their random
116 distribution. In the no-choice assays, 10 lobes of the same genotype were placed in a Petri
117 dish. Experimental unit was the Petri dish with 10 lobes in the first assay (in total five Petri
118 dishes, 50 replicates). For the second assay, the experimental unit was the same Petri dish but
119 with five lobes (in total 10 Petri dishes, 50 replicates).

120

121 ***Oviposition preference.*** For the choice assays, a leaf lobe (average length 3 cm) of each
122 genotype was placed on humid foam and then arranged in a circle inside a Petri dish (200 ×
123 15 mm) as shown in Figure 1. Twenty pairs (male and female) of CGM adults, 24 h post
124 emergence, were placed on CMC-40 leaf lobes at the centre of a Petri dish (50 for each
125 genotype, 10 petri dishes with 10 lobes in each of the petri dishes.) (Figure 1A). For the no-
126 choice assays, a similar procedure was followed with 20 pairs of mites per arena placed on
127 CMC-40 leaf discs, but now each Petri dish contained only lobes of a single genotype (Figure
128 1B) (one experimental run in which 20 mite pairs were released within a single Petri dish).

129 Oviposition was evaluated for eight (8) days and estimated as the average number of
130 eggs laid per female on 50 lobes for each genotype (choice assays) and the average number of
131 eggs laid per female on each genotype (no-choice). In each case, this was assessed counting
132 the total number of eggs laid per female during twice observations per day. The two
133 observations did not show statistical differences; hence for the analysis the total diaries were
134 used. The free and non-free preference tests were carried out for 10 and 12 days. Count
135 started from the petiole (upper rib) and continued in the lower part of the rib. The number of

136 eggs at 24h and 48h was compared in order to detect any early difference among genotypes.

137

138 ***Development time and sex ratio.*** Male and female mite adults, obtained from 6-month-old
139 CMC-40 plants, were transferred to the underside of leaf lobes obtained from 6-month-old
140 plants, kept on humid foam inside Petri dishes (200 × 15 mm). The average size of the lobes
141 was 3 cm. After 12 h, the adults were eliminated, and eggs were randomly selected and
142 removed with a needle and a fine brush. Only one egg was left to continue its development
143 until reach adulthood. Observations were done every 2 h recording its physiological stage.
144 Fifty lobes of each genotype were evaluated for egg to adult development time and offspring
145 sex ratio.

146

147 ***Statistical analysis***

148 Differences among the mean values in the no-choice and choice tests on the various
149 genotypes were analysed using one-way ANOVA, followed by Tukey test for multiple mean
150 comparison tests. ANOVA was used to detect differences in fecundity, development time and
151 sex ratios. All analyses used the R statistical program (R Development Core Team, 2014).
152 The level of significance was 5%. All biological parameters evaluated had 50 technical
153 replicates in all assays.

154

155 **RESULTS**

156 ***Oviposition preference***

157 Significant differences were recorded between the numbers of eggs on the 10 genotypes, as
158 compared with CMC-40 (ANOVA $P < 0.0001$, followed by Tukey $P < 0.05$) (Table 2). The
159 oviposition rate ranged from 1.5 ± 0.09 to 27.1 ± 1.98 eggs/8 days for the assessed genotypes
160 (Table 2). Female mites showed the highest oviposition rates on genotype 60444 (27.1 ± 1.98
161 eggs) with average number of eggs approximately twice compared to the susceptible check
162 CMC-40 (14.8 ± 1.02 eggs). NAT-31 and ALT-6 displayed low oviposition rates (1.5 ± 0.09
163 eggs and 3.3 ± 0.16 eggs, respectively, Table 2). Significant differences were recorded among
164 genotypes ($P < 0.05$) at 24h and 48h (Table 2). A group of genotypes (PER-182, 60444,
165 CMC-40) are preferred at 24h while presence of females was substantially delayed on NAT-
166 31, ALT-6, ECU-72, ECU-160.

167 Ten genotypes with contrasting oviposition rates were selected and tested with choice
168 and no choice bioassays. The experiment confirmed the second trial, oviposition rates ranged
169 between 5.34 ± 0.99 and 23.7 ± 4.3 eggs/female/8 days for choice bioassays and 4.4 ± 0.28 and

170 13.34±2.97 eggs/female/8days for no choice bioassays (Tables 2 and 3). Oviposition rates
171 (number of eggs/genotype) on NAT-31 and ALT-6 had, respectively, 79.2% and 82%
172 reduction when compared to the oviposition rate of the susceptible check CMC-40 (Table 2).
173 Significant differences were noted between the numbers of eggs on the four genotypes
174 compared with those on CMC-40 ($P < 0.05$) (Figure 3). Oviposition ranged from 7.9±0.29-
175 35.42±1.21 eggs/8 days in the second choice bioassays and 4.67±0.49-14.03±0.97 eggs/8 days
176 in the no choice bioassay (Tables 2 and 3).

177 In the second bioassay, the oviposition preference for genotypes 60444 (31.11± 1.20
178 eggs) and ECU-72 (35.42± 1.21 eggs) was similar to CMC-40 (29.12± 1.40 eggs) (Tables 2
179 and 3), and NAT-31 remained the least preferred (7.90± 0.29 eggs) (Table 2). There were
180 significant differences in the number of eggs laid on NAT-31 and ALT 6 compared with the
181 susceptible genotype (CMC-40) (Tables 2 and 3) ($P < 0.05$) used as control. The least
182 preferred genotypes in the preliminary trial were NAT-31 (2.2±0.012 eggs) and ALT-6
183 (1.9±0.009 eggs), with 79.2% and 82% reduction in oviposition, respectively (Table 2). In the
184 second trial, genotypes 60444 (14.03±0.97 eggs) and ECU-72 (9.48±0.73 eggs) had higher
185 oviposition rates compared with CMC-40 (7.48±0.66 eggs) (Table 2). As in the preliminary
186 selection, NAT-31 was the green mite least preferred accession (4.67±0.49 eggs). As in the
187 first trial, at no choice assays, female mites preferred oviposit to at 24h and 48h but there were
188 significant differences among genotypes ($P < 0.05$) (Table 2).

189

190 ***Developmental time and sex ratio***

191 Development time on the selected genotypes were similar with the exception of ECU-160, on
192 which *M. tanajoa* had a significantly shorter development time as compared to the other
193 genotypes (Table 4). Despite a relatively homogenous egg-to-adult development time in most
194 genotypes, there were significant differences between genotypes for development time of
195 particular stages. The CMC40 genotype in all experiments and evaluated parameters behaves
196 as a slightly susceptible material when compared to 60444 (Tables 2 and 3; Figures 2 and 3).
197 For this reason, material 60444 was selected as a susceptible material when dealing with pests
198 such as the green mite. The CMC40 material can be compared to 60444, PER335 and ALT12.
199 The genotypes NAT-31, ECU-72 y ALT-12 displayed either reduction or increase in life
200 parameters of the acari. For instance, the developmental times were reduced when exposed to
201 NAT-31 being 1.10±0.15 for protonymph and 0.67±0.09 for deutonymph but increased
202 6.22±0.30 for eggs; ECU-72 reduced 0.0±0.0 the teleiochrysalid stage while increased the
203 larvae (1.55±0.14) and deutonymph (2.27±0.20). Finally, ALT-12 reduced in the egg stage

204 (3.5±0.18) and increased for teleiochrysalid (1.05±0.06) and adults (3.50±0.19). The egg
205 stage on the susceptible check CMC-40 was significantly shorter as compared to resistant
206 genotypes. The short egg stage on CMC-40 was outbalanced by a longer protochrysalide
207 stage (1.85±0.16 d) when compared, for example, to NAT-31 (0.7±0.07 d). On ECU-72, a
208 genotype previously reported to be resistant genotype to pests (Bohórquez, 2009), the egg
209 stage time (3.65±0.13 d) was comparable to the susceptible check CMC-40. The proportion
210 of females (0.9:0.1) was not affected on two of the genotypes; ALT12 and COL1505 (Table
211 4).

212

213 **DISCUSSION**

214 Overall, our results showed that *M. tanajoa* had higher preference for genotype 60444 than
215 CMC-40 (Tables 2 and 3, Figures 2 and 3). CMC-40 has been previously identified as the
216 most susceptible host to arthropod cassava pests (Bellotti, 2002; Burbano, 2007; Bohorquez,
217 2009). The free-choice bioassay proposed in the present study has been instrumental to
218 compare genotype preference. CMC-40 appeared to have properties that render this genotype
219 attractive for female colonization and oviposition. The genotype 60444, a model African
220 variety used in virology and biotech studies (Bull *et al.*, 2009; Anjanappa *et al.*, 2016),
221 displayed even higher preference to green mite as compared to CMC-40.

222 In both choice and no choice assays the permanence had a similar trend and shows
223 contrasting preferences for all accessions. Oviposition preference of free choice assays (Table
224 2) allows us to rank genotypes in seven groups (from highest to lowest) according their
225 suitability to host acari eggs. Thus: 60444; PER-335; ALT-12-CMC-40; COL-1505-ECU-72;
226 PER-182-ECU-160; ALT-6 and NAT31. In contrast, only three groups are identified from no
227 choice assays: 60444 and ECU-160; PER335-PER182-ALT12-COL1505-ECU72 and ALT6-
228 NAT31-CMC40. Thus, in the no choice assay experiment, disregard of the genotype, it was
229 possible to confirm the acari preference to oviposit on a given genotype. Our results indicate
230 60444 as the most preferred genotype while ALT-6 and NAT31 were the less preferred. These
231 results allow us to establish that the chosen accessions for this study were actually a
232 representative sample from the germplasm bank with a high resistance variability affecting
233 green mite fitness. Further work is required in order to identify the chemical and physical
234 barriers of the susceptible and resistance genotypes in the response of the green acari attack.
235 Among the former, pre-formed or constitutive agents could influence the adaptation of the
236 green mite to this genotype; among the latter, secondary metabolites that influence attraction
237 or repellence towards the genotype might be involved in susceptibility (Schoonhoven *et al.*,

238 2005; Dicke and Baldwin, 2010; Piesik *et al.*, 2011). All of these represent important issues to
239 be analysed.

240 Hence, *M. tanajoa* is likely to use diverse strategies for host plant selection than for
241 oviposition. A main strategy is the recognition of host, depending on the physicochemical
242 properties of the surface of the leaves. During this process, mites may stay longer in one
243 genotype than another, without indicating a clear host selection for oviposition. Another
244 possibility is that the mite chooses a genotype exclusively to feed on but another to lay its
245 eggs. This, actually, might represent a protection strategy. NAT-31 and ALT-6 were the least
246 preferred genotypes where the females remain, however the first was more preferred to
247 oviposit than the second (Tables 2, 3).

248 Developmental times in our study were similar to those observed by Yaseen and
249 Bennet (1977) and Yaninek *et al.* (1984). In those studies, the developmental time of *M.*
250 *tanjaja* was inversely proportional to temperature. Additionally, significant differences were
251 present among the cassava genotypes at different stages of development (Table 4). Our study
252 demonstrates a long development time in green mite (11.07-15.10 days) in all the genotypes,
253 being only variable in ECU-160 (Table 4), which was the only genotype showing a significant
254 difference compared to the other genotypes. Despite that no statistically significant difference
255 was detected in the total developmental time of the green acari on the tested genotypes,
256 differences were found when acari stages were analysed suggesting that each genotype exerts
257 an antibiotic mechanism on the immature stages. An analysis of this variability shows that
258 NAT-31, ECU-72 and ALT-12 genotypes appear to influence, either decreasing or increasing,
259 developmental times of three different acari stages when compared to the rest of genotypes
260 (ALT16, PER182, PER335, COL1505 and CMC40). In these cases, only a development stage
261 was the influent, while in ECU160 two stages did. Arias (1995) and Gómez (2004) already
262 reported a high mortality of nymphs when they fed on the ECU-72 material, concluding that
263 the mortality of nymphal instars along with the length of the acari's life cycle are a clear
264 mechanism of antibiosis. In our study, it was observed that ECU-72 increases the time in
265 stages of development such as larvae and deutonymph, while NAT-31 increases the egg stage,
266 which might indicative of the influence of these genotypes by antibiosis at the time of
267 development of the green mite. Table 2 shows the tendencies of genotypes NAT-31 and ALT-
268 6 towards low oviposition as compared to the genotype 60444 which experiences higher
269 levels of infestation. Our results are in agreement with previous observations of the green mite
270 on CMC-40 system developed by Mesa *et al.* (1987) being mite behavior on CMC-40 similar
271 to the parameters of oviposition and developmental time. As in the preliminary trial at both,

272 choice and no choice assays, NAT-31 was identified as the less preferred, while 60444 was
273 the most preferred in terms of green mite oviposition. NAT-31 is the less preferred probably
274 because the disruption of oviposition prevents continuity of the mite progeny (see also
275 Bohórquez, 2009; Carabali *et al.*, 2009). Bohórquez (2009) suggests that NAT-31 shows
276 antibiotic and antixenotic characteristics against *A. socialis*. However, Vargas *et al.* (2002)
277 were the first to report the benefits of NAT-31, a variant of cassava (*M. esculenta*) resistant to
278 whitefly (*A. socialis*) at the Valle Cálido of the Alto Magdalena. It is possible that resistance
279 is due to the lineage as the parents of that genotype are ECU-72 and BRA-12. ECU-72 has
280 previously been shown to be resistant to whitefly (Bohórquez, 2009) and recently reported to
281 have high levels of green mite resistance. Likely, resistance established in the NAT-31
282 genotype comes from one of its parents (ECU-72) whose genes confer resistance to whitefly.
283 Although the heritability of the resistance is unknown, most likely it is governed by several
284 genes (polygenic). Hence, one can speculate that the other parent (BRA-12) presents some
285 level of resistance to arthropods conferring an additive effect to NAT-31. However, there is a
286 need to evaluate the possible resistance of BRA-12 to attack of the green mite. Genotypes
287 ECU-72, ECU-160, PER-182 and PER-335 showed similar trends for mite oviposition
288 preference and oviposition rate. These results mirror previous studies, which suggest that
289 these genotypes are key elements in developing resistance to whiteflies (Burbano *et al.* 2007;
290 Bohórquez, 2009; Carabalí *et al.*, 2010a; 2010b; 2013), of these, NAT-31, ECU-72, 60444
291 genotypes were previously prioritized for in-depth screening (Burbano *et al.*, 2007; Carabalí
292 *et al.* 2010a, b). A particular response exists depending on the type of pest; in the case of
293 green mites, one can hypothesise the capacity of adaptation and the ample host range the pests
294 could prompt their coevolution with cassava. All of this might push the mite to behave in a
295 polyphagous manner. Nevertheless more studies are needed on the host adaptability to
296 *Manihot* relatives to evaluate and confirm the possible polyphagous mite behavior.

297 In all the cassava genotypes, *M. tanajoa* females began to oviposit within the first 24
298 h. Nearly 90-100% of the eggs had been oviposited onto the selected genotypes by the fourth
299 day, (Figures 2 and 3). Since this oviposition rate illustrates the preference of the green mite
300 towards different cassava genotypes, it is plausible to consider that cassava accessions show
301 similar patterns of infestation and defensive responses in the first 24 h. Nevertheless, the high
302 rates of oviposition recorded among the other genotypes were 35% lower than that observed
303 in 60444. *M. tanajoa* females were observed to have high values oviposition preference and
304 oviposition rates on the latter accession (Tables 2, 3 and 4).

305 In our study, NAT-31 displayed short development times for proto- and deutonymph,

306 key stages in the mite's life cycle. ECU-72 and ECU-160 tended to suppress the quiescent
307 stages; hence, variants NAT-31, ECU-72 and ECU-160, suppressing and displaying
308 development times, could possess an antibiosis mechanism that might partially explain
309 various levels of resistance. In all genotypes, except ALT12 and COL1505, the proportion of
310 females (0.9:0.1) was not affected (Table 4), within the established observations on male
311 presented a constant motion seeking female's quiescence states to fertilize. Another feature of
312 the male is to feed very little when compared with females. It is important to note that the
313 females decide which eggs will be male, due in large part to their haplo-diploid condition
314 (Yaninek *et al.*, 1988). Overall, results of the biology and preference for oviposition
315 demonstrate that genotype NAT-31 exhibits resistance to *M. tanajoa*. Further, the different
316 levels of resistance observed in the evaluated genotypes also suggest, variable levels of
317 antixenosis and antibiosis. These findings are due mainly to the development time, suggesting
318 that factor as responsible for the differences established between CMC-40 and the other
319 genotypes. According to Sabelis (1985) changes in development time is the most crucial
320 factor for the growth of mite populations.

321 In conclusion, oviposition preference, development time and sex ratio of the green
322 mite were parameters allowing the identification of different levels of resistance (antixenotic
323 and antibiosis) in the cassava germplasm.

324 Firstly, 60444 was the accession with levels of susceptibility higher than CMC-40
325 previously used in pest-cassava studies as susceptible check. Hence is plausible to conclude,
326 in general, that 60444 can be considered as the most susceptible genotype indicating better
327 adaptation of the mite to this host. The mite possesses a number of characteristics to assist in
328 this behaviour, such as its high mutation rate and its aggregated distribution in the fields via
329 colonies, which greatly reduces genetic crosstalk among organisms and makes resistance
330 dilution difficult (Mesa *et al.*, 1987; Saito *et al.*, 1983). This response needs to be examined at
331 the gene and molecular levels to explain the plant's behaviour. Secondly, NAT-31 showed
332 low population levels of *M. tanajoa*, which might indicate resistance to the green mite. This
333 result could be exploited in genetic improvement programs for assisted selection of resistance
334 to one of the most significant pests in the Americas and Africa (CIAT, 2006). Identification
335 and characterization of accessions highly resistant to green mites will be particularly
336 instrumental to investigate the molecular determinants of the resistance against green mite in
337 cassava. Recent large-scale omics studies in cassava have helped to identify proteins
338 associated with improved traits in cassava (Owiti *et al.*, 2011; Vanderschuren *et al.*, 2014).
339 Similar studies with accessions contrasting for resistance against green mite (*i.e.* 60444,

340 CMC-40, ECU-72 and NAT-31) could lead to the identification of genes, transcripts and
341 protein expression patterns associated with pest resistance.

342

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486

487

488 **Figure captions**

489 **Figure 1.** Design of the (A) choice and (B) no-choice assays for oviposition preference of
490 cassava green mite on leaf lobes of various cassava genotypes. Initially mite responses were
491 screened on leaves of 10 genotypes (left) and subsequently responses were assessed on five
492 genotypes (right) after 1, 2 and 8 days.

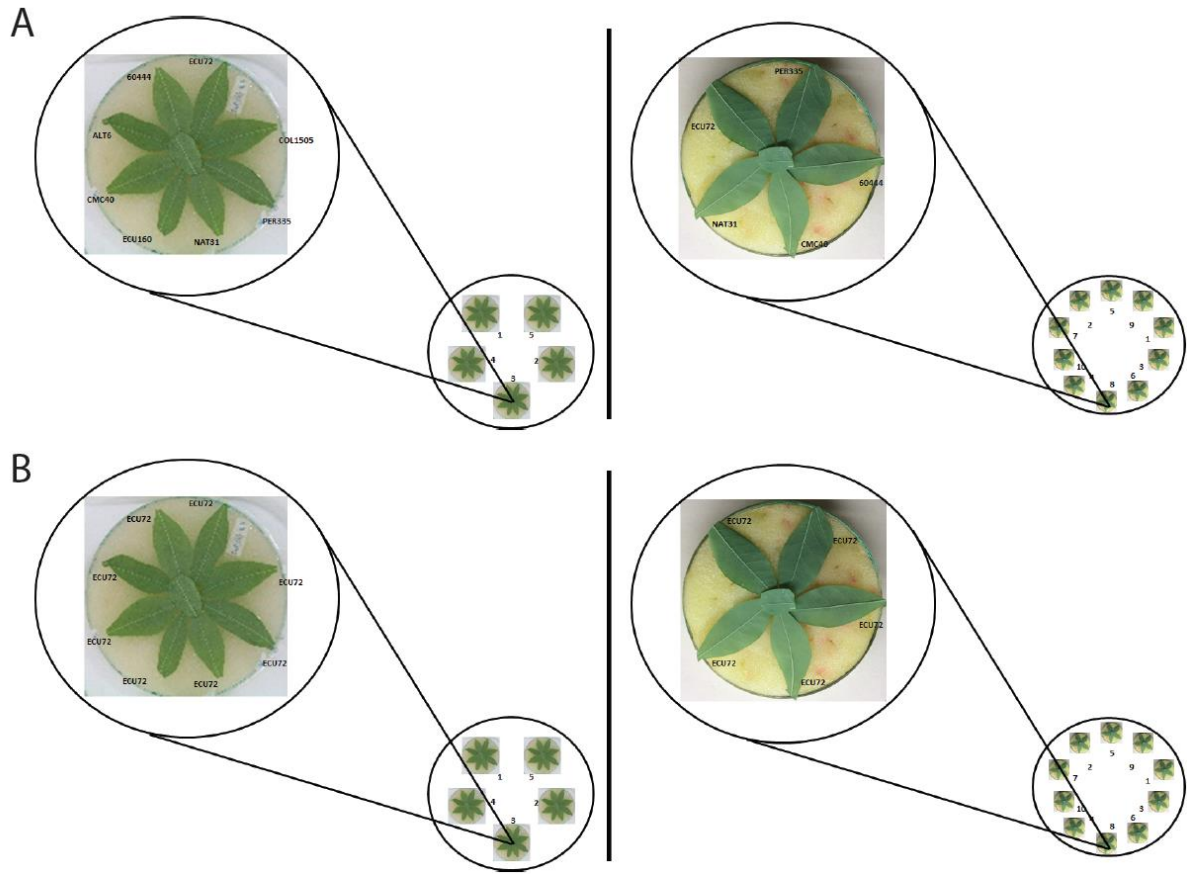
493

494 **Figure 2.** Test to free (A) and not free (B) preference for oviposition in 10 cassava
495 genotypes, first selection. Evaluating in days the preference of the green mite to lay eggs.

496

497 **Figure 3.** Test to free (A) and not free (B) preference for oviposition in 5 cassava genotypes,

498 second selection. Evaluating in days the preference of the green mite to lay eggs.



499

500 **Figure 1**

501

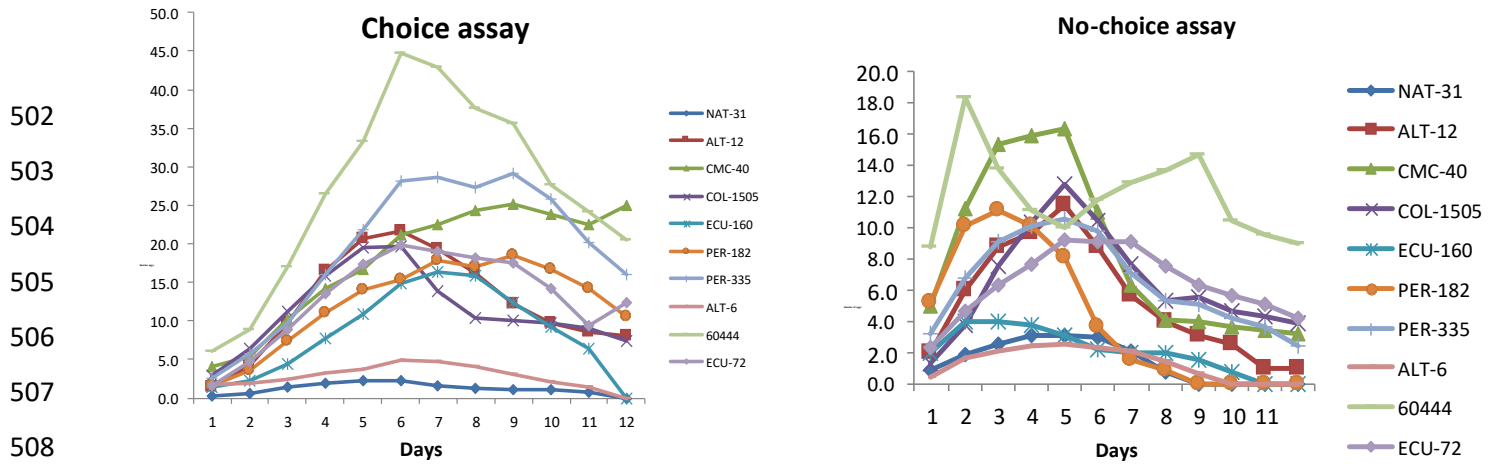


Figure 2

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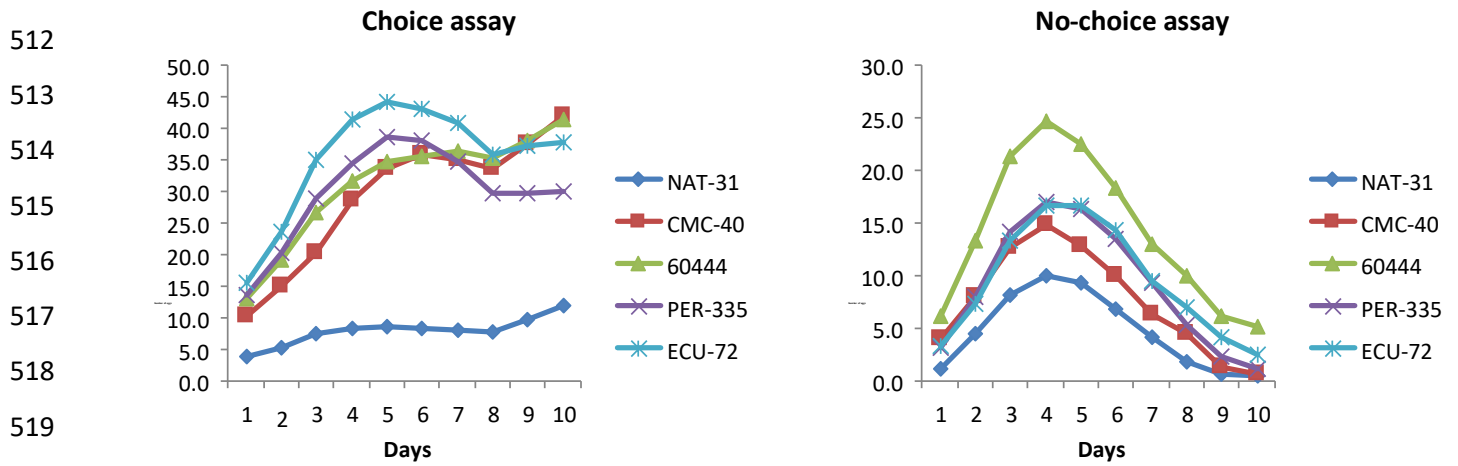


Figure 3

522

523 **Table 1** Recorded cassava genotypes with variable levels of resistance or tolerance to arthropod pests.

Accession	Mites	Whiteflies	Other pests	Resistance/tolerance	References
ALT-6	<i>Mononychellus tanajoa</i>			Tolerance	CIAT, 2004
ALT-12	<i>M. tanajoa</i>			Tolerance	CIAT, 2004
COL-1505	-	-	-	-	-
ECU-72		<i>Aleurotrachelus socialis</i> , <i>Bemisia tabaci</i>		Resistance	Bellotti and Arias, 2001; Gómez, 2004; Carabalí <i>et al.</i> , 2009; Bohorquez, 2009; Omongo <i>et al.</i> , 2012; Parsa <i>et al.</i> , 2015
ECU-160	<i>M. tanajoa</i>			Tolerance	Burbano <i>et al.</i> , 2007
NAT-31 (CG 489-31)		<i>A. socialis</i>		Resistance	Vargas <i>et al.</i> , 2002
PER-182	<i>M. tanajoa</i>			Tolerance	Boaventura <i>et al.</i> , 2006
PER-335	<i>M. tanajoa</i>	<i>A. socialis</i>		Tolerance	Bellotti and Arias, 1981; Boaventura <i>et al.</i> , 2006
60444			<i>Erinnyis ello</i>	Tolerance	Herrera <i>et al.</i> , 2011; CIAT, 2004

524

525 **Table 2** Choice assay for oviposition preference of *Mononychellus tanajoa*: mean (\pm SE) number of eggs laid after 24 and 48 h and preference for oviposition
 526 measured by no. eggs/genotype and average oviposition rate (N=500).

Accession	First trial				Second trial	
	No. eggs after 24 h	No. eggs after 48 h	No. eggs after 8 days	Oviposition rate (no. eggs/ Per day and per females)	No. eggs after 8 days	Oviposition rate (no. eggs/ Per day and per females)
60444	6.14 \pm 7.93 ^a	8.88 \pm 11.93 ^a	27.1 \pm 1.98 ^a	9.9 \pm 0.27 ^a	31.11 \pm 1.20 ^a	19.12 \pm 3.25 ^a
PER-335	2.66 \pm 4.32 ^{bc}	5.7 \pm 9.0 ^b	17.5 \pm 1.39 ^{ab}	12.6 \pm 0.3 ^{ab}	29.72 \pm 1.04 ^a	20.16 \pm 3.67 ^a
PER-182	1.6 \pm 3.2 ^{cd}	3.54 \pm 6.62 ^{bc}	11.0 \pm 0.81 ^{bcd}	2.9 \pm 0.19 ^{bcd}	-	-
ALT-12	1.44 \pm 2.43 ^{cd}	4.16 \pm 5.57 ^{bc}	13.7 \pm 1.01 ^b	2.74 \pm 0.27 ^b	-	-
ALT-6	1.8 \pm 3.07 ^{cd}	1.86 \pm 3.05 ^{cd}	3.3 \pm 0.16 ^{cd}	0.8 \pm 0.005 ^{cd}	-	-
COL1505	2.84 \pm 5.6 ^{bc}	6.32 \pm 9.86 ^{ab}	12.4 \pm 0.79 ^{bc}	2.8 \pm 0.34 ^{bc}	-	-
ECU-160	1.46 \pm 4.15 ^{cd}	2.32 \pm 4.6 ^{cd}	9.2 \pm 0.81 ^{bcd}	2.3 \pm 0.08 ^{bcd}	-	-
NAT-31	0.28 \pm 0.9 ^d	0.62 \pm 1.74 ^d	1.5 \pm 0.09 ^d	0.42 \pm 0.03 ^d	7.90 \pm 0.29 ^b	5.34 \pm 0.99 ^b
ECU-72	1.54 \pm 2.89 ^{cd}	4.7 \pm 7.97 ^{bc}	12.9 \pm 0.93 ^{bc}	3.2 \pm 0.31 ^{bc}	35.42 \pm 1.21 ^a	23.70 \pm 4.3 ^a
CMC-40	4.0 \pm 5.8 ^b	5.46 \pm 6.1 ^b	14.8 \pm 1.02 ^b	3.7 \pm 0.14 ^b	29.12 \pm 1.40 ^a	14.92 \pm 2.26 ^a
F	6.948	4.6985	10.851		7.7825	
d.f.	9 - 490	9 - 490	9 - 490		4 - 245	
P	<1.855e ⁻⁰⁹ ***	<5.331e ⁻⁰⁶ ***	1.889e ⁻¹⁵ ***		6.412e ⁻⁰⁶ ***	

527 Means within a column followed by the same letter are not significantly different (Tukey's HSD test: P>0.05).

528

529 **Table 3** No-choice assays for oviposition preference of *Mononychellus tanajoa*: mean (\pm SE) number of eggs laid after 24 and 48 h and preference for
 530 oviposition measured by No. eggs/genotype and average oviposition rate of *M. tanajoa* a no-free choice (N=500).

Accession	First trial				Second trial	
	No. eggs after 24 h	No. eggs after 48 h	No. eggs after 8 days	Oviposition rate (no. eggs/Per day and per females)	No. eggs after 8 days	Oviposition rate (no. eggs/ Per day and per females)
60444	8.73 \pm 13.7 ^a	18.3 \pm 34.73 ^a	12.5 \pm 0.38 ^e	4.5 \pm 0.96 ^e	14.03 \pm 0.97 ^a	13.34 \pm 2.97 ^a
PER335	3.2 \pm 3.53 ^{bcd}	6.8 \pm 6.86 ^{bcd}	7.7 \pm 0.34 ^{ef}	2.2 \pm 0.3 ^{ef}	9.02 \pm 0.80 ^{ab}	7.96 \pm 1.83 ^{ab}
PER-182	5.2 \pm 6.87 ^b	10.1 \pm 17.53 ^{bc}	6.3 \pm 0.53 ^{ef}	1.7 \pm 0.49 ^{ef}	-	-
ALT-12	1.96 \pm 3.03 ^{cd}	6.0 \pm 7.37 ^{bcd}	7.0 \pm 0.41 ^{ef}	1.4 \pm 0.4 ^{ef}	-	-
ALT-6	0.43 \pm 1.22 ^d	1.63 \pm 2.41 ^d	1.9 \pm 0.009 ^f	0.5 \pm 0.11 ^f	-	-
COL1505	1.33 \pm 2.41 ^d	3.73 \pm 4.32 ^{cd}	7.4 \pm 0.5 ^{ef}	1.6 \pm 0.24 ^{ef}	-	-
ECU-160	2.0 \pm 3.73 ^{cd}	3.96 \pm 4.95 ^{cd}	4.0 \pm 0.0 ^e	1.0 \pm 0.19 ^f	-	-
NAT-31	0.9 \pm 1.9 ^d	1.83 \pm 2.37 ^d	2.2 \pm 0.12 ^f	0.62 \pm 0.09 ^f	4.67 \pm 0.49 ^b	4.4 \pm 0.28 ^b
ECU-72	2.3 \pm 2.84 ^{bcd}	4.66 \pm 5.94 ^{bcd}	7.0 \pm 0.32 ^{ef}	1.8 \pm 0.24 ^{ef}	9.48 \pm 0.73 ^{ab}	7.3 \pm 1.41 ^{ab}
CMC-40	4.96 \pm 7.93 ^{bc}	11.2 \pm 12.83 ^b	2.2 \pm 0.12 ^f	0.5 \pm 0.009 ^f	7.48 \pm 0.66 ^{ab}	7.98 \pm 1.69 ^{ab}
F	6.5079	4.8212	4.3402		3.3728	
d.f.	9 - 290	9 - 290	9 - 290		5 - 294	
P	1.904e ^{-08 ***}	5.179e ^{-06 ***}	2.545e ^{-05 ***}		0.005596 **	

531 Means within a column followed by the same letter are not significantly different (Tukey's HSD test: P>0.05).

532

533 **Table 4.** Time development per stages and proportion of *Mononychellus tanajoa* on selected cassava genotypes (n=50).

Accession	Egg	Larvae	Protochrysalid	Protonymph	Deutochrysalid	Deutonymph	Teleiochrysalid	Adult	Egg-adult development time	Proportion of females
NAT-31	6.22±0.30 ^a	0.95±0.14 ^{abc}	0.77±0.07 ^{bcd}	1.10±0.15 ^c	1.05±0.11 ^{ab}	0.67±0.09 ^d	0.55±0.07 ^b	2.42±0.25 ^b	13.75±0.59 ^a	0.87 ^a
ALT-12	3.5±0.18 ^c	1.25±0.12 ^{abc}	1.05±0.07 ^{bc}	1.55±0.12 ^{bc}	1.02±0.05 ^{ab}	1.60±0.14 ^b	1.05±0.06 ^a	3.50±0.19 ^a	14.52±0.21 ^a	0.55 ^b
ALT-6	4.32±0.25 ^{bc}	1.05±0.14 ^{abc}	0.60±0.09 ^{cd}	2.87±0.11 ^a	1.0±0.07 ^{ab}	1.67±0.09 ^{ab}	0.07±0.05 ^c	2.47±0.21 ^{ab}	14.07±0.28 ^a	0.87 ^a
COL-1505	5.82±0.19 ^a	1.12±0.21 ^{abc}	1.07±0.16 ^{bc}	1.67±0.18 ^{bc}	1.25±0.13 ^{ab}	0.92±0.12 ^{cd}	0.50±0.10 ^b	2.25±0.25 ^b	14.62±0.35 ^a	0.66 ^b
PER-182	5.57±0.22 ^a	0.67±0.08 ^c	1.02±0.07 ^{bc}	1.27±0.11 ^c	1.17±0.10 ^{ab}	0.85±0.09 ^{cd}	0.50±0.07 ^b	2.15±0.25 ^b	13.22±0.40 ^a	0.90 ^a
PER-335	6.27±0.33 ^a	0.72±0.12 ^{bc}	0.45±0.10 ^d	2.22±0.23 ^{ab}	1.10±0.14 ^{ab}	0.90±0.11 ^{cd}	0.10±0.05 ^c	2.75±0.25 ^{ab}	14.52±0.38 ^a	0.85 ^a
ECU-72	3.65±0.13 ^{bc}	1.55±0.14 ^a	1.20±0.19 ^b	1.42±0.09 ^c	0.92±0.09 ^{ab}	2.27±0.20 ^a	0.0±0.0 ^c	2.32±0.28 ^b	13.35±0.54 ^a	0.90 ^a
ECU-160	4.0±0.21 ^{bc}	1.40±0.18 ^{ab}	0.80±0.08 ^{bcd}	1.30±0.14 ^c	0.80±0.10 ^b	1.72±0.23 ^{ab}	0.0±0.0 ^c	1.05±0.19 ^c	11.07±0.58 ^b	0.82 ^a
60444	6.12±0.06 ^a	1.30±0.14 ^{abc}	0.85±0.12 ^{bcd}	1.55±0.18 ^{bc}	1.30±0.10 ^a	0.95±0.09 ^{cd}	0.75±0.09 ^{ab}	2.27±0.18 ^b	15.10±0.28 ^a	0.77 ^a
CMC-40	4.52±0.18 ^b	1.45±0.20 ^a	1.85±0.16 ^a	1.32±0.15 ^c	1.15±0.13 ^{aba}	1.35±0.14 ^{bc}	0.15±0.05 ^c	2.55±0.25 ^{ab}	14.35±0.31 ^a	0.75 ^a
F	29.67	6.034	12.67	5.172	1.667	32.8	18	5.137		
d.f.	9 - 30	9 - 30	9 - 30	9 - 30	9 - 30	9 - 30	9 - 30	9 - 30		
P	1.5e ⁻¹² ***	8.21e ⁻⁰⁵ ***	5.16e ⁻⁰⁸ ***	0.000292 ***	0.141	3.96e ⁻¹³ ***	8.46e ⁻¹⁰ ***	0.000308 ***		

534 Means within a column followed by the same letter are not significantly different (Tukey's HSD test: P>0.05).