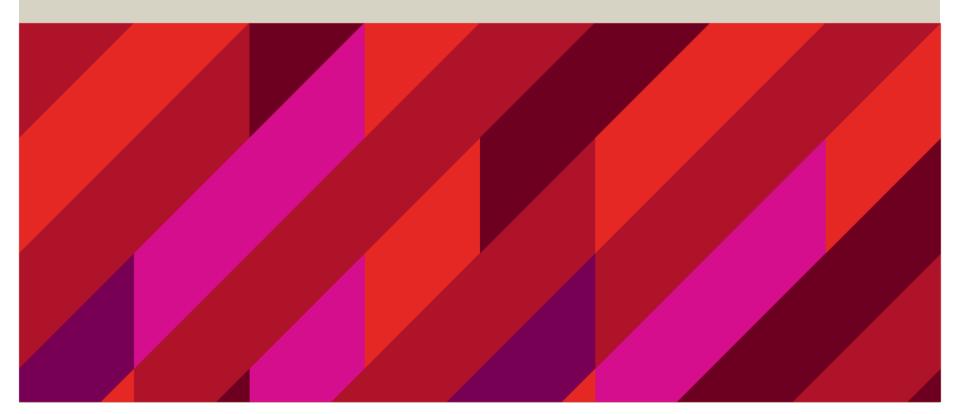


BIOL3110 Conservation & Ecological Genetics

LECTURE 3: GENETIC VARIATION





Assignment 1: Commentary

WORTH 5 % **DUE FRIDAY WEEK 3 (7/3/22) MONDAY 5PM**

Criterion	Marks
Get it between 500-600 words	1
Relevance of paper selection	1
Presentation, spelling, grammar	1
Genuine effort to interpret the paper	2

TIPS:

- Don't include quotations
- Cite the focal paper (at the end)
- Can include an image plus SHORT caption
- Hone in on the relevance of VG for conservation
- Choose a paper that you find most interesting
- Consider your seminar!







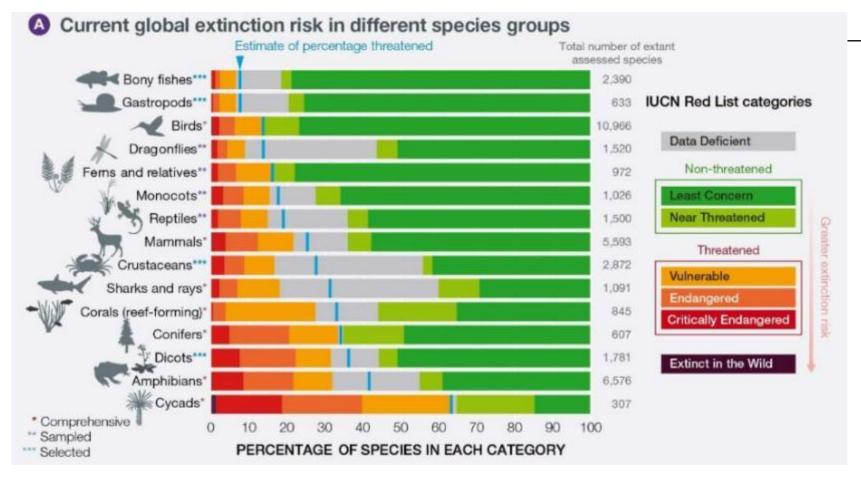






Globally, > one million species are threatened □







Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (2019)

BIOL3110 3

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IMPORTANCE (ACCORDING TO IUCN):

- Key constituent of biodiversity;
- 2. Required for adaptation
- Necessary for reducing inbreeding





TODAY:

- Review what it is and where it comes from
- Its role in guiding conservation
- Methods for measuring $V_G >>$
- Some examples of cons relevance











WHAT IS IT?

SIMPLY: DIFFERENCES IN DNA SEQUENCES

170 180 190
ATCTCTTGGCTCCAGCATCGATGAAGAACGCA
TCATTTAGAGGAAGTAAAAGTCGTAACAAGGT
GAACTGTCAAAACTTTTAACAACGGATCTCTT
TGTTGCTTCGGCGGGGCCCGCAAGGGTGCCCG
GGCCTGCCGTGGCAGATCCCCAACGCCGGGCC
TCTCTTGGCTCCAGCATCGATGAAGAACGCAG
CAGCATCGATGAAGAACGCATCGATGAAGAAC
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC
ACAACGGATCTCTTGGCTCCAGCATCGATGAA
CGGATCTCTTGGCTCCAGCATCGATGAACAC
GATGAAGAACGCAGCGAAACGCATCGATGAA



This week (Lectures 3 & 4)



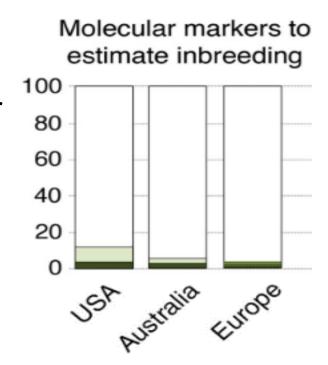
Whole Organism (Phenotype) V_G individual traits

Next week (Lectures 5 & 6)

Are genetic processes appropriately considered



> 300 threatened species recovery plans assessed for consideration of evolutionary factors (genetics)



Pierson et al (2016). Frontiers in Ecology and the Environment 14: 433-440

MEASUREMENT INDICES



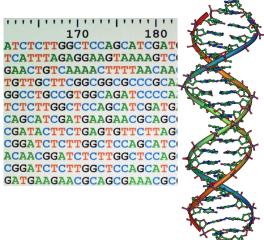
For individual loci:



- Polymorphism (P)
 - = proportion of polymorphic loci;



- Average heterozygosity (H)
 - = proportion of heterozygous loci per individual;
- Allelic diversity (A)
 - = average number of different alleles per locus.



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POLYMORPHISM (P)

Simple ratio of the number of polymorphic loci Eg:

Locus	Allele frequencies			
A	0.56	0.33	0.11	
В	0.70	0.20	0.10	
C	0.80	0.20		
D	1.0			
E	1.0			

$$\frac{\sum N_P}{N_T}$$

Where: N_P = number of polymorphic loci N_T = total number of loci

$$P = 3/5 = 0.6$$





HETEROZYGOSITY (H)

For a single locus (H for monomorphic locus =0) Eg:

Locus	Alleles & frequencies			
	A1 A2		A3	
ADA	0.56	0.33	0.11	

$$H = 1-(0.56^2 + 0.33^2 + 0.11^2)$$

= 1-(0.434)
= 0.564

$$H = 1 - \sum_{i} P_i^2$$

Where P_i = frequency of allele i



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AVERAGE HETEROZYGOSITY (H)

For multiple loci Simple average across them Eg:

$$\frac{\sum H_i}{N_T}$$

Where: $H_i = H$ at locus i $N_T = \text{total number of loci}$

Locus	Alleles & frequencies			Н
	A1			
ADA	0.56	0.33	0.11	0.564
BDA	1.00	0	0	0.000

Average H =
$$(0.564 + 0.000)/2$$
 = 0.282

MACQUARIE University

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ALLELIC DIVERSITY (A)

Simple average number of alleles per locus. Eg:

Locus	Allele frequencies			
A	0.60	0.25	0.13	0.12
В	0.70	0.10	0.10	0.10
C	0.50	0.30	0.20	
D	0.55	0.45		
E	0.85	0.15		
F	0.90	0.10		

$$A = \frac{\sum (N_A)}{N_T}$$

Where:

 N_A = number of different alleles across all loci N_T = total number of loci examined

$$A = 17/6 = 2.83$$

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(Example Chap 3 in textbook)

Calculate:

Polymorphism (P)

Average Heterozygosity (H)

Allelic diversity (A)



Locus	Allele frequencies			Н
ADA	0.56	0.33	0.11	0.564
DIAB	0.61	0.39		0.476
ESI	0.88	0.12		0.211
GPI	0.85	0.15		0.255
GPT	0.89	0.11		0.196
MPI	0.92	0.08		0.147
20 others	1.00			0.00

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6 of 26 loci polymorphic:

$$P = \frac{6}{26} = 0.23$$

H for the **average individual**:

$$\frac{\sum H}{26} = \frac{(0.564 + 0.476 + 0.211...)}{26} = 0.071$$

Allelic diversity (A):

$$\frac{[(1 \times 3) + (5 \times 2) + (20 \times 1)]}{26} = \frac{33}{26} = 1.27$$

Hence, an average of 1.27 alleles per locus



Locus	Allele frequencies			Н
ADA	0.56	0.33	0.11	0.564
DIAB	0.61	0.39		0.476
ESI	0.88	0.12		0.211
GPI	0.85	0.15		0.255
GPT	0.89	0.11		0.196
MPI	0.92	0.08		0.147
20 others	1.00			0.00

Individual H

- is it close to HWE expectations?
- What does this imply?

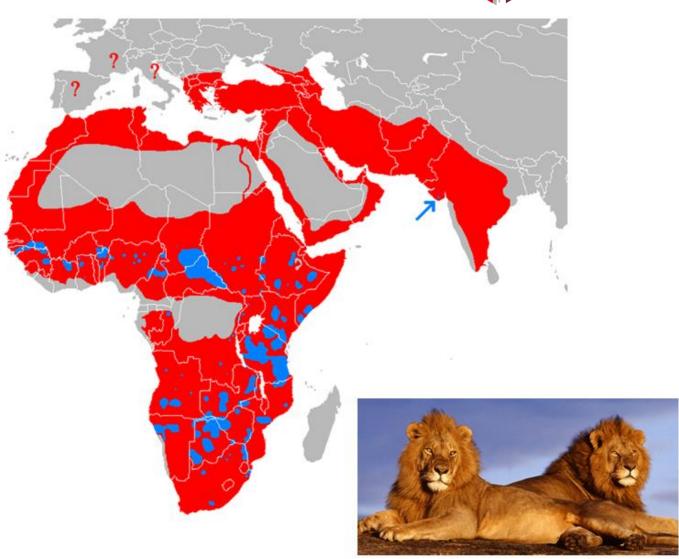
Panthera leo



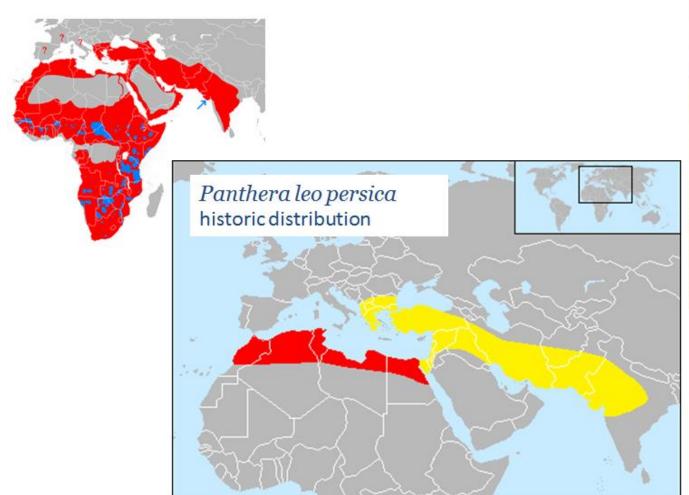
Distribution:

Historic

Current



Panthera leo persica Asiatic lion







15

Panthera leo persica





1974: 180 individuals **2010:** 411 individuals

- 97 adult males

162 adult females

- 75 sub-adults

77 cubs



भारत INDIA

16

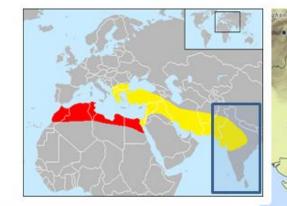
300

पैन्थेरा लिओ पर्सिका Panthera leo persica

Panthera leo persica

Genetic diversity

50 allozyme (protein) loci DNA fingerprints







	Alloz	DNA fingerprints	
	P	H	Н
Asiatic lion	0.00	0.000	0.038
African lion (outbred)	0.04-0.11	0.015-0.300	0.450

- Indicative of extreme bottleneck in recent past (N~20 in early 1900's)
- Problematic for inbreeding depression, lack of population resilience and reduced adaptive potential

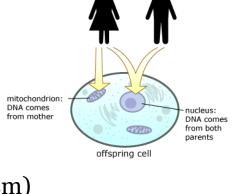
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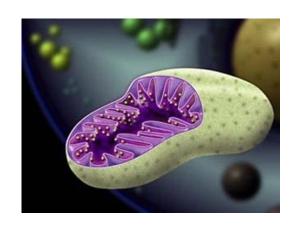
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ASSESSMENT AT SINGLE LOCUS LEVEL

- **Proteins** (allozyme electrophoresis)
- Nuclear DNA amplification via PCR
 - Microsatellites (sequence repeats)
 - SNPs (single nucleotide polymorphism)
 - AFLP (amplified fragment length polymorphism)
 - RAPD (Randomly amplified polymorphic DNA)
 - Sequencing
 - Plus other techniques... (see Box 3.3 Frankham *et al.*)
- Mitochondrial DNA







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MICROSATELLITES

- Repeats of 1-5bp sequences
 - 1. Simple Sequence Repeats (STRs)
 - 2. Short Tandem Repeats (STRs)

6 Repeats of 2bp segment e.g: XCACACACACAY
XGTGTGTGTGTY

- Highly variable
- Mostly **neutral DNA** (non-coding regions)
- Potential for non-invasive sampling

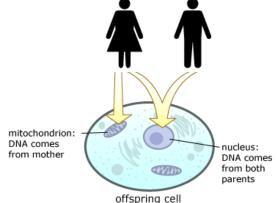
AKA GENETIC VARIATION OR VARIANCE

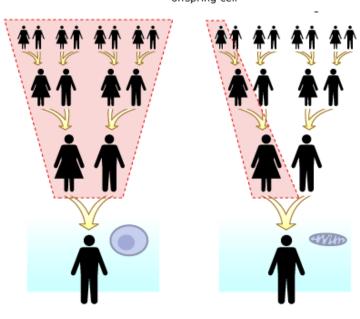
MITOCHONDRIAL DNA

- Haploid maternally-inherited DNA
- No recombination
- Useful in cons gen to:
 - 1. Resolve taxonomic uncertainties
 - 2. Define management units (haplotypes)
 - 3. Understand species biology

DNA in plant chloroplasts is equivalent







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MAJOR HISTOCOMPATABILITY COMPLEX

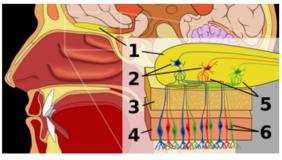


- Code for proteins for surface antigens in 2 classes:
 - Class I

Recognize intracellular pathogens and 'tag' the cell for immune system components (T-cells, phages etc).

- Class II
- Highly polymorphic loci with very high allelic diversity
- Sexual selection implicated in maximising population heterozygosity: mate choice for MHC diversity (via olfactory cues in humans)



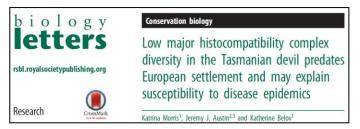


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MHC DIVERSITY & DEVIL FACIAL TUMORS (DFTD)

Historically low VG in MHC:

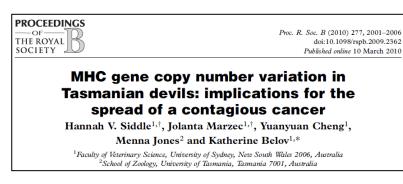


Recovery implications:

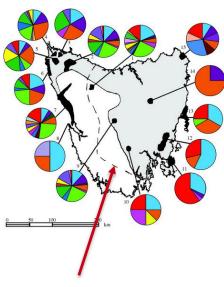
Most DFT cells express MHC classes 1 & 2 20% of devils only have class 1 or 2 genes MHC1 devils may detect DFT cells

expressing MHC1&2

Counterintuitive example

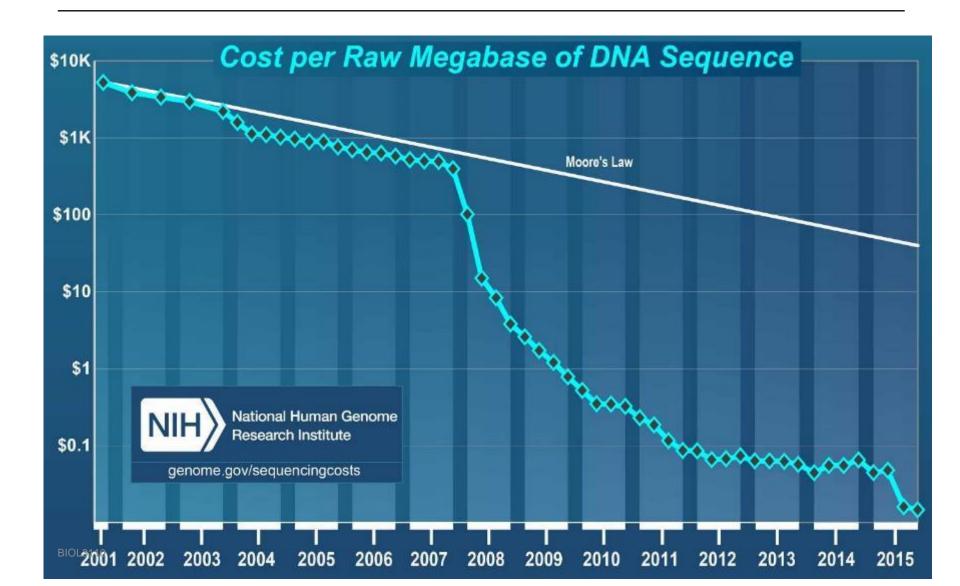






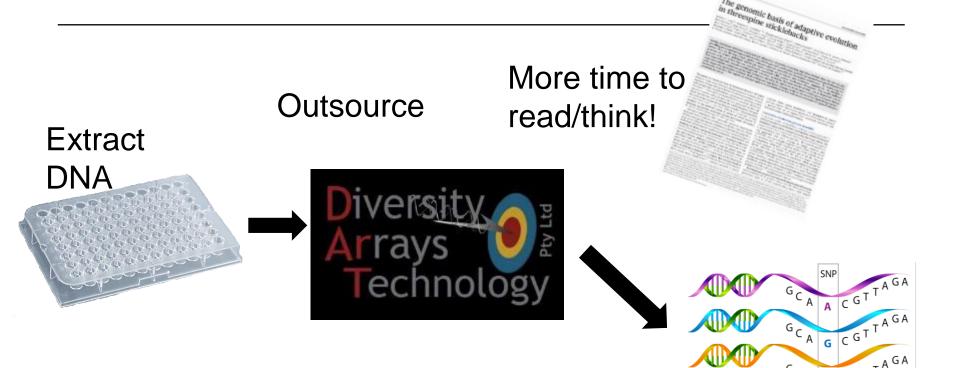
Extent of spread





Modern genomic workflow





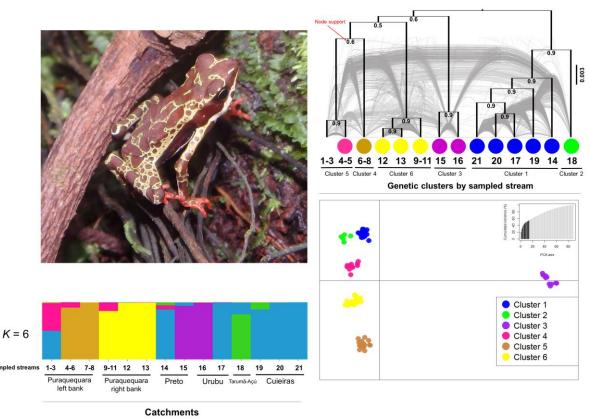


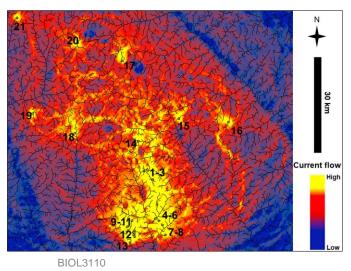
More time to develop bioinformatic skills

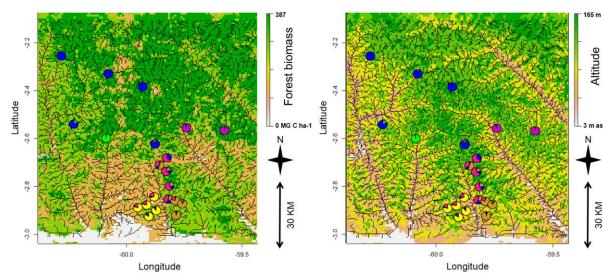


- 1) Biodiversity patterns- diversity, distribution,distinctiveness
- 2) Estimating dispersal, genetic connectivity

3) Identifying processes







Next lecture:



Characterising V_G for single loci More detail & examples

