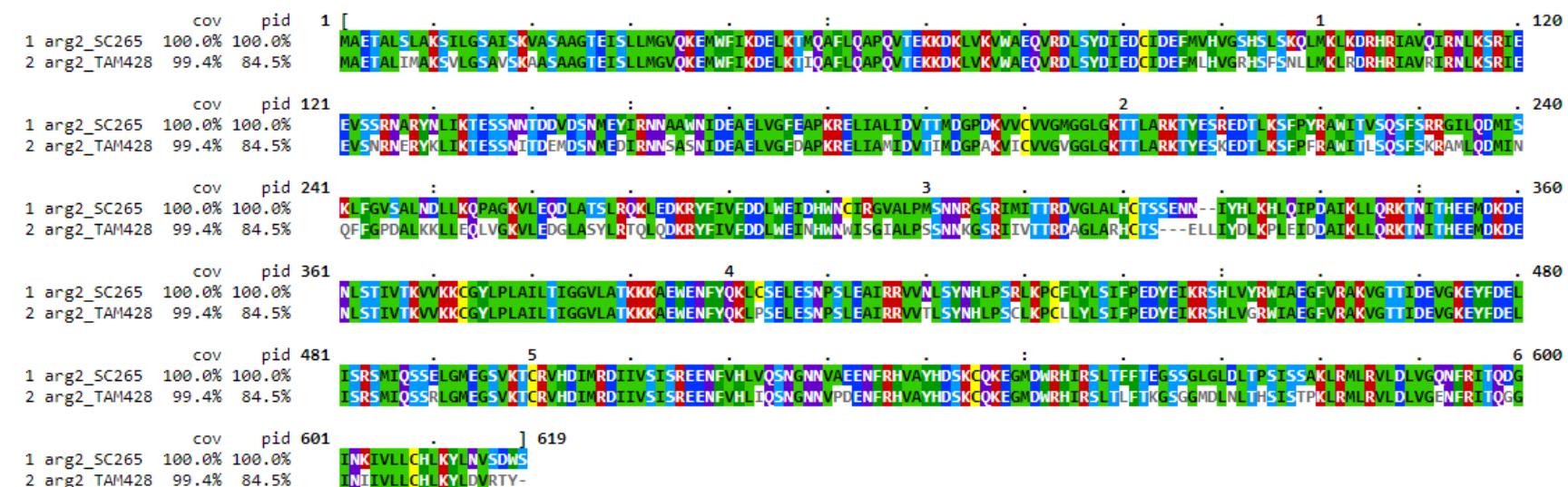**Supplemental_file_2_Demeke_thesis - two alignments of the deduced amino acid sequences of *ARG2* that correspond to pages 55 and 56 in the main thesis file.**

Alignment 1

The mutant *arg2* allele in TAM428 carries carry about 15% non-synonymous amino acids in the shortest ORF as compared to that of SC265 that carries another premature stop codon in a different position.

```
              cov     pid    1 [                                                                                                      1                . 120
1 arg2_SC265  100.0% 100.0%    MAETALSLAKSILGSAISKVASAAGTEISLLMGVQKEMWFIKDELKTKQAFLQAPQVTEKKDKLVKWAEQVRDLSYDIEDCIDEFMVHVGSHSLSKQLMKLKDRHRIAVQTRNLKSRIE
2 arg2_TAM428 99.4%  84.5%    MAETALIMAKSVLGSAVSKAASAAGTEISLLMGVQKEMWFIKDELKTIQAFLQAPQVTEKKDKLVKWAEQVRDLSYDIEDCIDEFMLIVGRHSFSNLLMKLRDRHRIAVRIRNLKSRIE

              cov     pid  121                                                                                                      2                . 240
1 arg2_SC265  100.0% 100.0%    EVSSRNARYNLIKTESSNNTDDVDSNKEYIRNNAAWNIDEAELVGFEAPKRELIALIDVTTKDGPDKVVCVVGMGGLGKTTLARKTYESREDTLKSFPYRAWITVSQSFSRRGILQDMIS
2 arg2_TAM428 99.4%  84.5%    EVSNRNERYKLIKTESSNITDEMDSNKEDIRNNSASNIDEAELVGFDAPKRELIAMIDVTIKDGPAKVICVVGVGGLGKTTLARKTYESKEDTLKSFPFRAWITLSQSFSKRAMLQDMIN

              cov     pid  241                                                                                                      3                . 360
1 arg2_SC265  100.0% 100.0%    KLFGVSALNDLLKQPAGKVLEQDLATSLRQKLEDKRYFIVFDDLWEIDHWNCIRGVALPMSNNRGSRIMITTRDVGLALHCTSSENN---IYHLKHLQIPDAIKLLQRKTNITHEEKDKDE
2 arg2_TAM428 99.4%  84.5%    QFFGPDALKKLLEQLVGKVLEDGLASYLRTQLQDKRYFIVFDDLWEINHWNWISGIALPSSNNKGSRIIVTTRDAGLARICTS---ELLIYDLKPLEIDDAIKLLQRKTNITHEEKDKDE

              cov     pid  361                                                                                                      4                . 480
1 arg2_SC265  100.0% 100.0%    NLSTIVTKVVKKCGYLPLAILTIGGVLATKKKAEWENFYQKLCSELESNPSLEAIRRVVNLSYNHLPSRLKPCFLYLSIFPEDYEIKRSHLVYRWIAEGFVRAKVGTTIDEVGKEYFDEL
2 arg2_TAM428 99.4%  84.5%    NLSTIVTKVVKKCGYLPLAILTIGGVLATKKKAEWENFYQKLPSELESNPSLEAIRRVVTLSYNHLPSCLKPCLLYLSIFPEDYEIKRSHLVGRWIAEGFVRAKVGTTIDEVGKEYFDEL

              cov     pid  481                                            5                                                        6 600
1 arg2_SC265  100.0% 100.0%    ISRSMIQSSELGMEGSVKTCRVHDIMRDIIVSISREENFVHLVQSNGNNVAEENFRHVAYHDSKCQKEGMDWRHIRSLTFFTEGSSGLGLDLTPSISSAKLRMLRVLDLVGQNFRITQDG
2 arg2_TAM428 99.4%  84.5%    ISRSMIQSSRLGMEGSVKTCRVHDIMRDIIVSISREENFVHLIQSNGNNVPDENFRHVAYHDSKCQKEGMDWRHIRSLTLFTKGSGGMDLNLTHSISTPKLRMLRVLDLVGENFRITQGG

              cov     pid  601           ] 619
1 arg2_SC265  100.0% 100.0%    INKIVLLCHLKYLNVSDWS
2 arg2_TAM428 99.4%  84.5%    INIIVLLCHLKYLDVRTY-
```

Alignment 2 – corresponds to the second paragraph on pages 55 and 56 in the main thesis document.

The two ARG2 amino acid sequence types [as the resistance allele in SC328C and mutant allele in BTx623] are highly divergent though both types maintain the complete ORF.

Dissertation, Demeke Mewa Bayable, Department of Botany and Plant Pathology - Purdue University (December 2020)

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7 arg2_Malisor84-7  98.5%  82.0%   LNIIVLLCHLKYLDVRTYWSTLYSLPSDIGKLHGLQILNIGYTYITTLPTQLTKLEDLRAIRCDRNFP-NYLDPDEPVHCLFATLRLPILLADSKSRDRAIGDLHMGCSSGWSRTSRNGV
8 arg2_BTx623       98.5%  82.0%   LNIIVLLCHLKYLDVRTYWSTLYSLPSDIGKLHGLQILNIGYTYITTLPTQLTKLEDLRAIRCDRNFP-NYLDPDEPVHCLFATLRLPILLADSKSRDRAIGDLHMGCSSGWSRTSRNGV

                     cov    pid   721          .           :           .           :           .           .           8           .           .           840
1 ARG2_SC382C      100.0% 100.0%  RVPRGIGNLKELQILESVDIRRTSSKAVKELGELTRIRKLAIGTDWASKKKCKILCKSIEKISSIRSLTVRAGEHQGRGLGWLISSSSPPPHLRSLSLYCYIGEMTDWFRNLTHLVKIFL
2 ARG2_SbRio       100.0% 100.0%  RVPRGIGNLKELQILESVDIRRTSSKAVKELGELTRIRKLAIGTDWASKKKCKILCKSIEKISSIRSLTVRAGEHQGRGLGWLISSSSPPPHLRSLSLYCYIGEMTDWFRNLTHLVKIFL
3 ARG2_Keller      100.0% 100.0%  RVPRGIGNLKELQILESVDIRRTSSKAVKELGELTRIRKLAIGTDWASKKKCKILCKSIEKISSIRSLTVRAGEHQGRGLGWLISSSSPPPHLRSLSLYCYIGEMTDWFRNLTHLVKIFL
4 ARG2_SC237       100.0% 100.0%  RVPRGIGNLKELQILESVDIRRTSSKAVKELGELTRIRKLAIGTDWASKKKCKILCKSIEKISSIRSLTVRAGEHQGRGLGWLISSSSPPPHLRSLSLYCYIGEMTDWFRNLTHLVKIFL
5 arg2_ICSV745      98.5%  82.0%  RVPRGIGNLKELQILERVDIRRTSSNAVKELGELTRIRKLATGTTGASKKKCKILCESIEKISSIRSLTVWAGENQDRGLGWLISSSSPPPHLRSLMLSCYIGEMTDWFRNLTHLVKLSL
6 arg2_IS8525       98.5%  82.1%  RVPRGIGNLKELQILERVDIRRTSSNAVKELGELTRIRKLATGTTGASKKKCKILCESIEKISSIRSLTVWAGENQDRGLGWLISSSSPPPHLRSLMLSCYIGEMTDWFRNLTHLVKLSL
7 arg2_Malisor84-7  98.5%  82.0%  RVPRGIGNLKELQILERVDIRRTSSNAVKELGELTRIRKLATGTTGASKKKCKILCESIEKISSIRSLTVWAGENQDRGLGWLISSSSPPPHLRSLMLSCYIGEMTDWFRNLTHLVKLSL
8 arg2_BTx623       98.5%  82.0%  RVPRGIGNLKELQILERVDIRRTSSNAVKELGELTRIRKLATGTTGASKKKCKILCESIEKISSIRSLTVWAGENQDRGLGWLISSSSPPPHLRSLMLSCYIGEMTDWFRNLTHLVKLSL

                     cov    pid   841          :           .           :           .           .           9           .           .           960
1 ARG2_SC382C      100.0% 100.0%  YKSQLKEDKTMEILGELPKLMLLRIDYHAY---LGDKLVFGTGAFLNLRTLEIWDSMDNLKEIRFEEGASRQMERIEINFCILKSGIIGVKHLPCIKVISLTG-SKVARLGMLEEEVNAH
2 ARG2_SbRio       100.0% 100.0%  YKSQLKEDKTMEILGELPKLMLLRIDYHAY---LGDKLVFGTGAFLNLRTLEIWDSMDNLKEIRFEEGASRQMERIEINFCILKSGIIGVKHLPCIKVISLTG-SKVARLGMLEEEVNAH
3 ARG2_Keller      100.0% 100.0%  YKSQLKEDKTMEILGELPKLMLLRIDYHAY---LGDKLVFGTGAFLNLRTLEIWDSMDNLKEIRFEEGASRQMERIEINFCILKSGIIGVKHLPCIKVISLTG-SKVARLGMLEEEVNAH
4 ARG2_SC237       100.0% 100.0%  YKSQLKEDKTMEILGELPKLMLLRIDYHAY---LGDKLVFGTGAFLNLRTLEIWDSMDNLKEIRFEEGASRQMERIEINFCILKSGIIGVKHLPCIKVISLTG-SKVARLGMLEEEVNAH
5 arg2_ICSV745      98.5%  82.0%  WDSQLKEDKTMEILGELPKLMLLRI-Y--FRASLGEKLVFGTGAFLNLRTLEIWN-MDGLKEIRFEEGTSRQMERIEINFCNLKSGIIGVKHLLCIKVISL-GDSTVARLGMLEEEVNTH
6 arg2_IS8525       98.5%  82.1%  WDSQLKEDKTMEILGELPKLMLLRI-Y--FRASLGEKLVFGTGAFLNLRTLEIWN-MDGLKEIRFEEGTSRQMERIEINFCNLKSGIIGVKHLLCIKVISL-GDSTVARLGMLEEEVNTH
7 arg2_Malisor84-7  98.5%  82.0%  WDSQLKEDKTMEILGELPKLMLLRI-Y--FRASLGEKLVFGTGAFLNLRTLEIWN-MDGLKEIRFEEGTSRQMERIEINFCNLKSGIIGVKHLLCIKVISL-GDSTVARLGMLEEEVNTH
8 arg2_BTx623       98.5%  82.0%  WDSQLKEDKTMEILGELPKLMLLRI-Y--FRASLGEKLVFGTGAFLNLRTLEIWN-MDGLKEIRFEEGTSRQMERIEINFCNLKSGIIGVKHLLCIKVISL-GDSTVARLGMLEEEVNTH

                     cov    pid   961          .           .           .           0           .           .         ] 1030
1 ARG2_SC382C      100.0% 100.0%  LNRPVLRLQEDRSYHGLGDLEGS-----HAE---VEATESIPDHAGEISQVITPTTTNSEIQPASSstop
2 ARG2_SbRio       100.0% 100.0%  LNRPVLRLQEDRSYHGLGDLEGS-----HAE---VEATESIPDHAGEISQVITPTTTNSEIQPASSstop
3 ARG2_Keller      100.0% 100.0%  LNRPVLRLQEDRSYHGLGDLEGS-----HAE---VEATESIPDHAGEISQVITPTTTNSEIQPASSstop
4 ARG2_SC237       100.0% 100.0%  LNRPVLRLQEDRSYHGLGDLEGS-----HAE---VEATESIPDHAGEISQVITPTTTNSEIQPASSstop
5 arg2_ICSV745      98.5%  82.0%  LNHPVLRLSDDRSYHDLEDVEGSPMRRWKQQNPFL----TMP--AREISQVITPTTTNSEIQTASSstop
6 arg2_IS8525       98.5%  82.1%  LNHPVLRLSDDRSYHDLEDVEGSPMRRWKQQNPFL----TMP--AREISQVITPTTTNSEIQTASSstop
7 arg2_Malisor84-7  98.5%  82.0%  LNHPVLRLSDDRSYHDLEDVEGSPMRRWKQQNPFL----TMP--AREISQVITPTTTNSEIQTASSstop
8 arg2_BTx623       98.5%  82.0%  LNHPVLRLSDDRSYHDLEDVEGSPMRRWKQQNPFL----TMP--AREISQVITPTTTNSEIQTASSstop
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