

Marine Ecological Genetics

02. Hardy-Weinberg equilibrium | computer practical

- Calculate allele and genotype frequencies
- Test for Hardy-Weinberg equilibrium
- Learn to interpret HW test results
- Become familiar with microsatellite data

Martin Helmkamp



Access files for practical

Download files from GitHub:

<https://github.com/mhelmkamp/meg24.git> (Code | Download ZIP)

Alternatively, run git from terminal:

```
git clone https://github.com/mhelmkamp/meg24.git
```

Open R script called **Mar_Ecol_Gen_week2.R** in RStudio

Is this population in Hardy-Weinberg equilibrium?

Exercise 1

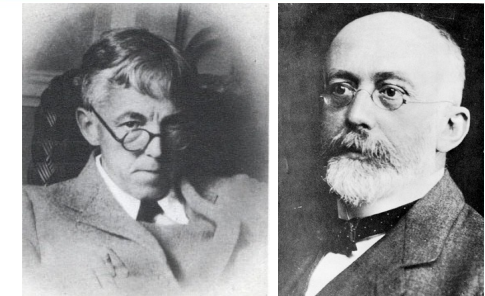
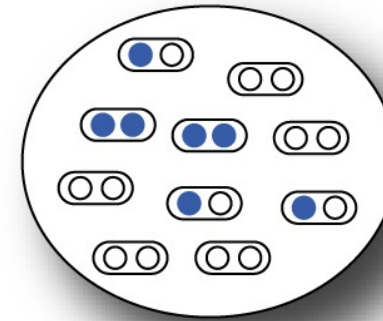
Diploid, sexual reproduction, 1 locus, 2 co-dominant alleles (yellow, blue)



HARDY-WEINBERG (1908)

Godfrey H. Hardy (1877-1947)

Wilhelm Weinberg (1862-1937)

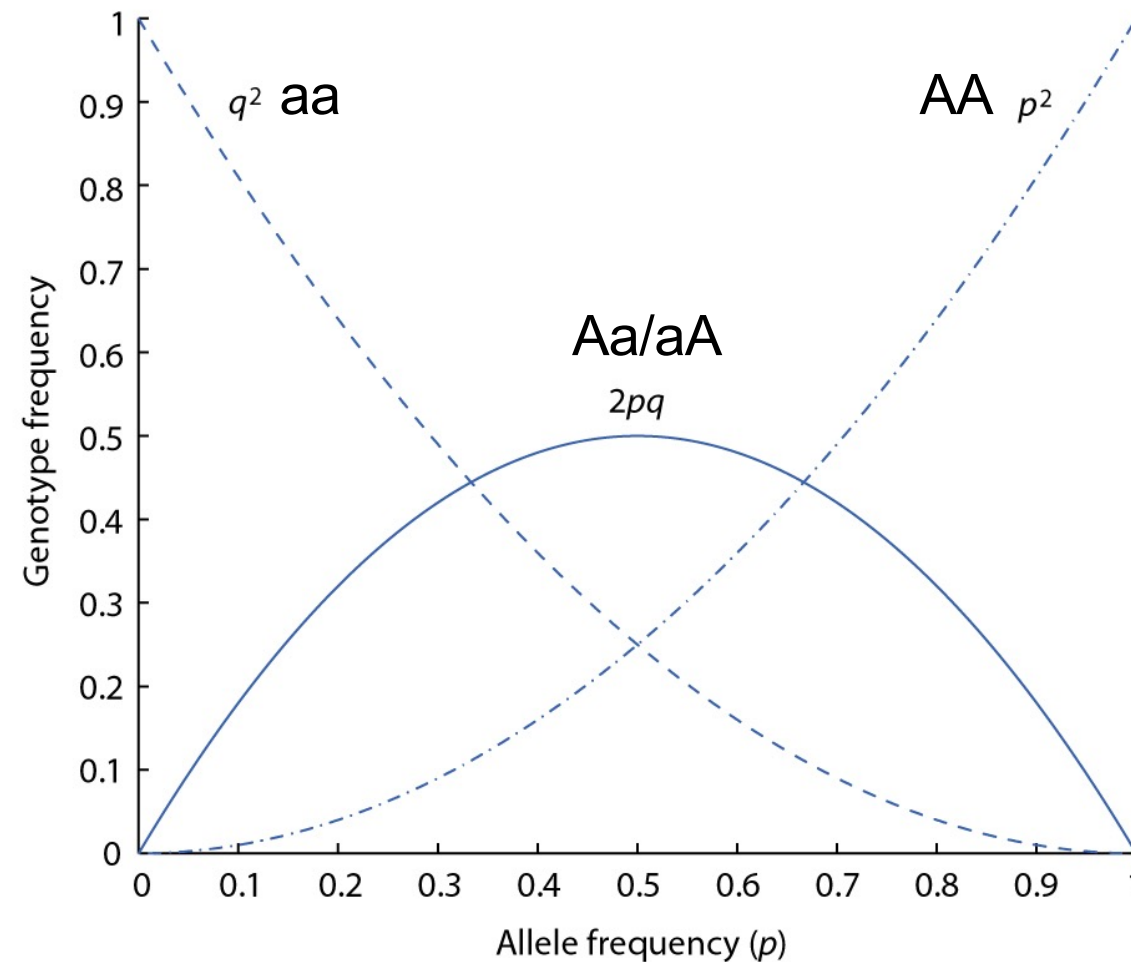


Establish the relationship between allele frequencies and genotype frequencies in a population

$$p^2 + 2pq + q^2 = 1$$

AA Aa/aA aa

p and q : allele frequencies for a locus with two alleles (A and a)
($p + q = 1$)



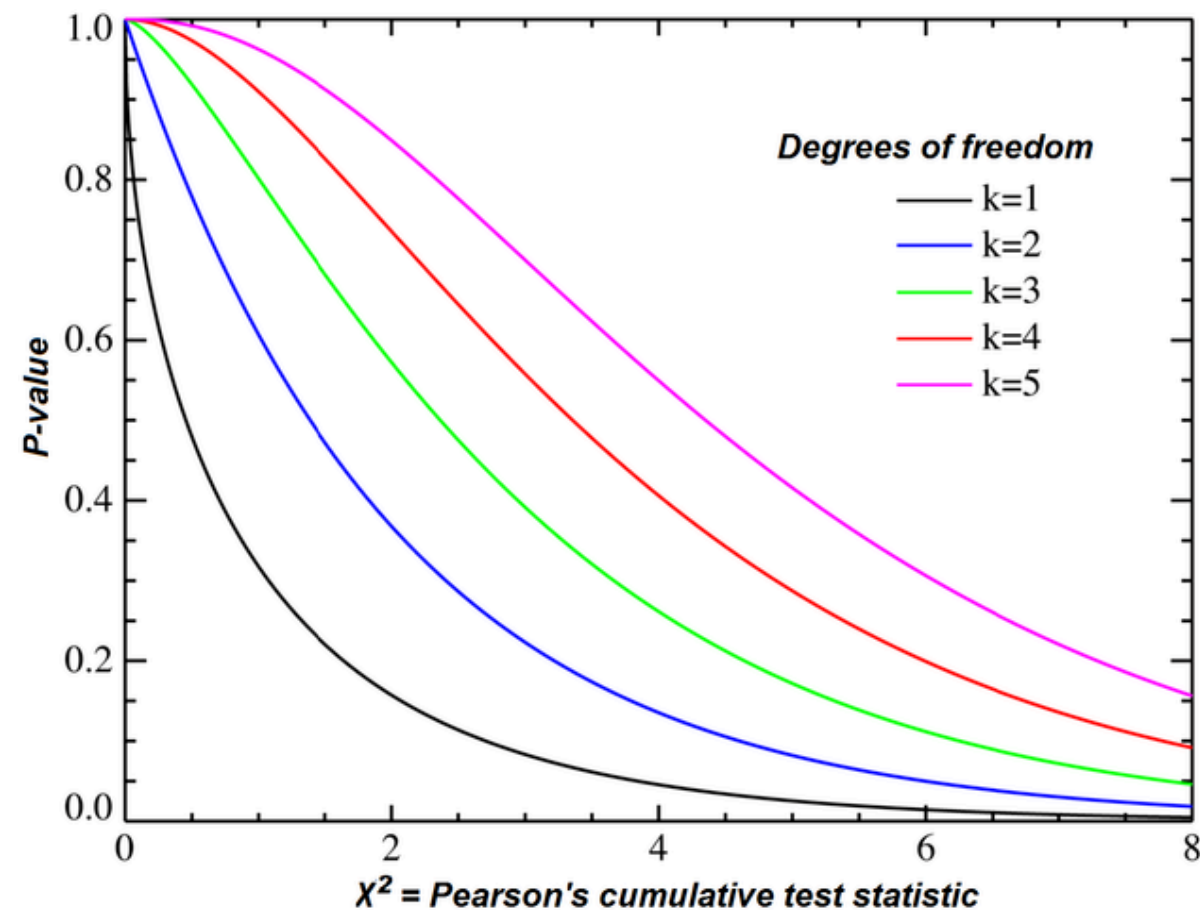
Pearson's chi-squared test

Exercise 1

Chi-square statistic:

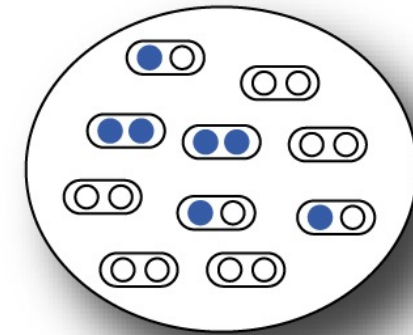
$$\chi^2 = \sum_{i=1}^n \frac{(O_i - E_i)^2}{E_i}$$

Chi-square distribution:



HETEROZYGOSITY

In one population



H_o = proportion of heterozygote individuals, observed heterozygosity

$H_e = 2pq = 1 - p^2 - q^2$, expected heterozygosity (assuming HW equilibrium)

$$F = \frac{H_e - H_o}{H_e}$$

Fixation index: *proportion by which heterozygosity is reduced or increased relative to the heterozygosity of a population at HW equilibrium with the same allele frequencies.*

Divided by $H_e \rightarrow$ *proportion* (of expected heterozygosity)

Varies between -1 and 1

$F < 0$: heterozygote excess

$F > 0$ heterozygote deficit (homozygote excess)

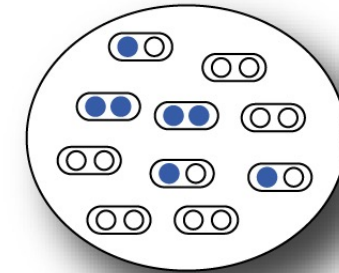
May be averaged over several loci \rightarrow reduces bias

May be extended to k alleles

A single generation of reproduction will result in a population that meets the expected Hardy-Weinberg frequencies, i.e. is at Hardy-Weinberg (HW) equilibrium

Assuming an “ideal” population, i.e. :

- Diploid organisms
- Sexual reproduction (as opposed to clonal)
- Random mating (as opposed to e.g. assortative) with respect to genotype
- Random union of gametes
- Discrete, non-overlapping generations
- Very large (infinite) population
- No migration
- No population structure
- No natural selection
- Two alleles
- Identical allele frequencies in both sexes



-> Departures from HW equilibrium may indicate:

- Inbreeding
- Assortative mating
- Self-fertilization
- Natural selection
- Population structure
- ...

Genepop format

Exercises 2/3

yellowblue.txt

Example data
Color
POP
ind01, yy
ind02, yy
ind03, yy
ind04, yy
ind05, yy
ind06, yy
ind07, yb
ind08, bb
ind09, bb
ind10, bb

puella_barbados.txt

Microsatellite genotypes of Hypoplectrus puella from Barbados

g2
gag010
h24
hyp001
hyp015
hyp018
e2
hyp008
hyp016
pam013
POP

Free text

Locus names

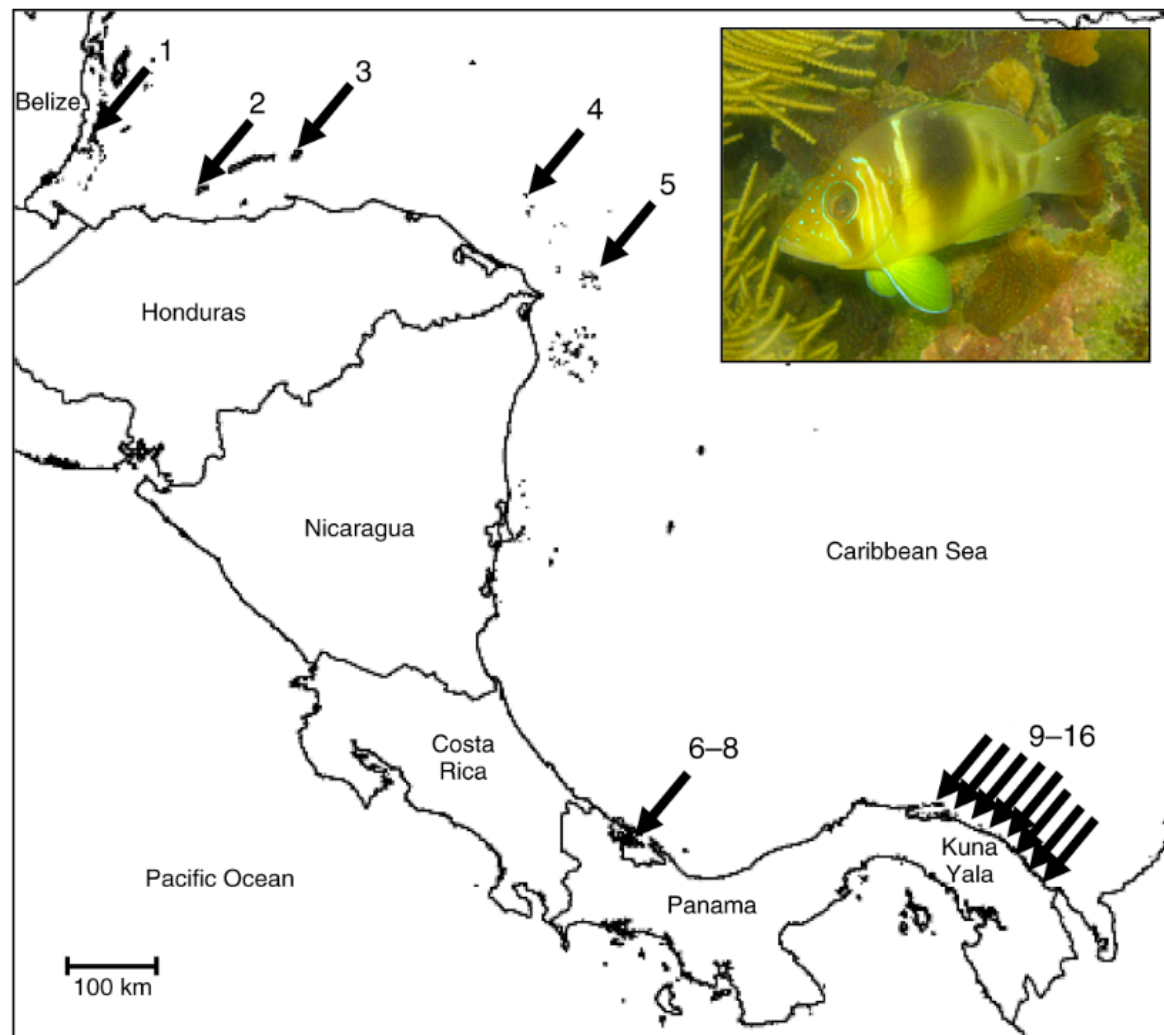
Sample / population

Alleles (000 = missing data)

barbados	ind#735	,	203235	121127	210248	225231	126132	190192	157157	236244	194220	114128
barbados	ind#736	,	205217	119119	204216	225229	126126	190192	157165	236236	216222	106144
barbados	ind#737	,	203203	135147	224226	233235	126136	190198	157163	238250	202226	126160
barbados	ind#738	,	211217	119121	228230	223231	126130	190190	157157	240244	220226	138160
barbados	ind#739	,	205225	121125	208216	227231	132132	192192	158159	244256	192196	146146
barbados	ind#740	,	217233	119121	216228	227233	126126	192198	157157	242256	194216	000000
barbados	ind#741	,	203209	000000	216222	223229	126130	192198	157157	234236	188226	118130
barbados	ind#742	,	203215	119119	222234	233233	130130	190190	157157	240246	182188	108126
barbados	ind#743	,	203243	111121	216224	231231	126126	190192	157159	234249	188198	118126
barbados	ind#744	,	203225	121135	206232	231231	126130	192198	157159	240249	182222	122156
barbados	ind#745	,	203211	121123	224236	227231	126132	192192	157163	238238	182204	138148
barbados	ind#746	,	227233	119123	216234	227233	126130	190190	157159	236245	186188	124142
barbados	ind#747	,	203223	133141	236240	231231	126126	192198	157157	234236	194204	118126
barbados	ind#748	,	203217	141145	222226	227235	126126	190192	145157	238240	182196	108108
barbados	ind#749	,	205221	125147	210238	223231	126132	192198	157157	234234	188200	106148
barbados	ind#750	,	203235	123123	230234	223231	126132	192198	157157	236256	188214	122136
barbados	ind#751	,	203211	121143	212248	223229	126132	190196	157159	234242	214216	118128
barbados	ind#752	,	213217	123169	204234	223231	126134	190198	157163	236248	193224	142148

Barred hamlet (*H. puella*) microsatellite dataset

Exercise 3



Ecology, 90(11), 2009, pp. 3087–3098
© 2009 by the Ecological Society of America

Estimating dispersal from genetic isolation by distance
in a coral reef fish (*Hypoplectrus puella*)

OSCAR PUEBLA,^{1,2,3} ELDREDGE BERMINGHAM,^{1,2} AND FRÉDÉRIC GUICHARD²

- 10 highly variable microsatellite loci
- 854 individuals
- 15 Caribbean locations

Take-home messages

- Testing for HWE can tell us whether a population is behaving like an ideal population or not
- Tests should be conducted over multiple loci, because not all loci may show the same pattern with respect to HWE
- Microsatellites are a widely used type of marker in population genetics