The importance of alternative host plants as a source of infestation in Kenyan French bean production areas

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Introduction

Western Flower Thrips (*Frankliniella occidentalis*) (WFT) is an important pest of French beans (*Phaseolus vulgaris*) in Kenya. Knowledge about issues such as gene flow between host plants and possible speciation processes can help to improve control strategies against WFT. But so far little is known about WFT population structure in Kenyan French bean production areas.

Research Questions

• Are weeds sources for infestation of French beans by WFT?

• Is there population structuring on the different host plants in French bean production areas?

• How strong is gene flow between WFT populations from different host plants?
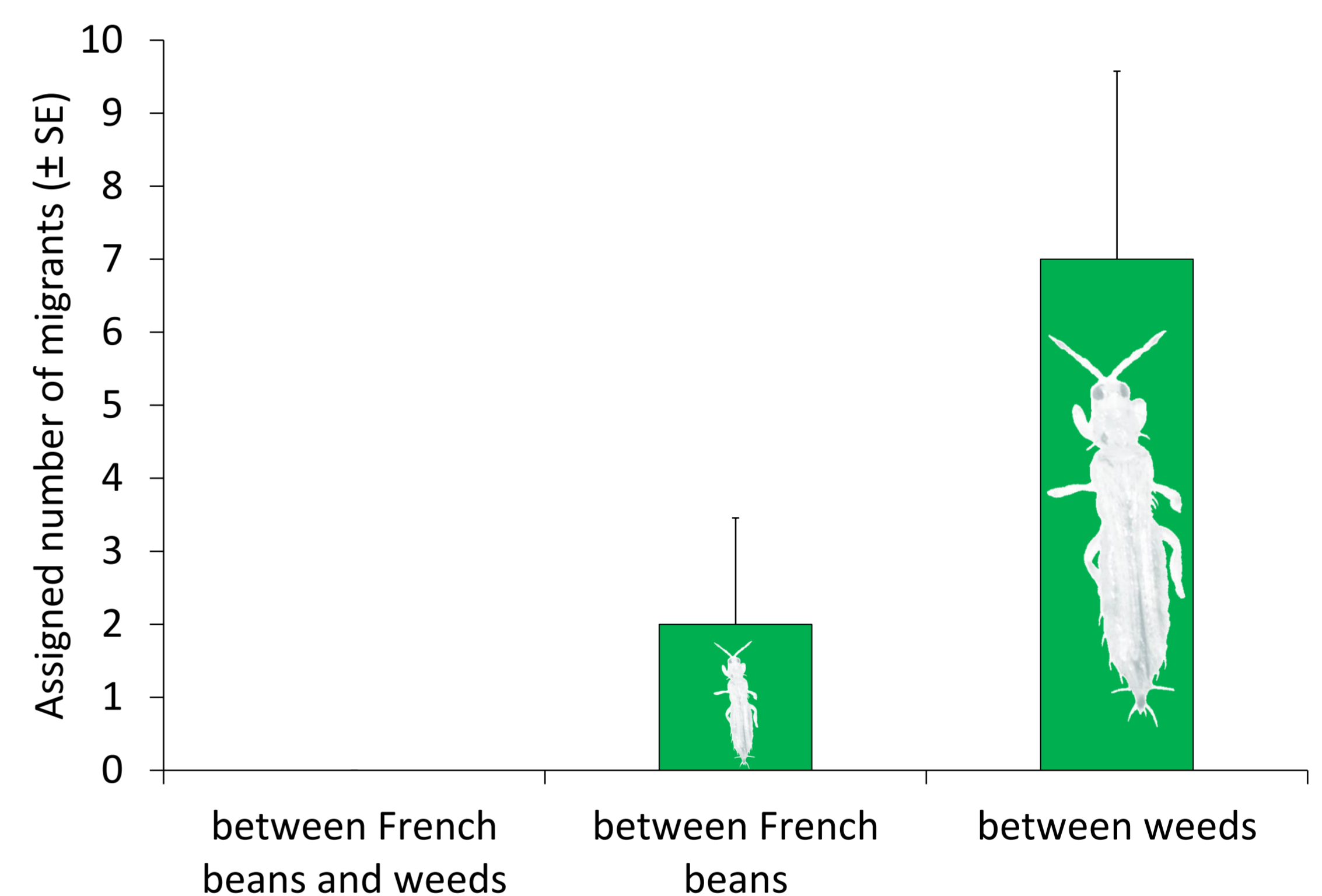
Conclusions

The results from several analyses all suggest that WFT populations from weeds and French beans are well separated with little genetic exchange, i.e. there is considerable population structuring. Reasons for this could be a different suitability of host plants and altered preferences of WFT biotypes for host plant species, leading to a certain degree of specialisation. For plant protection strategies the results indicate that weeds seem to be unimportant as a source of WFT infestations in French beans.
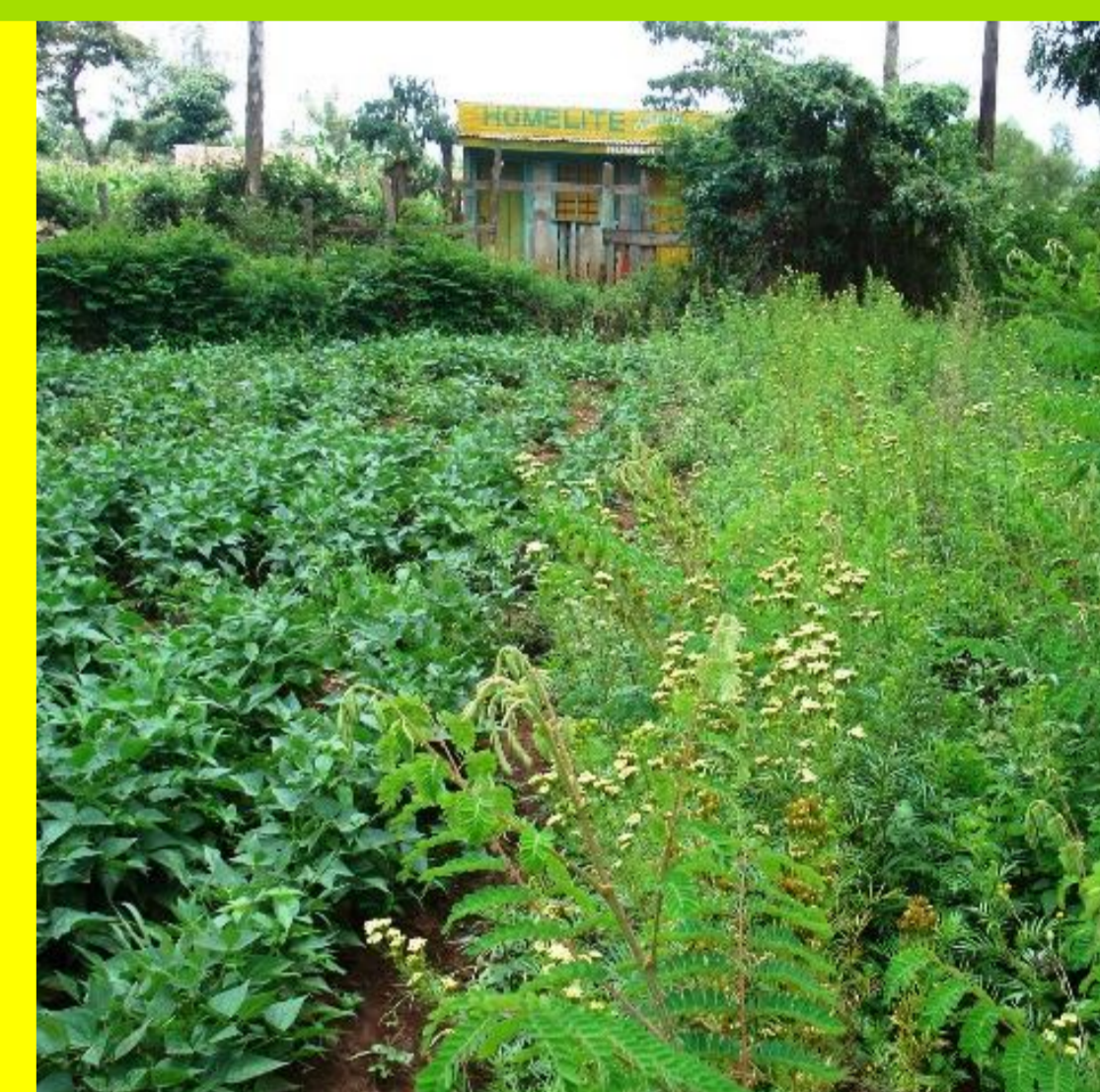
Results

• Considerable and highly significant population structuring (global F_{ST} = 0.253, p = 0.00693)

• AMOVA (Tab. 1): with two predefined groups 12 % of the total genetic variance attributable to host plant (weeds or French beans) could be explained (p = 0.02653)

• Assignment test (Fig. 1): no migrants between weed and French bean populations, a few among bean populations and several among weed populations

• Neighbor-joining tree (Fig. 2): clear separation of WFT populations collected on different host plants

Fig. 1: Migrants between potential source populations as detected by an assignment test (exclusion threshold = 0.01; Monte Carlo resampling; 1000 simulated individuals).

Tab. 1: Analysis of molecular variance (AMOVA) of *F. occidentalis* samples from Kenyan French bean production areas. Two groups (weeds and French beans) were defined a priori.

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among groups	1	738.443	10.29145	12.07
Among populations within groups	12	2448.652	11.31131	13.27
Within populations	168	10695.053	63.66103	74.66
Total	181	13882.148	85.26379	100.00
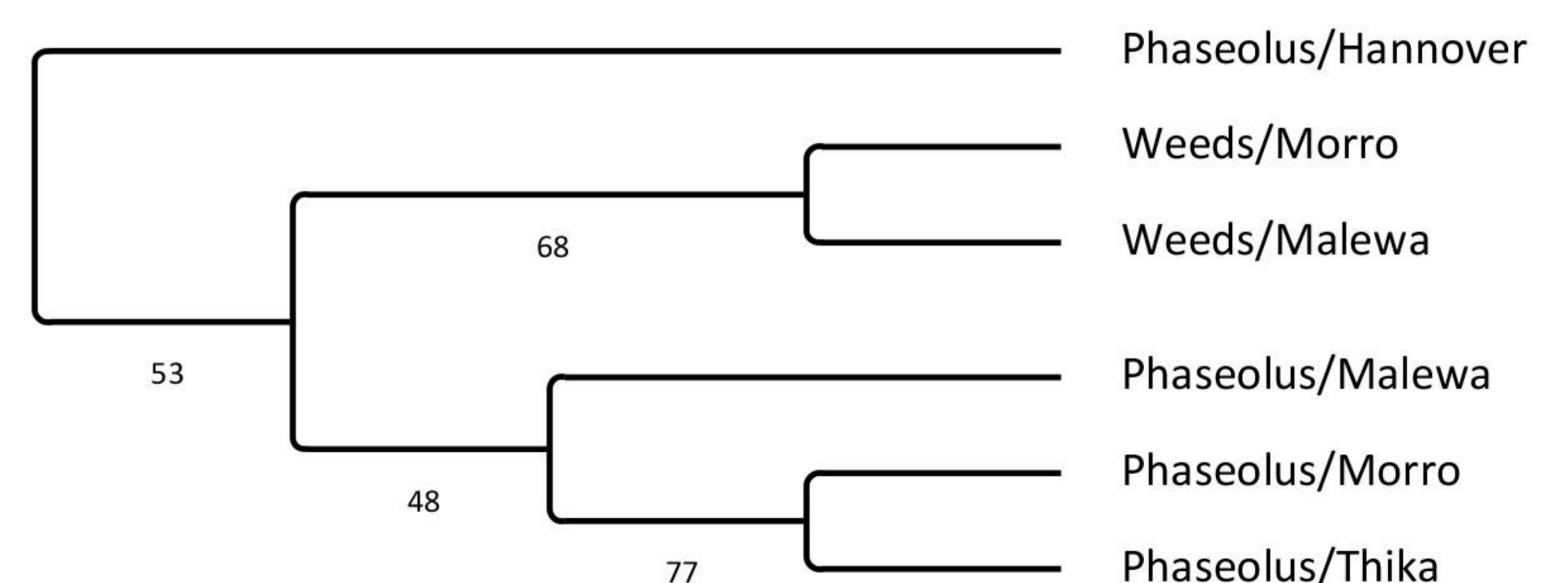
Fig. 2: Unrooted NJ-Tree based on Nei's genetic distance (D_A) between Kenyan WFT populations which were pooled by vicinity and host plant populations. Numbers indicate bootstrap support (1000 bootstraps). Hannover = Outgroup.

Experimental Design

• WFT collection: 7 different sites; on French beans and 4 weed species (*Galinsoga parviflora, Sesbania sesban, Nicandra physaloides, Amaranthus hybridus*); 2 Kenyan provinces, key growing areas of French beans

• Genotyping: 101 WFT females; 6 microsatellite loci (Yang et al. 2012)

• Data analysis: Populations 1.2.32 (genetic distance), Arlequin 3.5.1.3 (AMOVA) and Geneclass2 (partly Bayesian assignment test); individuals from adjacent sites pooled by host plant (i.e. weeds, beans)