

Online Resource 1 Primer pairs described in Loiseau *et al.* (2009) used in this study for three multiplex PCR sets. The table includes the repeat motifs, fluorescent dye labels (FAM, VIC, NED, and PET), allelic size range (bp) and the observed number of alleles (N_A) for each of the 15 loci for *Harmonia axyridis* individuals included in this study.

PCR set	Locus	Repeat motif	Label	Size range (bp)	# alleles (N_A)
PCR 1	Ha-244	(TG)10TC(TG)2	FAM	81-96	8
	Ha-201	(CA)8	FAM	306-319	6
	Ha-555	(CA)10	VIC	75-85	6
	Ha-605	(GA)16	VIC	134-167	11
	Ha-281	(TG)7	NED	134-147	12
	Ha-627	(GA)11	NED	227-254	11
	Ha-565	(GA)10	NED	326-334	3
	Ha-234	(CA)8	PET	128-138	7
PCR 2	Ha-267	(AC)8	FAM	177-187	6
	Ha-005	(GA)5	FAM	275-279	3
	Ha-105	(GA)5	VIC	240-243	4
PCR 3	Ha-194b	(GCA)4	NED	80-83	2
	Ha-215	(CA)7	NED	174-182	5
	Ha-223	(TG)6	NED	229-233	2
	Ha-094	(TAGA)5	PET	350-359	6

Online Resource 2: Results from tests comparing hypothetical scenarios to determine the most likely colonisation history of *Harmonia axyridis*. Tests were conducted in DIYABC v2.1.0 (Cornuet et al. 2014) which uses Approximate Bayesian Computations (ABC) to compare intricate population histories using simulations based on summary statistics (Guillemaud *et al.* 2010; Cornuet et al. 2014). Historical records of the successive invasions of *H. axyridis* across the world and the genetic groups identified from population structure analyses were used to build all plausible hypothetical scenarios for each successive group. The logic behind each set of scenarios is described within the table. Support estimates for the most likely scenario choice including posterior probability estimates with 95% confidence. The DIYABC software could not manage the large number of hypothetical ethical scenarios tested for Greece. Therefore, the scenarios for Greece were split into two sets. The scenarios with the two highest probability estimates were then selected from each set and included into a final third set to test for the most likely outcome. The scenario with the highest posterior probability estimate is highlighted in bold. The following site samples were used as “reference” locations in the data set to represent each genetic group or geographical location: Asia 1 (PRM), Asia 2 (WUH), Asia 3 (IRK) East North America (MIN), West North America (VAN), South America (SAN), Europe (RAK), South Africa (STB), and Greece (THS).

Genetic/ Geographic group	Logic	Scenario	True scenario	Posterior probability (95% CI)
East North America	First observations of this beetles in the wild occurred in east North America in 1988. Therefore, it was most likely colonised by beetles from the native region.	Asia 1 → East North America	1	0.1129 [0.1080,0.1178]
		Asia 2 → East North America	2	0.1450 [0.1394,0.1506]
		Asia 3 → East North America	3	0.0577 [0.0545,0.0609]
		Asia 1 + Asia 2 → East North America	4	0.4040 [0.3961,0.4120]
		Asia 2 + Asia 3 → East North America	5	0.1947 [0.1884,0.2011]
		Asia 3 + Asia 1 → East North America	6	0.0856 [0.0817,0.0896]
West North America	West North America falls into the same genetic cluster as Asian native samples (Asia 1). Because of the chronological order of invasion, it makes sense that west North America was invaded by individuals from a native population. Therefore, I'm did test any hypothetical scenarios for this region.			
South America	South America groups closely with east North America in the population structure analyses including STRUCTURE and neighbour-joining tree. It would therefore be reasonable to assume that it was either colonised by samples originating from east North America, or had a very similar introduction history to east North America	Asia 1 + Asia 2 → South America	1	0.0063 [0.0034,0.0093]
		East North America → South America	2	0.9937 [0.9907,0.9966]

Europe

The scenarios testing the colonization history of European populations of *Harmonia axyridis* include all plausible introduction scenarios including introductions from single locations and admixture events between two locations and includes an unsampled population.

Asia 1 → Europe	1	0.0096 [0.0000,0.0348]
Asia 2 → Europe	2	0.0000 [0.0000,0.0276]
Asia 3 → Europe	3	0.0000 [0.0000,0.0276]
East North America → Europe	4	0.0022 [0.0000,0.0287]
West North America → Europe	5	0.0008 [0.0000,0.0282]
Unsampled → Europe	6	0.0000 [0.0000,0.0276]
Asia 1 + Asia 2 → Europe	7	0.0001 [0.0000,0.0277]
Asia 1 + Asia 3 → Europe	8	0.0046 [0.0000,0.0307]
Asia 1 + WNA → Europe	9	0.0266 [0.0000,0.0542]
Asia 1 + ENA → Europe	10	0.0077 [0.0000,0.0323]
Asia 1 + Unsampled → Europe	11	0.1321 [0.0589,0.2052]
Asia 2 + Asia 3 → Europe	12	0.0000 [0.0000,0.0276]
Asia 2 + WNA → Europe	13	0.0000 [0.0000,0.0276]
Asia 2 + ENA → Europe	14	0.0000 [0.0000,0.0276]
Asia 2 + Unsampled → Europe	15	0.0000 [0.0000,0.0276]
Asia 3 + WNA → Europe	16	0.0001 [0.0000,0.0277]
Asia 3 + ENA → Europe	17	0.0000 [0.0000,0.0276]
Asia 3 + Unsampled → Europe	18	0.0000 [0.0000,0.0276]
ENA + WNA → Europe	19	0.0000 [0.0000,0.0276]
ENA + Unsampled → Europe	20	0.1513 [0.0449,0.2577]
WNA + Unsampled → Europe	21	0.6647 [0.5238,0.8056]

<p>South Africa</p> <p>Europe and South Africa had its first record of <i>Harmonia axyridis</i> in the wild in the same year (2001). Therefore, they have identical sets of competing scenarios. The scenarios include all plausible introduction scenarios including introductions from single locations and admixture events between two locations and includes an unsampled population.</p>	Asia 1 → South Africa	1	0.0000 [0.0000,0.0792]
	Asia 2 → South Africa	2	0.0000 [0.0000,0.0792]
	Asia 3 → South Africa	3	0.0000 [0.0000,0.0792]
	East North America → South Africa	4	0.2736 [0.0633,0.4839]
	West North America → South Africa	5	0.0000 [0.0000,0.0792]
	Unsampled → South Africa	6	0.0000 [0.0000,0.0792]
	Asia 1 + Asia 2 → South Africa	7	0.0003 [0.0000,0.0793]
	Asia 1 + Asia 3 → South Africa	8	0.0000 [0.0000,0.0792]
	Asia 1 + WNA → South Africa	9	0.0000 [0.0000,0.0792]
	Asia 1 + ENA → South Africa	10	0.0006 [0.0000,0.0795]
	Asia 1 + Unsampled → South Africa	11	0.0000 [0.0000,0.0792]
	Asia 2 + Asia 3 → South Africa	12	0.0000 [0.0000,0.0792]
	Asia 2 + WNA → South Africa	13	0.0000 [0.0000,0.0792]
	Asia 2 + ENA → South Africa	14	0.0002 [0.0000,0.0793]
	Asia 2 + Unsampled → South Africa	15	0.0000 [0.0000,0.0792]
	Asia 3 + WNA → South Africa	16	0.0000 [0.0000,0.0792]
	Asia 3 + ENA → South Africa	17	0.0006 [0.0000,0.0796]
	Asia 3 + Unsampled → South Africa	18	0.0000 [0.0000,0.0792]
	ENA + WNA → South Africa	19	0.0003 [0.0000,0.0793]
	ENA + Unsampled → South Africa	20	0.7244 [0.5139,0.9349]
	WNA + Unsampled → South Africa	21	0.0000 [0.0000,0.0792]

Greece Set 1

The first set of two tests for the colonization history of populations of *Harmonia axyridis* in Greece include plausible introduction scenarios including introductions from single locations and admixture events between two locations and includes an unsampled population

Asia 1 → Greece	1	0.0000 [0.0000,1.0000]
Asia 2 → Greece	2	0.0007 [0.0000,1.0000]
Asia 3 → Greece	3	0.0000 [0.0000,1.0000]
East North America → Greece	4	0.0005 [0.0000,1.0000]
West North America → Greece	5	0.4148 [0.0000,1.0000]
South America → Greece	6	0.0141 [0.0000,1.0000]
Europe → Greece	7	0.0073 [0.0000,1.0000]
South Africa → Greece	8	0.0000 [0.0000,1.0000]
Unsampled → Greece	9	0.0000 [0.0000,1.0000]
Asia 1 + Asia 2 → Greece	10	0.0004 [0.0000,1.0000]
Asia 1 + Asia 3 → Greece	11	0.0000 [0.0000,1.0000]
Asia 1 + WNA → Greece	12	0.0004 [0.0000,1.0000]
Asia 1 + ENA → Greece	13	0.0000 [0.0000,1.0000]
Asia 1 + South America → Greece	14	0.0000 [0.0000,1.0000]
Asia 1 + Europe → Greece	15	0.0013 [0.0000,1.0000]
Asia 1 + South Africa → Greece	16	0.0000 [0.0000,1.0000]
Asia 1 + Unsampled → Greece	17	0.0000 [0.0000,1.0000]
Asia 2 + Asia 3 → Greece	18	0.0000 [0.0000,1.0000]
Asia 2 + WNA → Greece	19	0.5180 [0.0000,1.0000]
Asia 2 + ENA → Greece	20	0.0000 [0.0000,1.0000]
Asia 2 + South America → Greece	21	0.0408 [0.0000,1.0000]
Asia 2 + Europe → Greece	22	0.0018 [0.0000,1.0000]

**Greece Set
2**

The second set of two tests for the colonization history of populations of *Harmonia axyridis* in Greece include plausible introduction scenarios including introductions from single locations and admixture events between two locations and includes an unsampled population

Asia 2 + South Africa → Greece	1	0.0936 [0.0000,1.0000]
Asia 2 + Unsampled → Greece	2	0.0031 [0.0000,1.0000]
Asia 3 + WNA → Greece	3	0.0000 [0.0000,1.0000]
Asia 3 + ENA → Greece	4	0.0000 [0.0000,1.0000]
Asia 3 + South America → Greece	5	0.0000 [0.0000,1.0000]
Asia 3 + Europe → Greece	6	0.0000 [0.0000,1.0000]
Asia 3 + South Africa → Greece	7	0.0000 [0.0000,1.0000]
Asia 3 + Unsampled → Greece	8	0.0000 [0.0000,1.0000]
ENA + WNA → Greece	9	0.0000 [0.0000,1.0000]
ENA + South America → Greece	10	0.0000 [0.0000,1.0000]
ENA + Europe → Greece	11	0.4682 [0.0000,1.0000]
ENA + South Africa → Greece	12	0.0024 [0.0000,1.0000]
ENA + Unsampled → Greece	13	0.0000 [0.0000,1.0000]
WNA + South America → Greece	14	0.0000 [0.0000,1.0000]
WNA + Europe → Greece	15	0.0000 [0.0000,1.0000]
WNA + South Africa → Greece	16	0.0000 [0.0000,1.0000]
WNA + Unsampled → Greece	17	0.0000 [0.0000,1.0000]
South America + Europe → Greece	18	0.0000 [0.0000,1.0000]
South America + South Africa → Greece	19	0.0000 [0.0000,1.0000]
South America + Unsampled → Greece	20	0.0000 [0.0000,1.0000]
Europe + South Africa → Greece	21	0.4327 [0.0000,1.0000]
Europe + Unsampled → Greece	22	0.0000 [0.0000,1.0000]
South Africa + Unsampled → Greece	23	0.0000 [0.0000,1.0000]

Greece Set 3	The third set of tests including four scenarios that indicated high probability values in Greece Set 1 and 2	West North America → Greece	1	0.1057 [0.0618,0.1495]
		Asia 2 + WNA → Greece	2	0.0012 [0.0000,0.0063]
		ENA + Europe → Greece	3	0.8773 [0.8326,0.9220]
		Europe + South Africa → Greece	4	0.0158 [0.0080,0.0235]

Online Resource 3 Prior distributions based on the parameters from Lombaert *et al.* (2011) used in the testing of all ABC analyses to infer the invasion history of *Harmonia axyridis*.

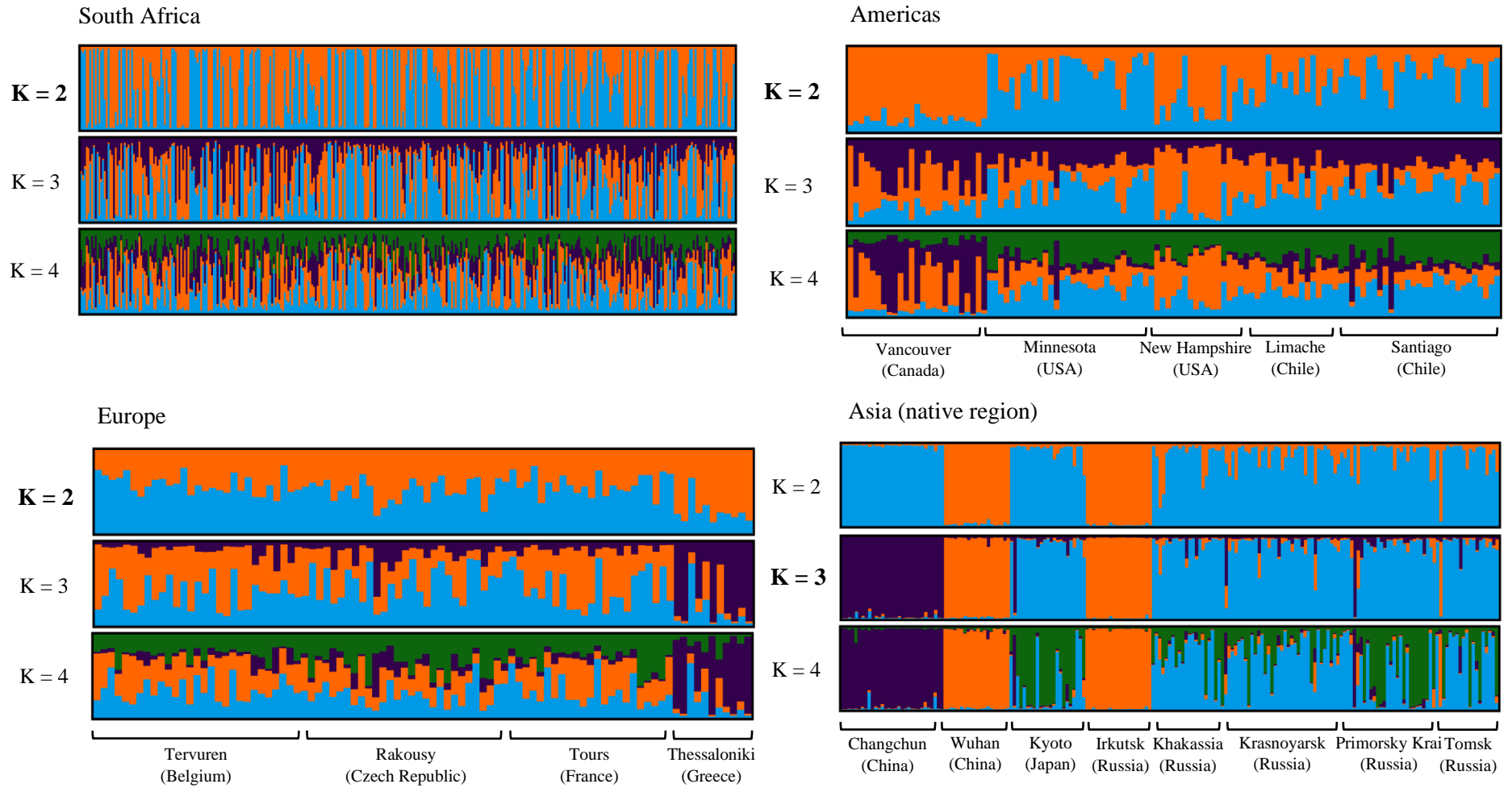
Parameter	Distribution
Effective population size	Uniform [100 – 20 000]
Effective number of founder individuals	Loguniform [2 – 1 000]
Duration of bottleneck (db)	Uniform [0 – 5]
Admixture rate (ra)	Uniform [0.1 – 0.9]
Timing of events (generations back in time): x = year of recorded introduction of population	Uniform [x-x+5]
Merging time of the sourced native population into unsampled native	Loguniform [100 – 2 500]
Merging time of two ancestral populations into unsampled ancestral	Uniform [100 – 3 000]
Mean mutation rate	Uniform [10^{-5} – 10^{-3}]
Mean geometric distribution	Uniform [0.1 – 0.3]
Mean SNI rate	Uniform [10^{-8} – 10^{-4}]

Online Resource 4 Results from one-sided Wilcoxon sign rank tests indicating whether 31 *Harmonia axyridis* populations experienced deviations from expected heterozygosity (deficit or excess). Heterozygote deficit indicates population contraction, while heterozygote excess indicates population expansion (which is indicative of a recent bottleneck). The results from two models are shown: TPM (two-phase model of mutation) and SMM (stepwise mutation model). Significant probability values are indicated in bold ($p < 0.05$).

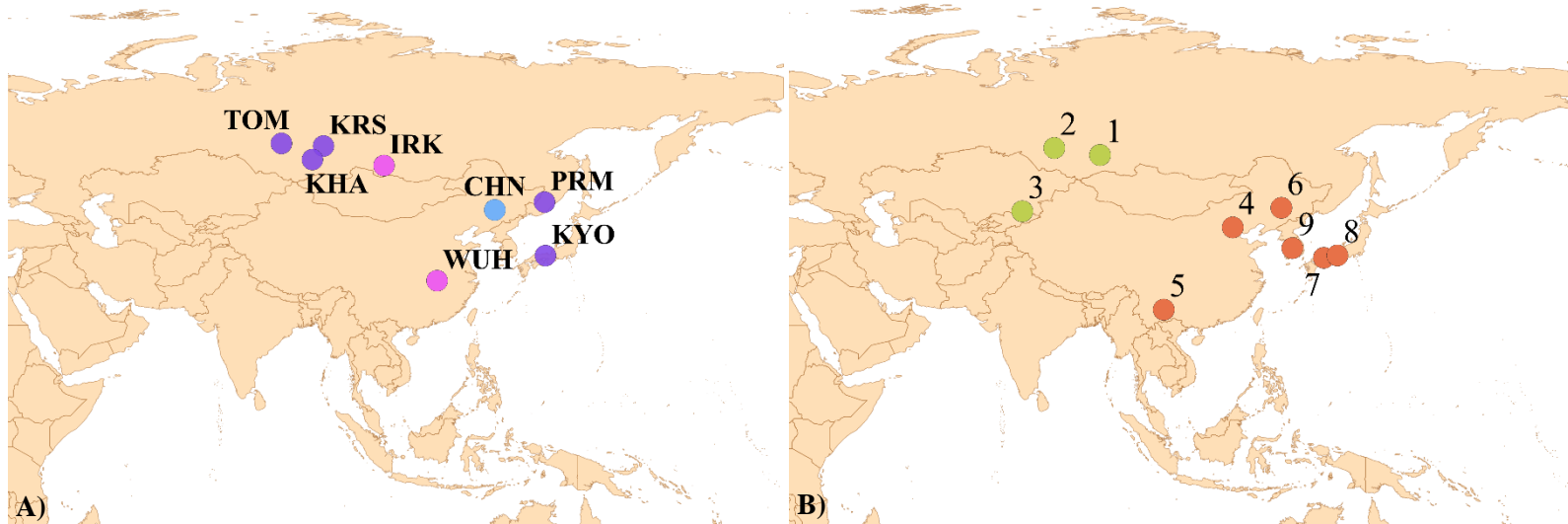
	Location	T.P.M		S.M.M	
		Deficit	Excess	Deficit	Excess
South Africa	Breyten	0.998	0.003	0.473	0.554
	Bredasdorp	0.997	0.007	0.879	0.134
	Clarens	0.976	0.029	0.446	0.580
	De Zalze Golf Estate	0.852	0.163	0.313	0.709
	George	0.936	0.073	0.342	0.682
	Goedehoop	0.988	0.015	0.548	0.476
	Hout Bay	0.980	0.024	0.342	0.682
	Impendile	0.984	0.020	0.342	0.682
	Marwaqa Nature Reserve	0.961	0.045	0.500	0.524
	Sandfontein	0.982	0.021	0.163	0.852
	Silverdale	0.999	0.001	0.830	0.188
	Springs	0.984	0.020	0.751	0.271
	Stellenbosch	0.961	0.045	0.380	0.643
	Sani Pass	0.996	0.011	0.729	0.294
Europe	Tervuren	0.423	0.598	0.009	0.992
	Rakousy	0.738	0.281	0.165	0.849
	Tours	0.976	0.028	0.820	0.195
	Greece	0.805	0.213	0.213	0.805
North America	Vancouver	0.489	0.532	0.021	0.982
	Minnesota	0.489	0.533	0.084	0.924
	New Hampshire	0.756	0.262	0.165	0.849
South America	Limache	0.719	0.300	0.115	0.896
	Santiago	0.966	0.042	0.381	0.640
Asia	Changchun	0.999	0.000	0.901	0.104
	Wuhan	0.837	0.179	0.476	0.548
	Kyoto	0.620	0.404	0.077	0.932
	Irkutsk	0.999	0.000	0.997	0.004
	Khakassia	0.575	0.445	0.015	0.987
	Krasnoyarsk	0.619	0.402	0.028	0.976
	Primorsky Krai	0.151	0.862	0.001	0.999
	Tomsk	0.467	0.555	0.024	0.979

Online Resource 5 Pairwise FST values between populations of *Harmonia axyridis*. Significant values are in bold ($p < 0.05$). Sample codes are described in full in Table 2.1.

	S-BRE	S-BDP	S-CLA	S-DEZ	S-GEO	S-GOD	S-HBY	S-IMP	S-MWA	S-SAN	S-SLV	S-SPR	S-STB	S-SPA	TER	RAK	TOU	THS	VAN	MIN	HAM	LIM	SNT	CHN	WUH	KYO	IRK	KHA	KRS	PRM	TOM
S-BRE	NA																														
S-BDP	0,03	NA																													
S-CLA	0,03	0,03	NA																												
S-DEZ	0,01	0,03	0,04	NA																											
S-GEO	0,02	0,03	0,03	0,02	NA																										
S-GOD	0,04	0,04	-0,01	0,05	0,03	NA																									
S-HBY	0,00	0,04	0,03	0,00	0,02	0,05	NA																								
S-IMP	0,02	0,04	0,00	0,04	0,02	0,01	0,03	NA																							
S-MWA	0,02	0,02	0,02	0,02	0,01	0,02	0,02	0,01	NA																						
S-SAN	0,01	0,03	0,01	0,02	0,01	0,01	0,02	0,01	0,01	NA																					
S-SLV	0,03	0,04	-0,06	0,04	0,03	-0,01	0,04	0,00	0,02	0,00	NA																				
S-SPR	0,04	0,05	0,00	0,06	0,06	0,00	0,06	0,02	0,04	0,03	0,00	NA																			
S-STB	0,00	0,03	0,03	0,00	0,02	0,04	0,01	0,02	0,02	0,01	0,03	0,05	NA																		
S-SPA	0,02	0,03	0,00	0,03	0,02	0,01	0,03	0,00	0,01	0,01	0,00	0,02	0,02	NA																	
TER	0,04	0,06	0,07	0,05	0,06	0,09	0,05	0,08	0,07	0,06	0,08	0,09	0,05	0,09	NA																
RAK	0,04	0,06	0,05	0,03	0,06	0,06	0,03	0,06	0,05	0,04	0,06	0,07	0,03	0,06	0,05	NA															
TOU	0,06	0,06	0,03	0,05	0,06	0,04	0,05	0,05	0,05	0,04	0,05	0,05	0,05	0,05	0,03	0,03	NA														
THS	0,07	0,08	0,02	0,08	0,09	0,03	0,08	0,04	0,07	0,04	0,01	0,02	0,06	0,05	0,09	0,06	0,04	NA													
VAN	0,03	0,05	0,05	0,03	0,05	0,07	0,03	0,06	0,05	0,04	0,06	0,08	0,03	0,06	0,03	0,02	0,04	0,08	NA												
MIN	0,04	0,05	0,02	0,04	0,05	0,04	0,03	0,05	0,05	0,03	0,03	0,04	0,03	0,04	0,06	0,04	0,04	0,05	0,04	NA											
HAM	0,05	0,04	0,06	0,04	0,06	0,08	0,06	0,08	0,06	0,06	0,08	0,08	0,05	0,08	0,05	0,05	0,05	0,08	0,04	0,05	NA										
LIM	0,02	0,05	0,05	0,03	0,05	0,06	0,02	0,05	0,04	0,04	0,06	0,06	0,01	0,05	0,03	0,02	0,03	0,07	0,01	0,02	0,04	NA									
SNT	0,03	0,11	0,04	0,03	0,04	0,06	0,02	0,05	0,04	0,03	0,05	0,06	0,02	0,05	0,03	0,03	0,04	0,07	0,02	0,02	0,05	0,00	NA								
CHN	0,10	0,14	0,11	0,10	0,11	0,12	0,11	0,11	0,12	0,09	0,10	0,13	0,09	0,12	0,09	0,09	0,11	0,12	0,07	0,09	0,10	0,07	0,09	NA							
WUH	0,13	0,06	0,13	0,10	0,15	0,15	0,12	0,15	0,14	0,13	0,12	0,14	0,12	0,14	0,16	0,12	0,14	0,12	0,12	0,11	0,11	0,14	0,13	0,20	NA						
KYO	0,04	0,15	0,05	0,03	0,05	0,06	0,03	0,05	0,06	0,04	0,05	0,07	0,03	0,06	0,04	0,04	0,04	0,06	0,02	0,04	0,05	0,03	0,03	0,08	0,10	NA					
IRK	0,13	0,07	0,13	0,11	0,13	0,15	0,13	0,14	0,14	0,13	0,16	0,17	0,13	0,15	0,15	0,14	0,14	0,17	0,14	0,12	0,13	0,14	0,14	0,22	0,20	0,13	NA				
KHA	0,05	0,07	0,05	0,04	0,06	0,06	0,04	0,07	0,07	0,04	0,06	0,07	0,04	0,06	0,07	0,04	0,05	0,07	0,04	0,04	0,06	0,04	0,03	0,10	0,11	0,02	0,12	NA			
KRS	0,04	0,05	0,07	0,03	0,06	0,08	0,04	0,08	0,07	0,05	0,07	0,09	0,04	0,07	0,06	0,05	0,06	0,09	0,03	0,06	0,04	0,05	0,05	0,10	0,10	0,02	0,13	0,01	NA		
PRM	0,03	0,05	0,05	0,02	0,05	0,06	0,02	0,06	0,06	0,04	0,05	0,08	0,02	0,05	0,05	0,02	0,05	0,08	0,01	0,03	0,04	0,02	0,01	0,08	0,11	0,02	0,13	0,01	0,02	NA	
TOM	0,03	0,02	0,04	0,01	0,05	0,06	0,03	0,05	0,05	0,04	0,04	0,06	0,02	0,05	0,06	0,03	0,05	0,06	0,02	0,03	0,03	0,03	0,03	0,08	0,08	0,01	0,12	0,00	-0,01	0,00	NA



Online Resource 6 Coancestry assignment results of *Harmonia axyridis* beetles from the programme STRUCTURE for South African, American, European and Asian subsets of data. Each bar indicates an individual in the order it appears in Table 1.1. Labels for the countries of origin are included on the x-axis. Best K according to the method described by Evanno *et al.* 2005 is highlighted in bold on the y axes. Because all populations within South Africa belonged to a single cluster, labels of location names are not included, but can be found in Table 1 and are presented here in the same order as they are in the table.



Online Resource 7 **A)** Genetic clustering in the native region of *Harmonia axyridis* from this study identifying three distinct clusters described in Figure 2.4 and Figure S. Sample codes are described in Table 1.1 **B)** Genetic clustering from Lombaert *et al.* 2014 identifying two distinct clusters in the native region: One in west Asia and a separate distinct cluster in east Asia. Sample location names are as follows: 1- Abakan, Russia; 2- Novosibirsk, Russia; 3- Almaty, Khazakhstan; 4- Beijing, China; 5- Shilin city, China; 6- Changhun city, China; 7- Fuchu, Japan; 8- Kyoto, Japan; 9- Daejon, South Korea. In both maps sample location points are coloured according to the genetic cluster it belongs to.

Online Resource 8 Analysis of molecular variance (AMOVA) for 31 populations of *Harmonia axyridis* for five different population structure scenarios. The scenarios were based on partitioned sampled populations according to geographic subdivision, coancestry results from STRUCTURE, and the genetic relationships inferred from the neighbour-joining tree. The table includes variance components among groups (Va), among populations within groups (Vb), and among individuals within populations (Vc).

Scenario 1: Subdivision by country (12 groups): South Africa + Belgium + Czech Republic + France + Greece + Canada + United States + Chile + China + Japan + Russia

Scenario	Among groups			Among populations within groups			Among individuals within populations		
	Va	Percentage	P	Vb	Percentage	P	Vc	Percentage	P
1	27.684	53.57	<0.0001	6.167	11.93	<0.0001	17.828	31.50	<0.0001
2	17.677	34.95	<0.0001	15.075	29.80	<0.0001	17.828	35.24	<0.0001
3	14.089	26.72	<0.0001	20.815	39.47	<0.0001	17.828	33.81	<0.0001
4	17.224	34.00	<0.0001	15.607	30.81	<0.0001	17.828	35.19	<0.0001
5	14.928	29.45	<0.0001	17.938	35.38	<0.0001	17.828	35.17	<0.0001

Scenario 2: Subdivision by geographical areas (6 groups): South Africa + Europe + South America + North America + North-West Asia (IRK, KHA, KRS, TOM) + East Asia (CHN, WUH, KYO, PRM)

Scenario 3: Subdivision based on coancestry from STRUCTURE (K=2): South Africa + World (Europe, Americas, Asia)

Scenario 4: Subdivision based on coancestry from STRUCTURE (K=6): South Africa + Americas (HAM, MIN, LIM, SNT) + Europe + Asia 1 (VAN, KYO, KHA, KRS, PRM, TOM) + Asia 2 (WUH, IRK) + Asia 3 (CHN)

Scenario 5: Subdivision based on genetic relationship from NJ tree (4 groups): [southern Africa] + [Americas (HAM, MIN, LIM, SNT)] + [Europe] + [China, Japan, Russia, Canada]

Online Resource 9 Results from separate Mantel's tests to investigate isolation-by-distance between South African populations closest to two of South Africa's seaport harbours: the Port of Durban and the Port of Cape Town, and those further inland. Impendile (S-IMP) and Marwaqa Nature Reserve (S-MWA) were used to represent populations closest to the Port of Durban and the populations from Hout Bay (S-HBY) and Stellenbosch (S-STB) were used to represent populations closest to the Port of Cape Town.

Seaport Harbour	Populations closest to seaport harbour	Populations further inland	Correlation co-efficient	p-value
Port of Durban	Impendile (S-IMP) and Marwaqa Nature Reserve (S-MWA)	Clarens (S-CLA)	0.53	0.33
		Goedehoop (S-GOD) and Breyten (S-BRE)	0.55	0.25
		Springs (S-SPR)	0.99	0.31
		Sandfontein (S-SAN)	0.73	0.33
Port of Cape Town	Hout Bay (S-HBY) and Stellenbosch (S-STB)	Bredasdorp	0.74	0.34