PHENOTYPIC CHARACTERIZATION OF THE RUDÁ x AND 277 COMMON BEAN RIL POPULATION

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Populations composed by recombinant inbred lines (RIL) are very useful to develop genetic linkage maps. Keep the genetic structure of these populations over the generation advancement is important to develop accurate and reliable linkage maps. The existence of genetic variability within those populations is essential for detection of the significant association between molecular markers and loci controlling quantitative or qualitative traits. For this reason, the main objective of this work was to quantify the phenotypic diversity of the RIL population derived from crosses between Rudá and AND 277, a potential new core mapping population for common bean.

As described by Sanglard *et al.* (2013), F_2 plants derived from the cross Rudá x AND 277 were conducted under greenhouse condition up to the F_{10} generation using the single seed descent (SSD) method to obtain the RIL population. In this work, a group of 393 RIL's, the parents, and five commercial control cultivars were screened in the field, in a 20 x 20 triple lattice design, for seven quantitative traits. Because of the low efficiency of the lattice, the data were analyzed in randomized blocks with additional treatments (parents) with three replications. The genetic dissimilarity of the RIL's and parents was estimated by the Mahalanobis generalized distance (D^2). The Tocher agglomerative method was used to group the genotypes into clusters of dissimilarity.

The RIL effect was significant for all evaluated traits ($P < 0.01$), showing the existence of genetic variability in this population. The RIL's *vs* parents contrast was significant for the traits number of days to flowering (DF), days to harvest (DH), grain yield (YLD), and weight of 100 seeds (W100), but no significant for architecture of plants (ARC), seed flattening (H), and seed shape (J). The significance of the mentioned contrasts indicates that the phenotypic mean of RIL's differs from the mean of the parent cultivars. Coincidence between these means is expected only in the absence of epistasis. Thus, these results indicate the occurrence of additive x additive epistatic interactions for DF, DH, YLD and W100. Heritability values for the evaluated traits ranged from 82.81 to 97.09%. The 393 RIL's were grouped into 10 different groups based on the Tocher agglomerative method, using the Mahalanobis generalized distance indexes (Table 1). The traits that most contributed to the genetic dissimilarity were W100 and DF, while ARC was the less one. In geral, it was observed that the population formed by the 393 RIL's (Rudá x AND 277) presented genetic variability for all evaluated traits, what is essential for detecting associations between these traits and molecular markers in coming up efforts of genetic mapping and QTL analysis.

REFERENCES

Sanglard *et al*. (2013) Rudá x AND 277 RILs: a potential new core mapping population for common bean. *Annual Report of the Bean Improvement Cooperative* 56:23-24.

Table 1. Clustering of 393 RIL's (Rudá x AND 277) and parent cultivars of common bean obtained by the Tocher agglomerative method based on the Mahalanobis generalized distance indexes.

Cluster	N[1]	Rudá x AND 277 RIL's (ID Code: UFV-RA)
I	329	34 106 223 354 94 78 147 57 97 344 301 5 83 329 115 289 7 173 2 287 376 359 4 357 196 185 215 163 193 213 22 145 246 8 88 89 132 39 253 197 25 272 384 232 347 342 91 60 211 381 84 76 201 337 310 130 353 139 131 269 41 318 181 280 160 43 221 36 126 268 12 50 70 283 53 28 149 27 205 202 326 317 325 52 349 373 291 166 46 65 87 251 62 167 298 188 273 81 15 379 74 44 1 189 276 146 24 371 48 80 104 29 255 161 294 154 285 346 172 47 334 295 218 42 388 13 119 231 300 77 314 240 361 293 250 236 331 93 10 111 284 351 116 308 31 303 368 73 151 239 237 123 142 169 216 281 33 96 207 262 171 254 174 103 316 156 319 49 124 138 90 19 82 137 26 122 358 121 217 134 21 92 292 32 263 370 17 369 153 341 264 219 233 11 377 150 30 203 6 279 85 71 14 305 313 112 177 9 100 374 117 247 378 392 206 58 278 304 228 311 56 327 40 186 257 212 155 222 296 282 178 190 141 101 140 175 309 307 258 364 133 393 290 363 210 176 37 338 199 345 183 227 336 238 105 383 328 302 180 179 113 120 61 324 195 200 184 356 45 389 267 157 67 18 3 64 252 72 107 209 164 274 129 391 271 330 367 386 16 321 339 192 109 375 312 230 229 198 158 352 118 382 385 286 98 55 244 372 260 59 136 54 220 306 235 226 99 38 102 51 148 182 159 362 320 214 256 315 355
II	16	95 162 143 108 245 288 114 20 266 333 350 204 69 135 225 35
III	7	66 265 348 323 380 168 187 Rudá
IV	2	297 387
V	31	152 194 366 275 241 208 125 332 75 248 335 249 299 234 242 340 261 224 170 343 322 365 390 128 68 191 79 243 86 165 259
VI	3	23 110 63
VII	2	144 270
VIII	1	127
IX	1	360
X	1	277
XI	-	AND 277

[1]Number of RIL's in each cluster.