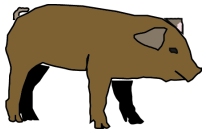
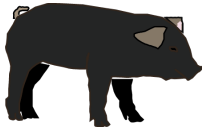
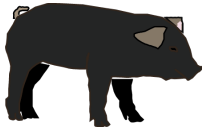
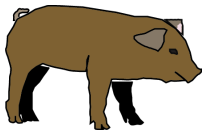
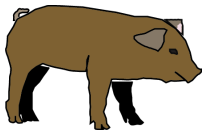
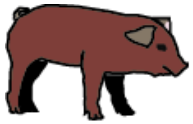
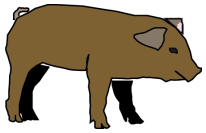
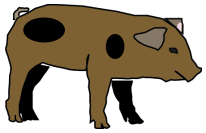
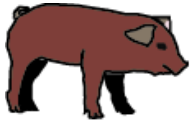
Pig Check

How accurately can we predict evolution?

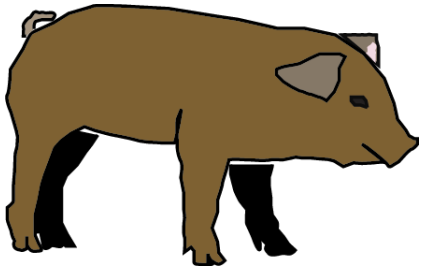
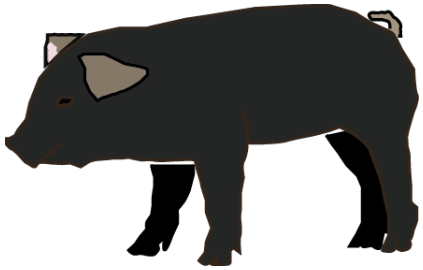
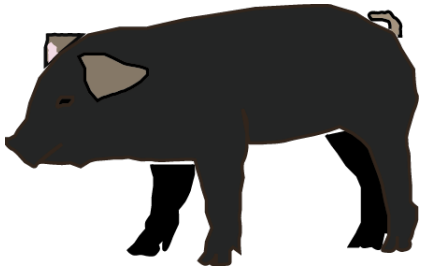
Analytical prediction vs. simulation results

WW Brown 	BW Black 	BB Black 	“Allele W is recessive to allele B”
WW Brown 	RW Brown 	RR Red 	“Allele W is dominant to allele R”
WW Spotless brown 	SW Bwn some spots 	SS Red many spots 	“Alleles W and S are codominant.”
RR Red 	RS Red some spots 	SS Red many spots 	“Alleles R and S show incomplete dominance.”

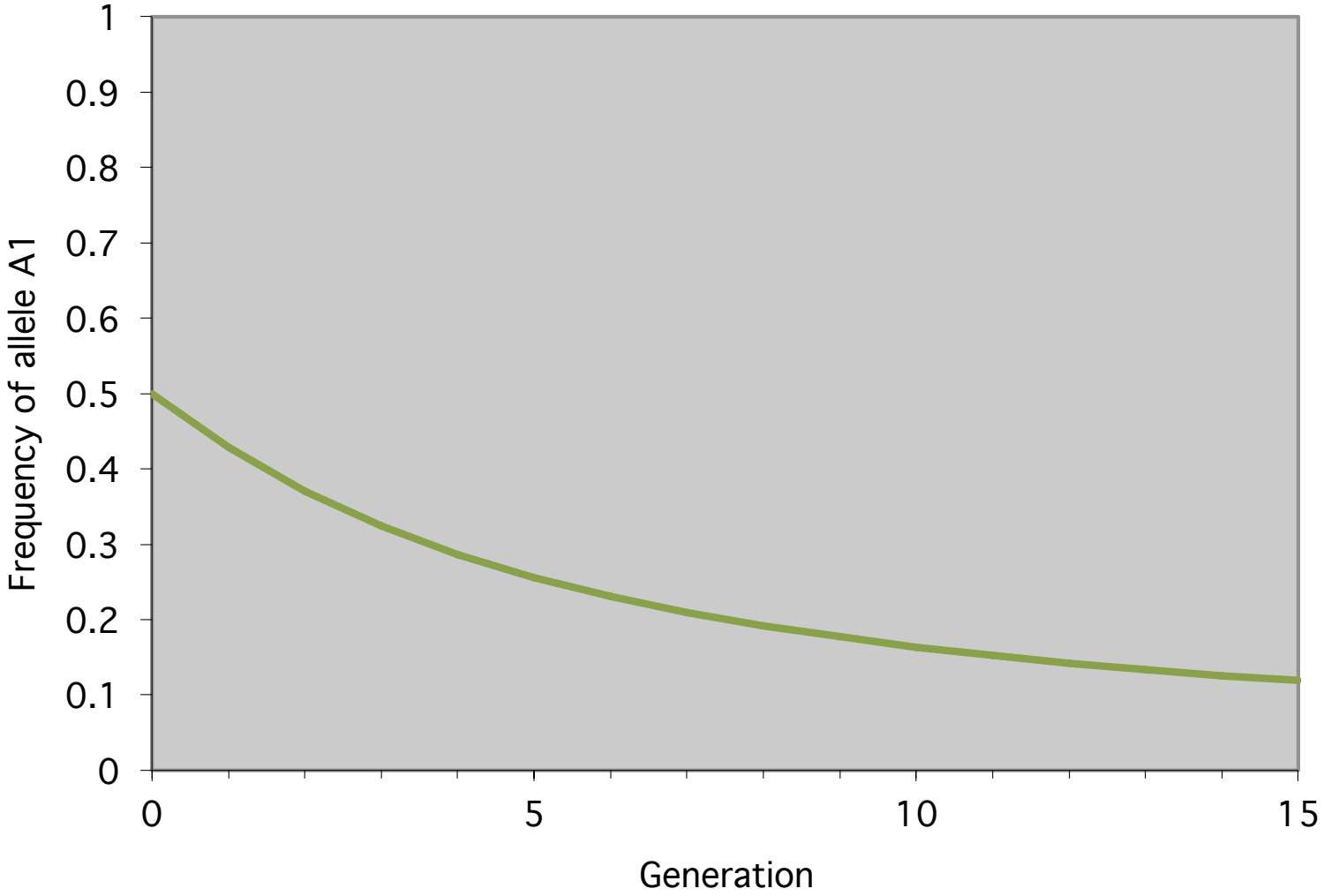
“Dominant” and “recessive” are not properties of alleles. They are descriptions of the phenotypes of heterozygotes.

Exercise 1

Pigs: Half pure brown, half pure black; Death rate 0.5 for brown
PigCheck: Starting Fr(A_1)=0.5; Fitnesses = 0.5, 1, 1

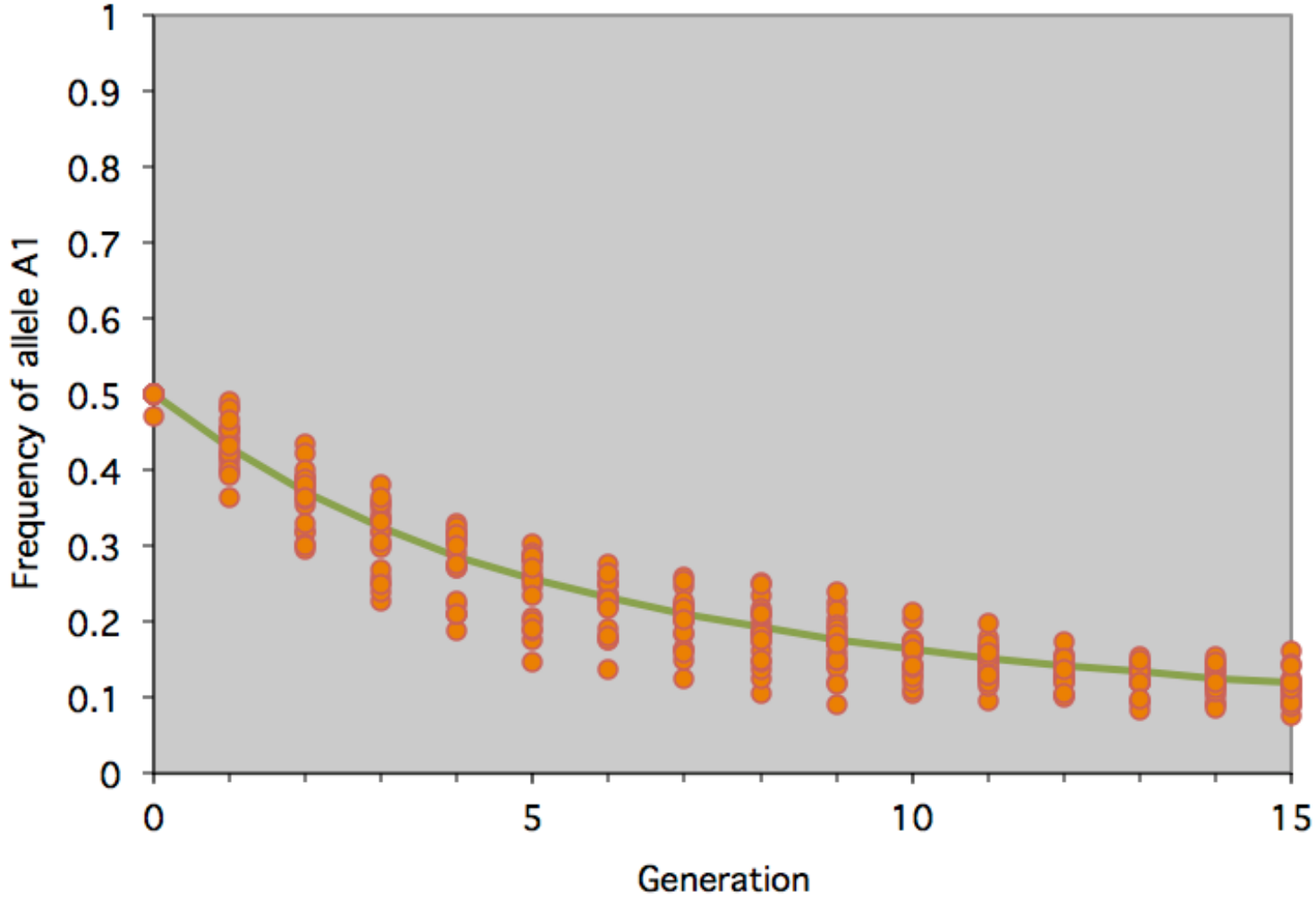
Results



Green line = prediction from model

Oragne dots = data from Mendelian Pigs

Results



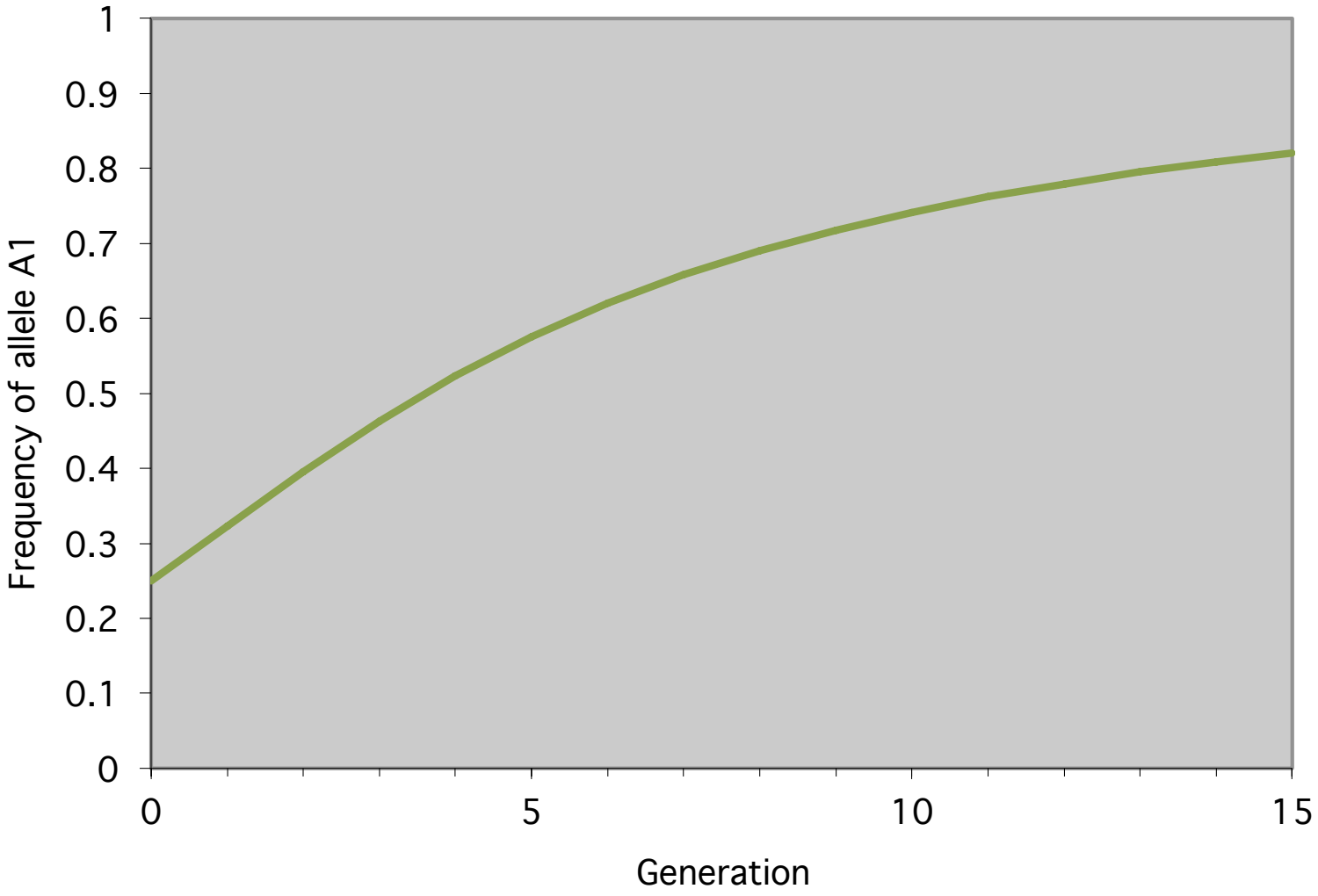
Green line = prediction from model

Orange dots = data from Mendelian Pigs

Exercise 2

Pigs: 25% pure red, 75% pure spotted; Death rate 0.4 for red, many spots
PigCheck: Starting Fr(A_1)=0.25; Fitnesses = 1, 1, 0.6

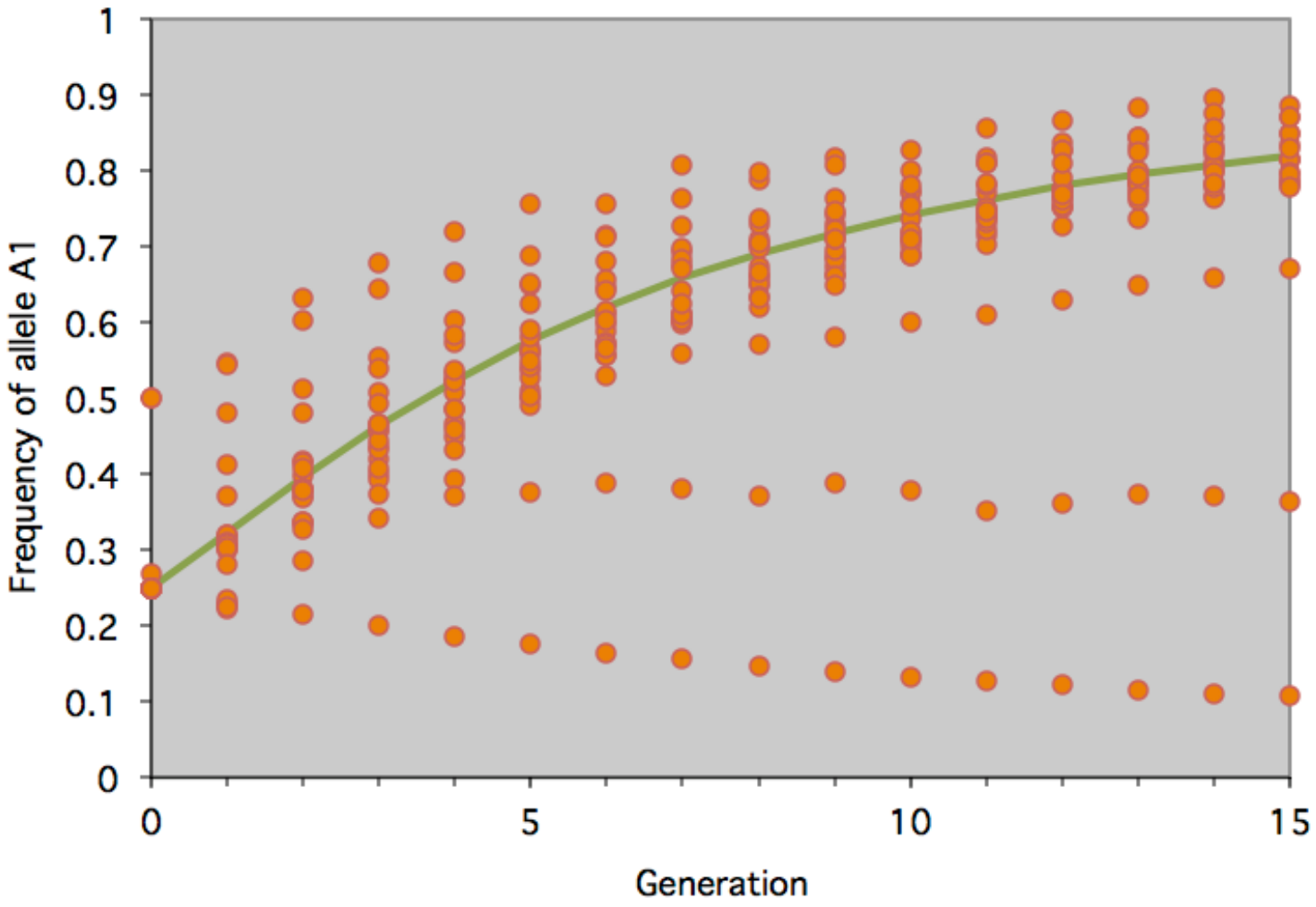
Results



Green line = prediction from model

Oragne dots = data from Mendelian Pigs

Results

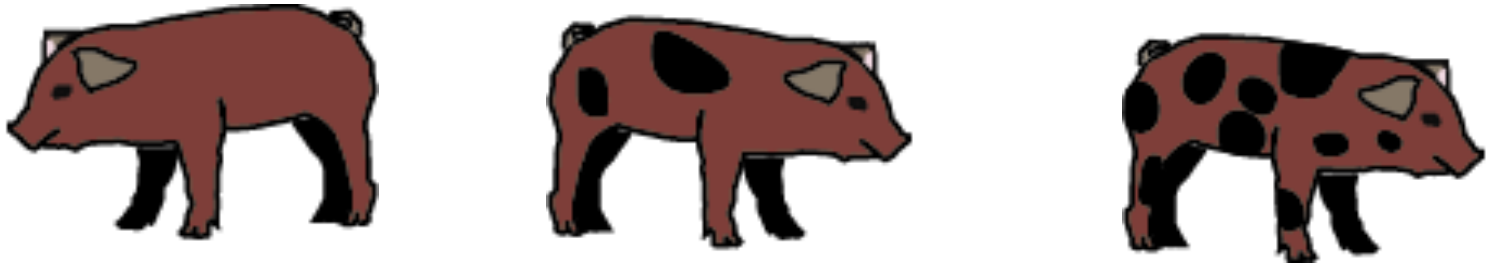


Green line = prediction from model

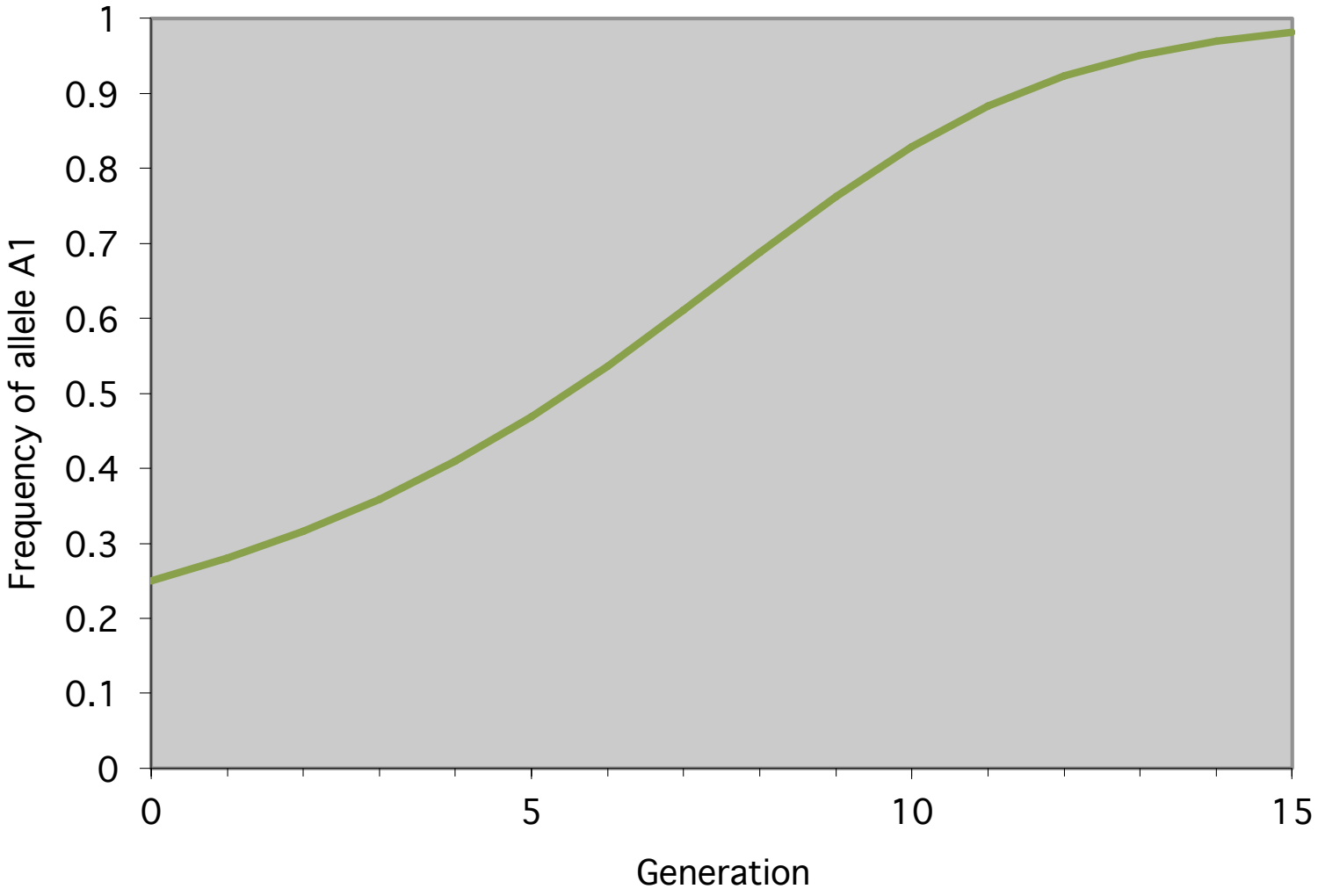
Orange dots = data from Mendelian Pigs

Exercise 3

Pigs: 25% pure red, 75% pure spotted; Death rate 0.4 for few spots & many spots
PigCheck: Starting Fr(A_1)=0.25; Fitnesses = 1, 0.6, 0.6



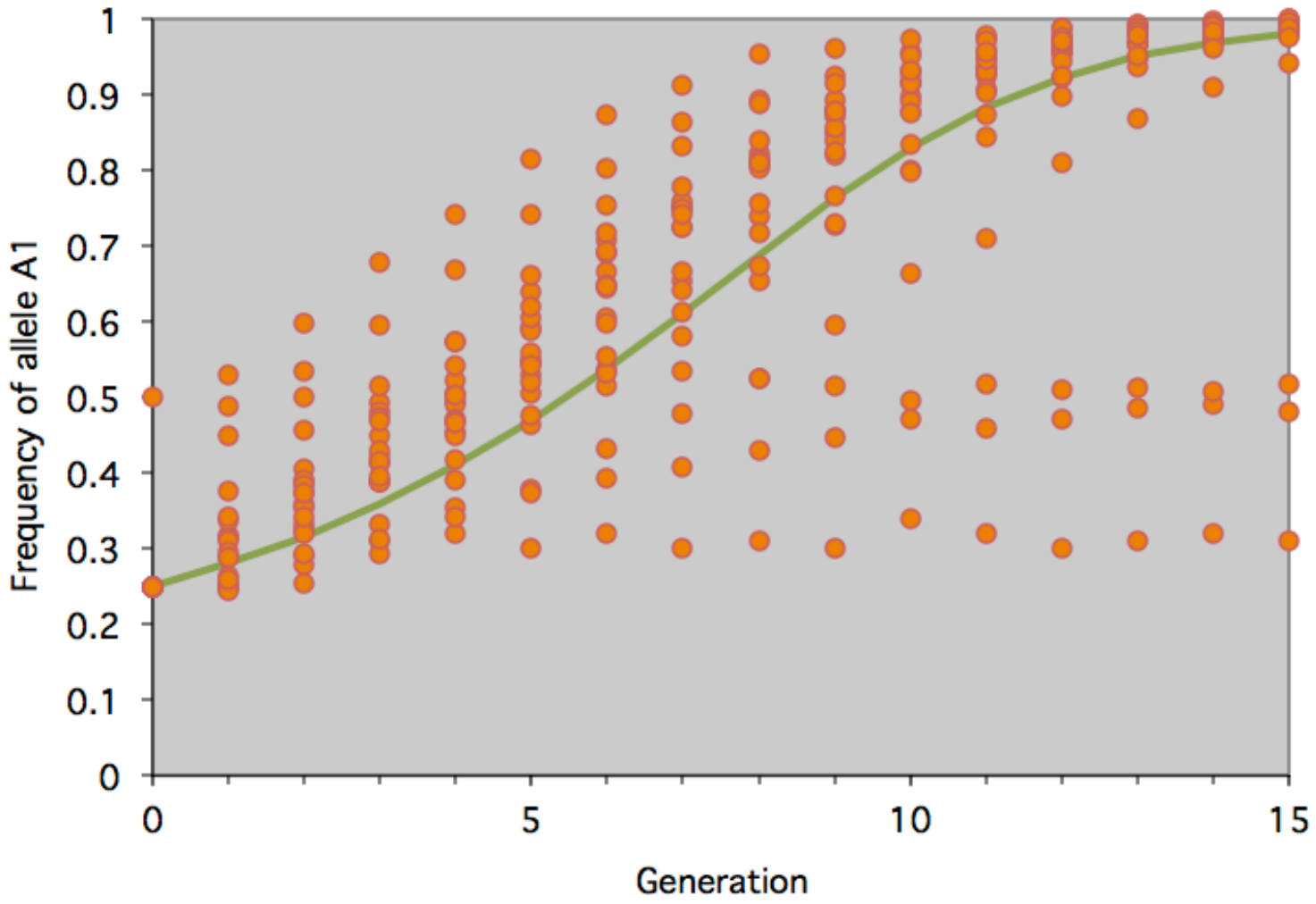
Results



Green line = prediction from model

Oragne dots = data from Mendelian Pigs

Results



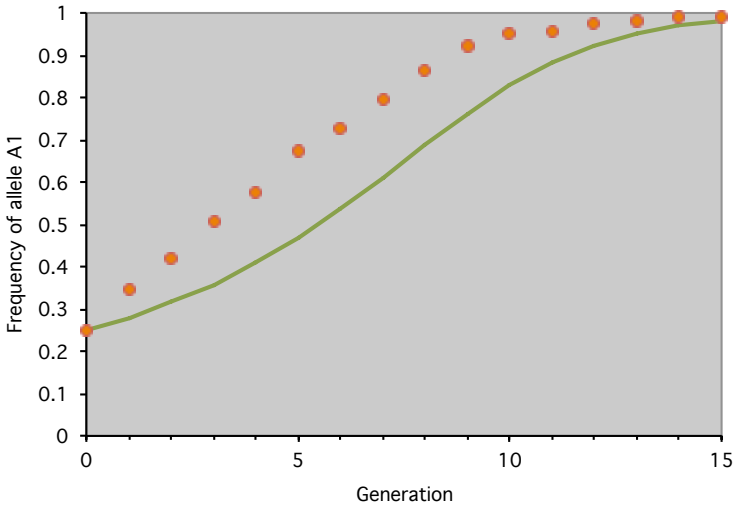
Green line = prediction from model

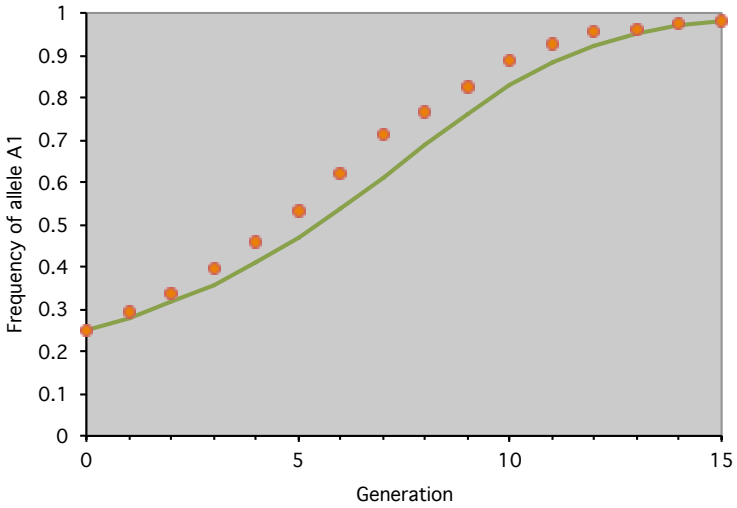
Orange dots = data from Mendelian Pigs

Exercise 3

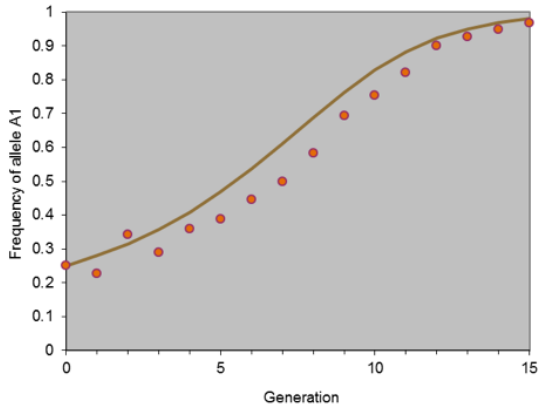
Pigs: 25% pure red, 75% pure spotted; Death rate 0.4 for few spots & many spots
PigCheck: Starting Fr(A_1)=0.25; Fitnesses = 1, 0.6, 0.6

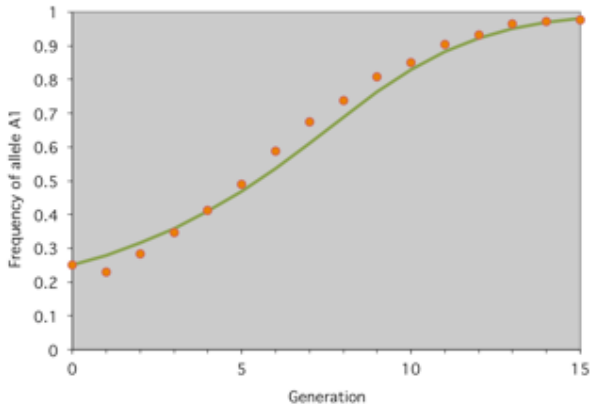
Jon's results:

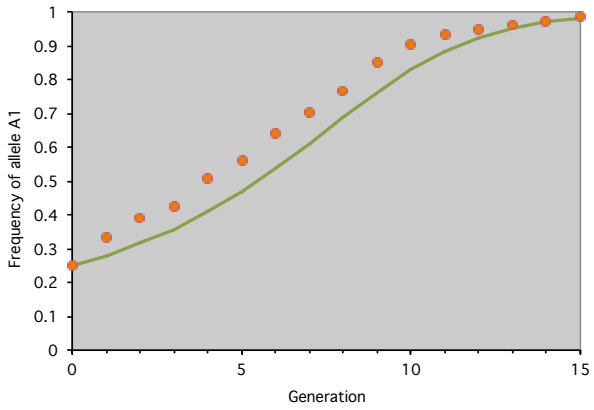


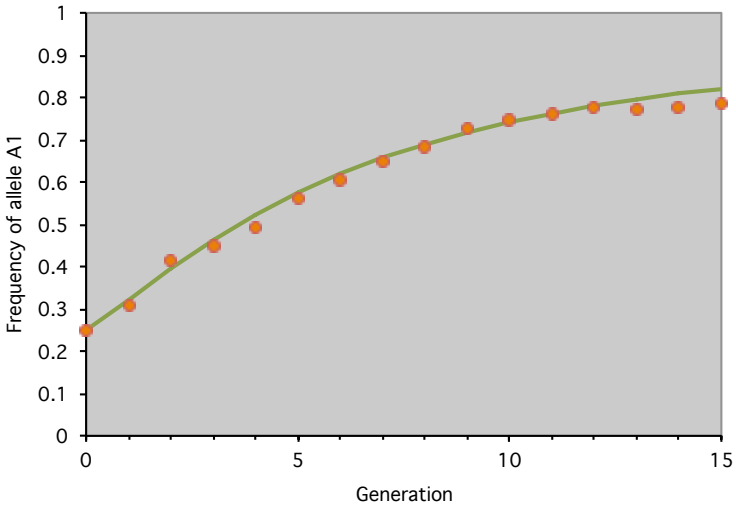


Students' results:

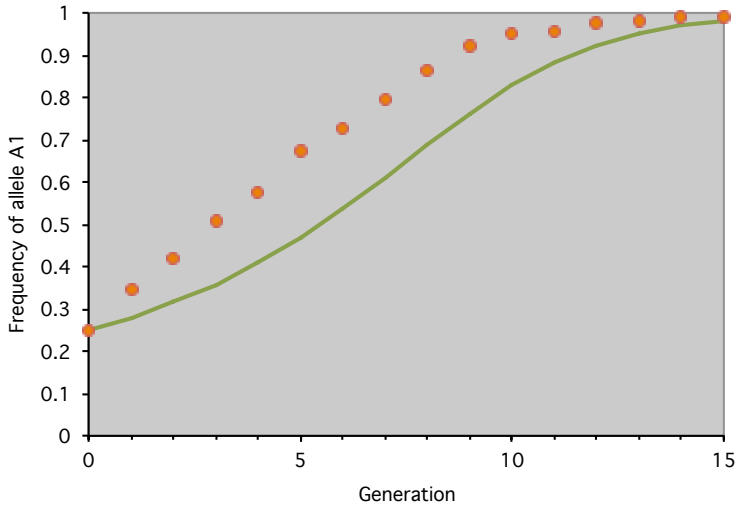








vs



$Fr(A_1)=0.25$; Fitnesses = 1, 1, 0.6

$Fr(A_1)=0.25$; Fitnesses = 1, 0.6, 0.6

Challenge:
Why was the prediction better for Ex. 2 than Ex. 3?