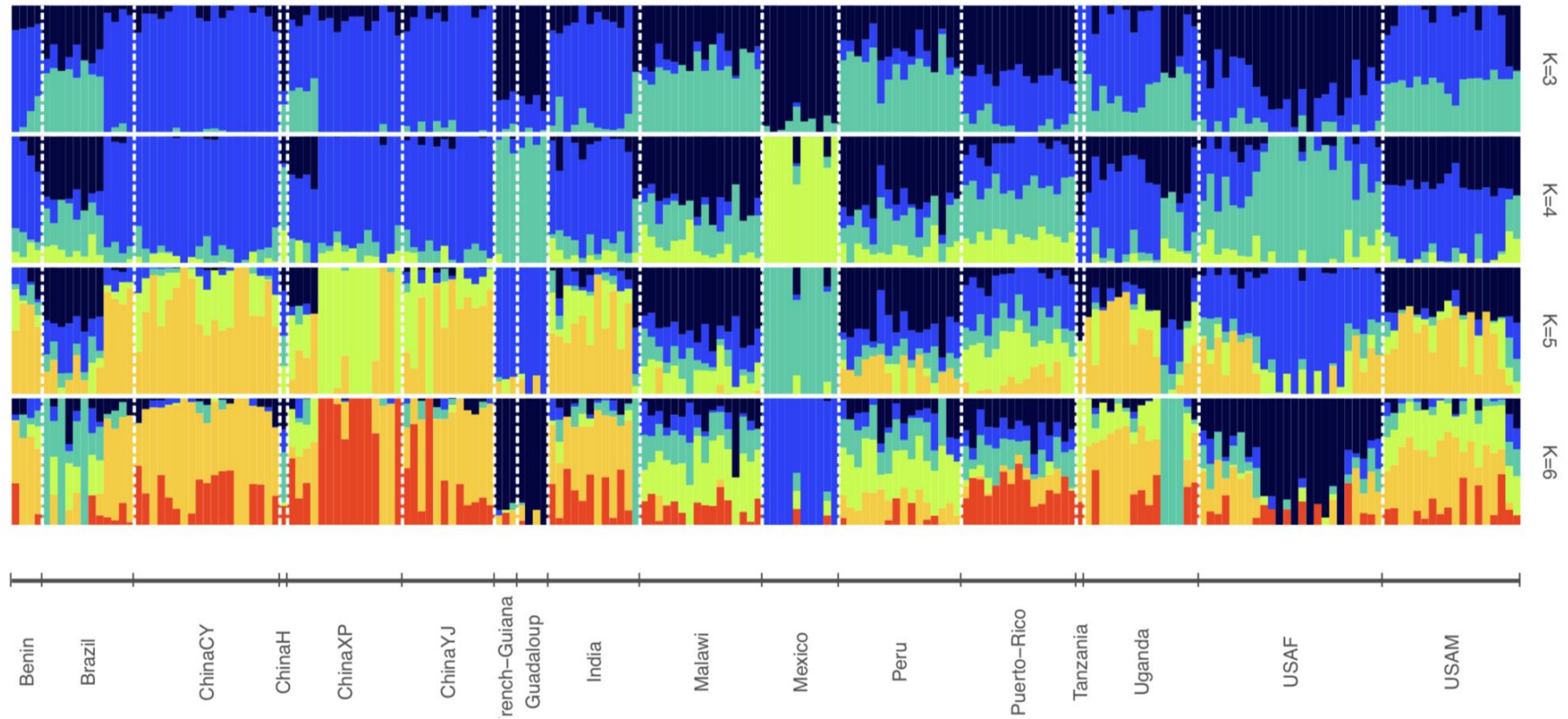


Global population genomic signature of *Spodoptera frugiperda* (fall armyworm) supports complex introduction events across the Old World

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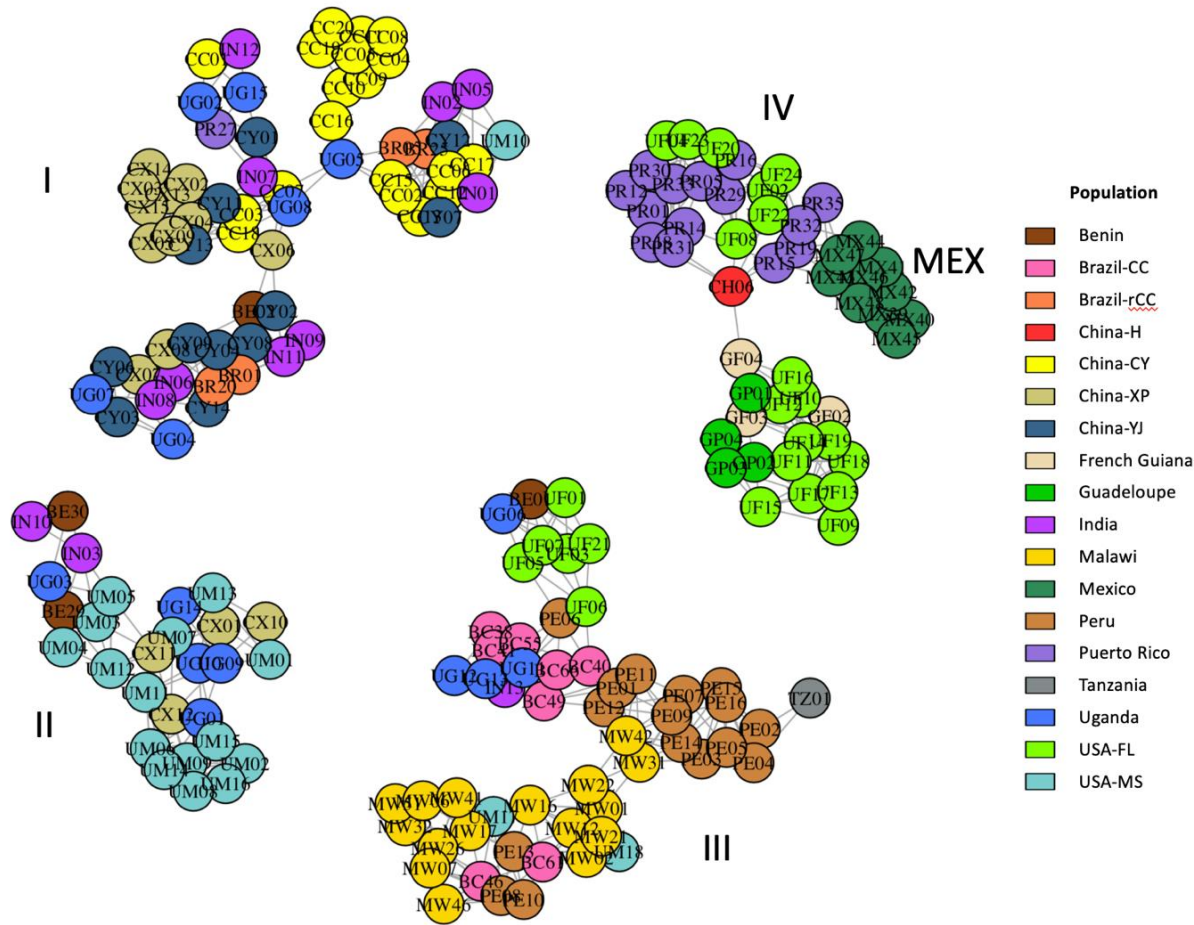
(a) Native and invasive *Spodoptera frugiperda* admixture analysis



Supplementary Figure 1: (a) Admixture analysis based on 870 unlinked and neutral genome-wide SNPs for FAW populations from both native (North, Central, South Americas) and invasive (Africa, Asia) ranges. The Mexican population represents the only New World native FAW population with most individuals having non-admixed genome patterns, and where all individuals also have the corn mitogenome haplotype.

	TPI	mtDNA
MX39	Green	Green
MX40	Yellow	Green
MX41	Green	Green
MX42	Green	Green
MX43	Green	Green
MX44	Green	Green
MX45	Green	Green
MX46	Green	Green
MX47	Green	Green
MX48	Green	Green

(b) Mitochondrial DNA genome and *Tpi* gene characterisation of Mexican FAW, showing one individual also have the rice *Tpi* signature (yellow colour cell). Corn mitochondrial genome and *Tpi* gene are in green colour.



Supplementary Figure 2: Maximum Likelihood (ML) network showing individuals belonging to the populations as given in the legend. The network was drawn using the plotAdmixture function in the R package NetView^{1,2}, and is based on a ML distance matrix calculated from the IQ-Tree shown in Fig. 3. using the R package ape³. The four major clusters, I – IV, correspond to those shown in the tree. Individuals are identified by country codes as follows: China XP (CX), China YJ (CY), China CY (CC), China CH06 (CH), India (IN), Uganda (UG), Tanzania (TZ), Malawi (MW), Benin (BE), Brazil CC (BC), Brazil rCC (BR), Peru (PE), French Guiana (GF), Mexico (MX), Guadeloupe (GP), Puerto Rico (PR), USA-Florida (UF), and USA-Mississippi (UM). See Supplementary Data 1 for complete information about the individuals.

Supplementary References

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