Supplementary Information

Genetic comparisons of fall armyworm populations from 11 countries spanning sub-Saharan Africa provide insights into strain composition and migratory behaviors.

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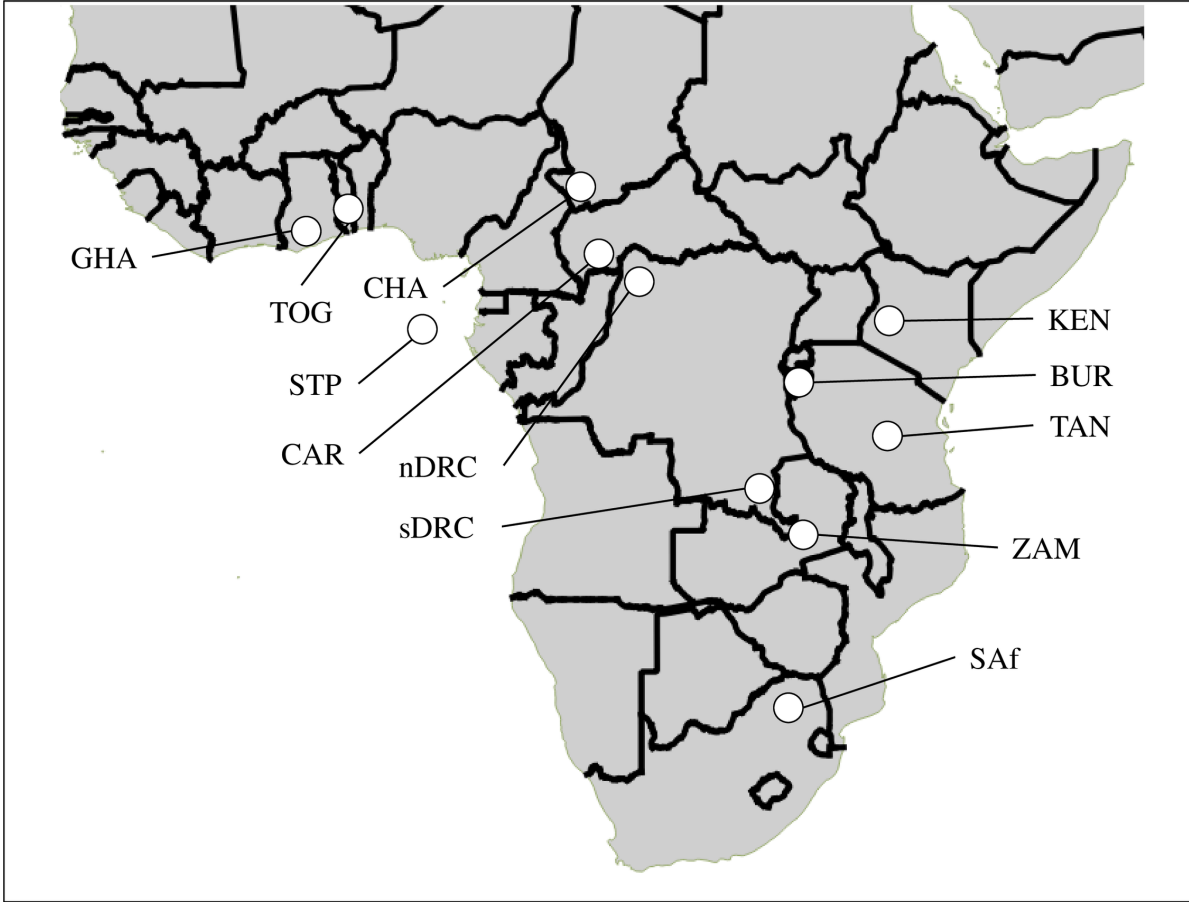
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Supplementary Figure legends

Supplementary Figure S1. Map of collection sites in Africa described in Table 1.

Supplementary Figure S2. Description of the COIB polymorphisms and the haplotypes observed in African fall armyworm. The consensus Western Hemisphere *COI*-CS (WHCOI-CS) and *COI*-RS (WHCOI-RS) sequences are in dark bold. The six COIB haplotypes observed in Africa are listed with two in the *COI*-CS and four in the *COI*-RS categories. Strain-specific polymorphisms are indicated by bold lettering. Differences within strain categories are denoted by dark bold. Sites polymorphic in the consensus are indicated by the IUPAC symbol R, which indicates a G or A alternative. Asterisk identifies site used for strain identity.

Supplementary Figure S3. Descriptions of the *Tpi* gene segments used in the fall armyworm analysis. Numbered locations indicate relevant polymorphic sites. A, haplotype sequences in the TpiE4 segment are shown with WHTpiR and WHTpiC the consensus sequences for the strain-specific *Tpi* haplotypes derived from Western Hemisphere data. Asterisks identify strain-specific polymorphic sites defined by Western Hemisphere populations. Note that site 165 is strain-specific in the Western Hemisphere but not in Africa. Dark and bold lettering indicate differences from the reference sequences. B, the six TpiI4 haplotypes found in Africa. Letters in dark bold identify polymorphisms. Site 131 was associated with consistently poor sequence quality and so was assumed to be the consensus G for all specimens. Dark triangle indicates insertion site in TpI4Ca1b of a 200-bp insertion.

Supplementary Figure S1

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                       1125                                          1164*              1176
                       |                                             |                  |
WHCOI-CS    CATTTCCATTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGRGGATTTATTCAT
COI-CSa1    CATTTCCTTTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGGGGATTTATTCAT
COI-CSa2    CATTTCCTTTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGAGGATTTATTCAT
WHCOI-RS    CATTTCCACTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGTGGATTTATTCAC
COI-RSa1    CATTTCCACTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGTGGATTTATTCAC
COI-RSa2    CATTTCCATTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGTGGATTTATTCAC
COI-RSa3    CATTTTCACTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGTGGATTTATTCAC
COI-RSa4    CATTTCCACTATGTTTTATCAATAGGAGCTGTATTTGCTATTTTAGGTGGATTTATTCAC

                   1182                1197                     1216
                   |                   |                        |
WHCOI-CS    TGATACCCATTATTTACTGGGTTATCTTTAAATCCTTATTTATTAAAAATTCAATTTTTT
COI-CSa1    TGATACCCATTATTTACTGGGTTATCTTTAAATCCTTATTTATTAAAAATTCAATTTTTT
COI-CSa2    TGATACCCATTATTTACTGGGTTATCTTTAAATCCTTATTTATTAAAAATTCAATTTTTT
WHCOI-RS    TGATATCCATTATTTACTGGATTATCTTTAAATCCTTAATTATTAAAAATTCAATTTTTT
COI-RSa1    TGATATCCATTATTTACTGGATTATCTTTAAATCCTTAATTATTAAAAATTCAATTTTTT
COI-RSa2    TGATATCCATTATTTACTGGATTATCTTTAAATCCTTAATTATTAAAAATTCAATTTTTT
COI-RSa3    TGATATCCATTATTTACTGGATTATCTTTAAATCCTTAATTATTAAAAATTCAATTTTTT
COI-RSa4    TGATATCCATTATTTACTGGATTATCTTTAAATCCTTCATTATTAAAAATTCAATTTTTT

                                                           1287
                                                           |
WHCOI-CS    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGRTT
COI-CSa1    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGGTT
COI-CSa2    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGGTT
WHCOI-RS    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGATT
COI-RSa1    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGATT
COI-RSa2    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGATT
COI-RSa3    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGATT
COI-RSa4    ATTATATTTATCGGAGTAAATTTAACTTTCTTCCCACAACATTTTTTAGGATT
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Supplementary Figure S2

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A. TpiE4          129             144                          165* 168*         180 183*        192     198
                   |               |                             \  |  /          \  |  /         |       |
       WHTpiR: TGGCAGCAACTGGGACAAGGTCGTACTAGCTTATGAACCTGTCTGGGCTATTGGCACTGGAAAGACYGCCACYCCA
       TpiRa1: TGGTAGCAACTGGGACAAAGTCGTACTAGCTTATGAACCCGTCTGGGCTATTGGGACTGGAAAGACCGCCACCCCA


       WHTpiC: TGGCAGCAACTGGGACAAGGTCGTACTAGCTTATGAACCCGTTTGGGCTATTGGCACCGGAAAGACYGCCACYCCA
       TpiCa1: TGGCAGCAACTGGGACAAGGTCGTACTAGCTTATGAACCCGTTTGGGCTATTGGCACCGGAAAGACCGCCACCCCA
       TpiCa2: TGGCAGCAACTGGGACAAGGTCGTACTAGCTTATGAACCCGTTTGGGCTATTGGCACCGGAAAGACTGCCACTCCA




B. TpiI4             28 29 31     38              53 55  58            70      77  80  84  87
                      \ / /        |               \ |  /             |        |   |   |   |
     TpiRa1a  TTAATTTGTTTTATAAAAATGCAGGATAAAAAATG---CATGCAAATCTTTATTGGTATTAAAAGTTTACTTCCATAATCTTG
     TpiCa1a  TTAATTTGTTTTAT--AAATAAACGATAAACAATGATACATGCAAATCTTGATTGGTATTAAAAGTTTACTTACATGATCTTG
     TpiCa1b  TTAATTTGTTTTAT--AAATAAACGATAAACAATGATACATGCAAATCTTGATTGGTATTAAAAGTTTACTTACATGATCTTG
     TpiCa2a  TTAATTTGTTTTAT--AAATAAAGGATAAAAAATGATACATGCAATTATTTATTGGTATTAACAGTTTATTTACATGATTTTG
     TpiCa2b  TTAATTTGTTTTAT--AAATAAAGGATAAAAAATGATACATGCAATTATTTATTGGTATTAACAGTTTATTTACATGATTTTG
     TpiCa2C  TTAATTTGTTTTAT--AAATAAAGGATAAAAAATGATACATGCAATTATTTATTGGTATTAACAGTTTATTTACATGATCTTG

                    96                               131  136           148     155          167 171
                     |                                |    |             |       |            |   |
     TpiRa1a  AACTGTGCTTATCTAGTAAATAGTGTTTAGAATTTAATCAGAATTGGTTTCAGTAATCAGTATGCTATTTAAAACCCATATG
     TpiCa1a  AACTGTGCTTATCTAGTAAATAGTGTTTAGAATTTAATCAGAATTGGTTTCAGTAATCAGTATGTTATTTAAAACCTATAGG
     TpiCa1b  AACTGTGCTTATC▼TAGTAAATAGTGTTTAGAATTTAATCAGAATTAGTTTCAGTAATCAGTATGTTATTTAAAACCTATAGG
     TpiCa2a  AACTGCGCTTATCTAGTAAATAGTGTTTAGAATTTAATCAGAATTGGTTTCAGTAATAAGTATGTTATTTAAAACCTATAGG
     TpiCa2b  AACTGCGCTTATCTAGTAAATAGTGTTTAGAATTTAATCAGAATTGGTTTCAGTAATCAGTATGTTATTTAAAACCTATAGG
     TpiCa2C  AACTGTGCTTATCTAGTAAATAGTGTTTAGAATTTAATCAGAATTGGTTTCAGTAATCAGTATGTTATTTAAAACCTATAGG


     TpI4Ca1b insertion(▼):  TCTATTATATAAAAATAAGTCGGGTTTTCCTTCCTGACGCTATAACTCCAGAATGCACGAACCGATT
                             TCCACGGTTTTGCATCCGTTGGAAAGGTCTCGGGCTCCGTGAGGTTTATAGCAAAGAAAATTCCGGA
                             TTAAAAAAAAAGCACGAGGACACTGAAAATCATTGGTGGCGAAACGGGGTTCGCCGGGTTTGCTAG
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Supplementary Figure S3