# A high throughput multi-locus insecticide resistance marker panel for tracking resistance emergence and spread in *Anopheles gambiae*

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Electronic Supplementary Material

Supplementary figures and tables
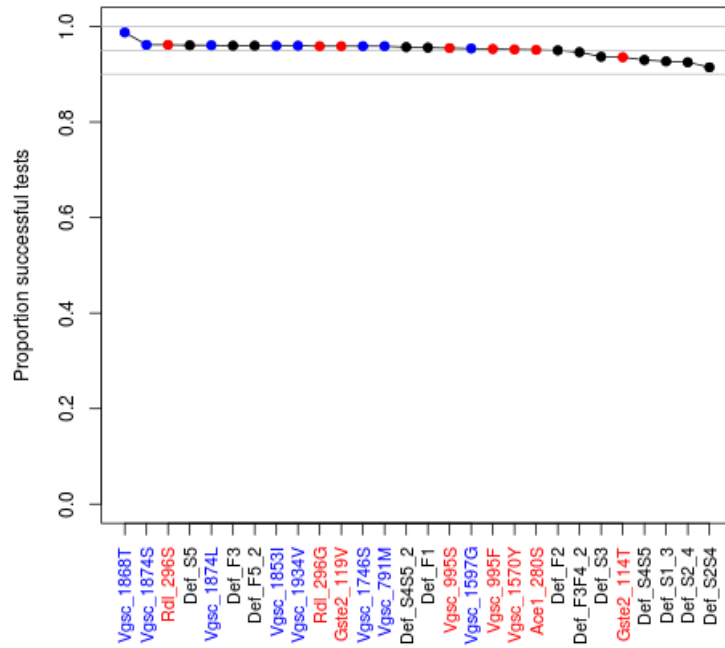
Fig. S1: Success rate of individual SNP assays in the multiplex sequenome assay was never lower than 90% (measured as the proportion of assays that were of high enough quality to give a genotype call). Red points indicate known resistance variants, blue points indicate variants found on the background of some *kdr* mutations and which may therefore be associated with either increased resistance or compensation for the costs of the *kdr* mutations, black points indicate SNPs used to distinguish between *kdr* mutant haplotype backgrounds.
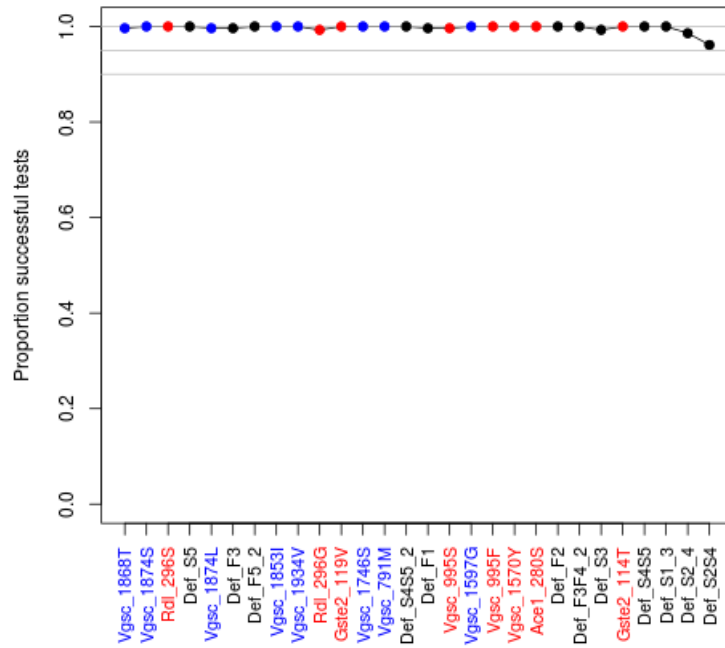
Fig. S2: Success rate of individual SNP assays among *An. coluzzii* samples was never lower than 95% (measured as the proportion of assays that were of high enough quality to give a genotype call). Red points indicate known resistance variants, blue points indicate variants found on the background of some *kdr* mutations, black points indicate SNPs used to distinguish between *kdr* mutant haplotype backgrounds.
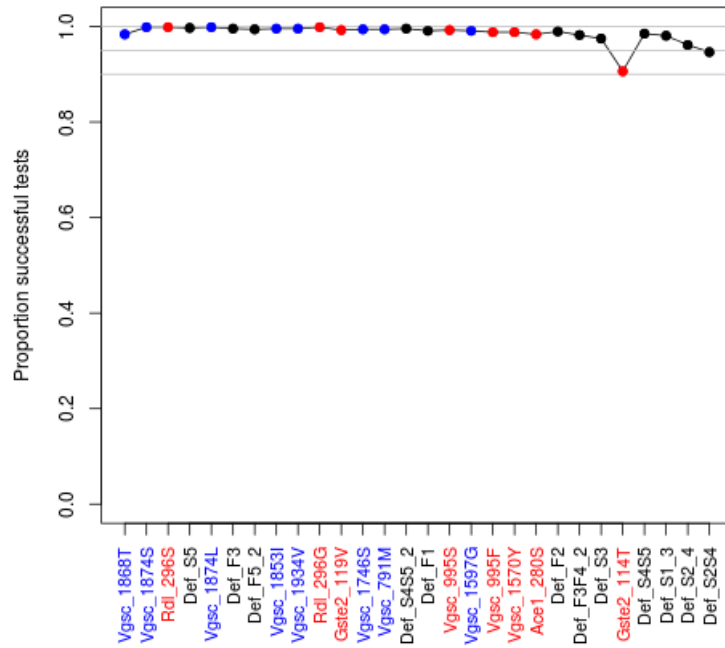
Fig. S3: Success rate of individual SNP assays among *An. gambiae* samples was never lower than 90% (measured as the proportion of assays that were of high enough quality to give a genotype call). Red points indicate known resistance variants, blue points indicate variants found on the background of some *kdr* mutations, black points indicate SNPs used to distinguish between *kdr* mutant haplotype backgrounds.
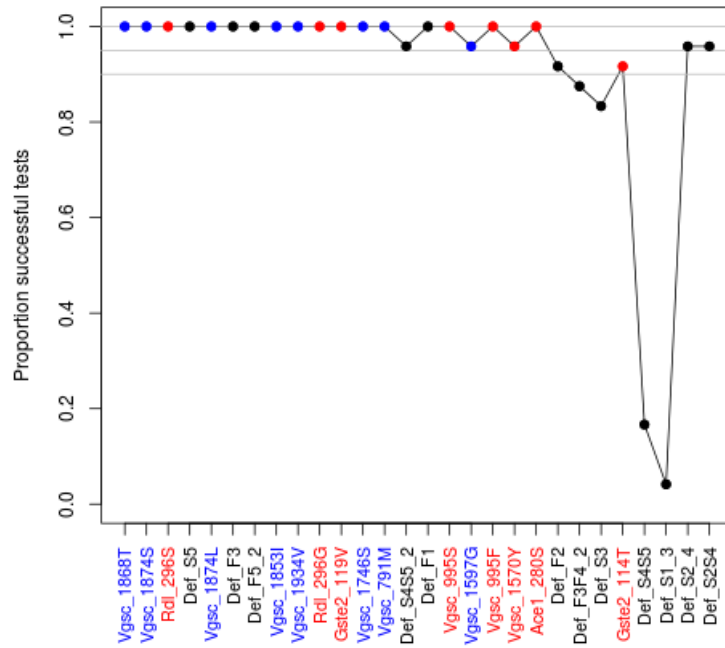
Fig. S4: Success rate of individual SNP assays among *An. arabiensis* samples was good overall, but some assays had a low rate of success (measured as the proportion of assays that were of high enough quality to give a genotype call). All four assays with success rates below 90% were ones used to distinguish between *kdr* haplotype backgrounds Red points indicate known resistance variants, blue points indicate variants found on the background of some *kdr* mutations, black points indicate SNPs used to distinguish between *kdr* mutant haplotype backgrounds.

Table **S1**: Bioassay results for samples from Burkina Faso (CDC bottle assay).

| | 20ppm Permethrin | | | |
Location	Dead	Live	Total	Mortality
Bakaridjan	30	11	41	73.2%
Bounouba	15	26	41	36.6%
Naniagara	15	33	48	31.3%
Tiefora	24	52	76	31.6%

Table **S2**: Bioassay results for samples from DRC (WHO tube assay).

| | 0.75% Permethrin | | | |
Location	Dead	Live	Total	Mortality
Pwamba	7	18	25	28.0%
Fiwa	98	83	181	54.1%
Bassa	101	45	146	69.2%

| | 0.05% Deltamethrin | | | |
Location	Dead	Live	Total	Mortality
Pwamba	40	23	63	63.5%
Fiwa	131	44	175	74.9%
Bassa	119	24	143	83.2%

Table **S3**: Bioassay results for samples from Ghana (WHO tube assay).

| | 0.75% Permethrin | | | |
Location	Dead	Live	Total	Mortality
Keta	61	50	111	55.0%

| | 0.05% Deltamethrin | | | |
Location	Dead	Live	Total	Mortality
Keta	75	45	121	62.0%

| | 4% DDT | | | |
Location	Dead	Live	Total	Mortality
Keta	43	66	110	39.1%

Table **S4**: Bioassay results for samples from Kenya WHO tube assay. Results are for *An. gambiae* s.l. in 2015.

| Location | 0.75% Permethrin | | | |
	Dead	Live	Total	Mortality
Bondo	522	569	1091	47.8%
Nyando	319	198	517	61.7%
Rachuonyo	670	218	888	75.5%
Teso	332	409	741	44.8%

| Location | 0.05% Deltamethrin | | | |
	Dead	Live	Total	Mortality
Bondo	1028	759	1787	57.6%
Nyando	537	342	879	61.1%
Rachuonyo	919	213	1132	81.2%
Teso	585	750	1335	43.8%

Table **S5**: SNPs VGC-1746S and VGC-791M are almost perfectly associated (only two samples give discordant calls). The wild-type alleles are G and C for 1746S and 791M respectively.

VGC-1746S

		GG	GT	TT
	CC	672	0	0
VGC-791M	CT	2	33	0
	TT	0	0	5