

# Identifying unique national genetic resources in an international setting

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Slide 1

## Introduction

- Benchmark sets
  - Safe set analysis
  - Core set diversity
- Mean kinships between and within populations
  - Estimated from marker genes

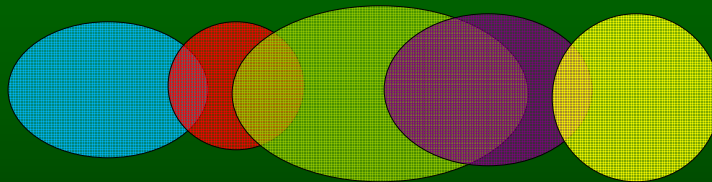
## Core sets: Intro

- Elimination of overlap
  - Plant breeding (Frankle and Brown, 1984)
  - In or out decision



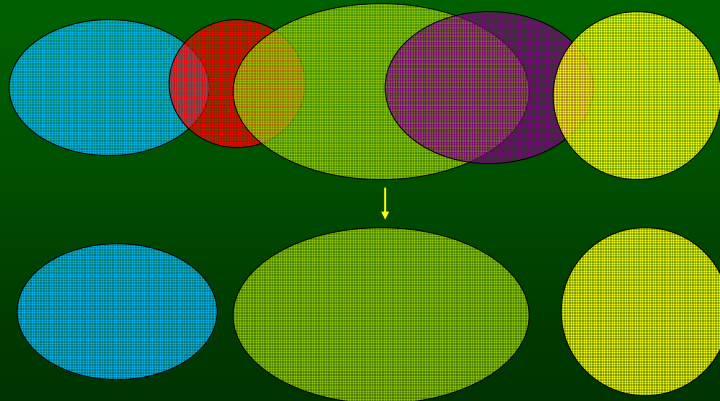
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    - Full sibs, parent offspring:  $f = 0.25$

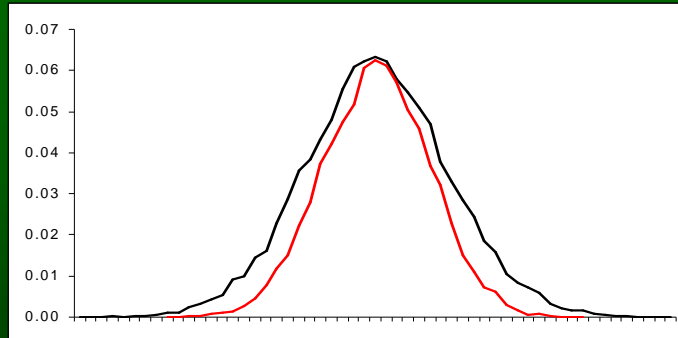


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  - What overlap?
- Mean kinship between populations
  - Kinship is defined as  $P(\text{allele } X = \text{allele } Y) = f$ 
    - Full sibs, parent offspring:  $f = 0.25$
  - But also  $\text{var}(G_t) = \text{var}(G_0) \times (1 - f)$ 
    - Falconer and MacKay, 1996



## Core set: Measure of diversity



$f =$   
0.25  
 $f = 0$

Genetische variatie

## Core sets : Measure of diversity

- Kinships
  - Common alleles
  - Decrease in genetic variance

## Core sets : Measure of diversity

- Kinships
  - Common alleles
  - Decrease in genetic variance
- Minimizing Kinship
  - Minimizing overlap
  - Maximizing genetic variance



## Core sets: Principle

- Suppose:

$$F = \begin{vmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 1 & 1 \end{vmatrix}$$

- Mean(F) =  $5/9 = 0.55$ 
  - Var(Gt) =  $0.45 \text{ var}(Go)$



## Core sets: Principle

•Suppose:

$$F = \begin{array}{c|ccc} & 1 & 0 & 0 \\ & 0 & 1 & 1 \\ & 0 & 1 & 1 \end{array}$$

•Mean(F) =  $5/9 = 0.55$

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•Suppose:

$$F = \begin{array}{c|ccc} & 1 & 0 & 0 \\ & 0 & 1 & 1 \\ & 0 & 1 & 1 \end{array}$$

•Mean(F) =  $5/9 = 0.55$

•Var(Gt) = 0.45 var(Go)

•Elimination of (3): Mean(F) =  $2/4 = 0.50$

•Var(Gt) = 0.50 var(Go): Diversity increased



## Core sets: Principle

- Solution: Contributions to Core set

$$F = \begin{array}{ccc|c} 1 & 0 & 0 & \frac{1}{2} \\ 0 & 1 & 1 & \frac{1}{4} \\ 0 & 1 & 1 & \frac{1}{4} \end{array}$$

- Mean(F) =  $(\frac{1}{2} * 1 + \frac{1}{4} * 4) / (3 * \frac{1}{2} + 2 * 3 * \frac{1}{4}) = 0.5$

- Var(Gt) = 0.50 var(Go)

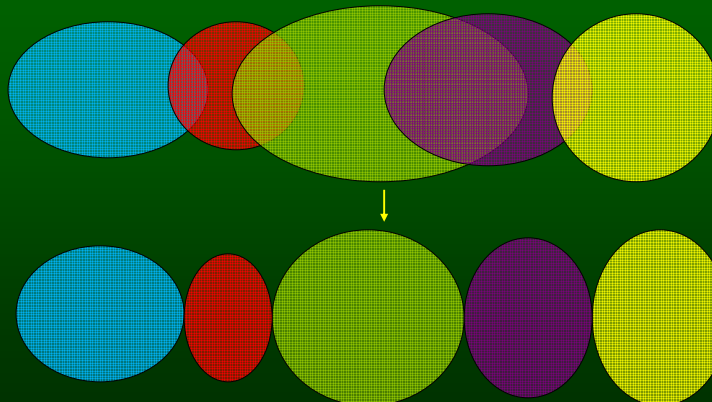
- Mean kinship (and thus overlap) is minimized



## Core sets: Principle

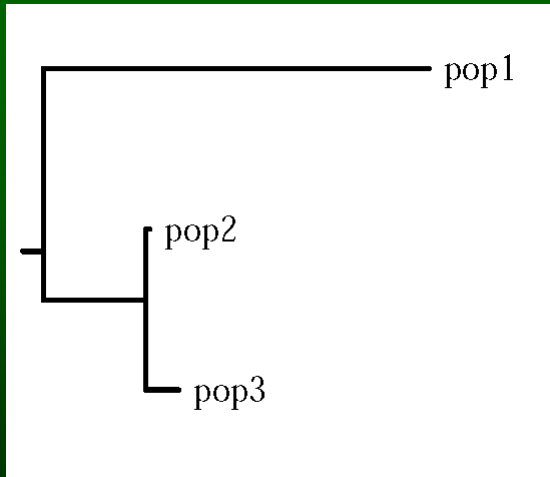
- Elimination of overlap

- By relative contributions:





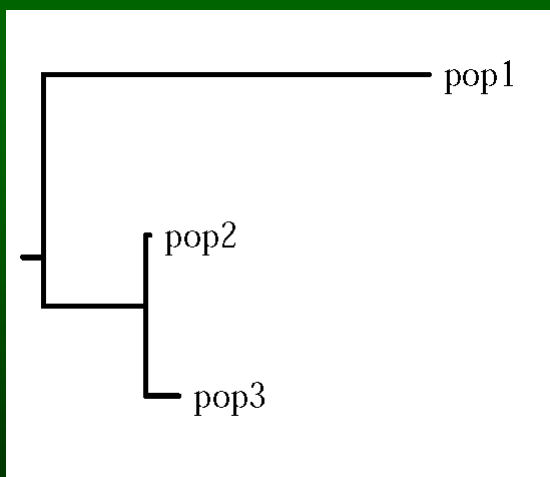
## MEK: Small example



|      |              |              |              |
|------|--------------|--------------|--------------|
| Pop1 | <b>0.361</b> | 0.000        | 0.013        |
| Pop2 |              | <b>0.100</b> | 0.096        |
| Pop3 |              |              | <b>0.127</b> |



## MEK: Small example



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| Pop1 | <b>0.361</b> | 0.000        | 0.013        |
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| Pop3 |              |              | <b>0.127</b> |

|      |              |
|------|--------------|
|      | <b>c</b>     |
| Pop1 | <b>0.217</b> |
| Pop2 | <b>0.774</b> |
| Pop3 | <b>0.009</b> |



## Core set: Conclusions

- Largest contributions
  - Populations with the least drift
  - Closest to original ancestors
    - Least number of extinct alleles
- Small contributions
  - High levels of drift/inbreeding
  - Sub population of larger population
- Core set tries to conserve founder variance



## Illustrations: National vs. International

- Mateus et al., 2004: Portuguese cattle
  - 11 indigenous breeds
    - Alentejana, Arouquesa , Barrosa , Barva de lide, Cachena, Garvonesa, Marinhola, Maronesa, Mertolenga, Minhota, Mirandesa
  - 4 exotics
    - Charolais (USA), Charolais (PT), Limousin, Holstein Friesian
- Analysis
  - Core set Portuguese indigenous breeds only
  - Core set including exotics
  - Safe set analysis; Exotics as Safe set

## Illustrations: National vs. International

### Core sets

|                      | <b>Porto</b> |
|----------------------|--------------|
| <i>Mertolenga</i>    | 0.238        |
| <i>Cachena</i>       | 0.220        |
| <i>Arouquesa</i>     | 0.027        |
| <i>Maronesa</i>      | 0.136        |
| <i>Marinhao</i>      | 0.000        |
| <i>Barrosa</i>       | 0.000        |
| <i>Garvonesa</i>     | 0.146        |
| <i>Alentejana</i>    | 0.000        |
| <i>Minhota</i>       | 0.152        |
| <i>Mirandesa</i>     | 0.023        |
| <i>Barva de lide</i> | 0.059        |

Mateus et al. (2004), Anim. Genet.

## Illustrations: National vs. International

### Core sets Incl. exotics

|                      | <b>Porto</b> | <b>Incl. exotics</b> |
|----------------------|--------------|----------------------|
| <i>Mertolenga</i>    | 0.238        | 0.310                |
| <i>Cachena</i>       | 0.220        | 0.215                |
| <i>Arouquesa</i>     | 0.027        | 0.034                |
| <i>Maronesa</i>      | 0.136        | 0.136                |
| <i>Marinhao</i>      | 0.000        | 0.008                |
| <i>Barrosa</i>       | 0.000        | 0.000                |
| <i>Garvonesa</i>     | 0.146        | 0.131                |
| <i>Alentejana</i>    | 0.000        | 0.000                |
| <i>Minhota</i>       | 0.152        | 0.108                |
| <i>Mirandesa</i>     | 0.023        | 0.053                |
| <i>Brava de lide</i> | 0.059        | 0.003                |

Mateus et al. (2004), Anim. Genet.

## Safe sets and benchmarks

- Safe set analysis
  - Construct a set of resources that are 'safe'
    - No immediate risk of extinction
    - Widely used
  - Add breed  $i$  to the Safe set
  - Calculate contributions to  $\text{Div}(s+i)$
- Reranking relative to whole set analysis

## Illustrations: National vs. International

|                      | Porto | Core sets     |       |       |
|----------------------|-------|---------------|-------|-------|
|                      |       | Incl. exotics | S + i | AD(i) |
| <i>Mertolenga</i>    | 0.238 | 0.310         | 0.463 | 0.021 |
| <i>Cachena</i>       | 0.220 | 0.215         | 0.399 | 0.018 |
| <i>Arouquesa</i>     | 0.027 | 0.034         | 0.392 | 0.014 |
| <i>Maronesa</i>      | 0.136 | 0.136         | 0.329 | 0.014 |
| <i>Marinhao</i>      | 0.000 | 0.008         | 0.319 | 0.013 |
| <i>Barrosa</i>       | 0.000 | 0.000         | 0.283 | 0.012 |
| <i>Garvonesa</i>     | 0.146 | 0.131         | 0.277 | 0.011 |
| <i>Alentejana</i>    | 0.000 | 0.000         | 0.261 | 0.011 |
| <i>Minhota</i>       | 0.152 | 0.108         | 0.258 | 0.010 |
| <i>Mirandesa</i>     | 0.023 | 0.053         | 0.190 | 0.009 |
| <i>Brava de lide</i> | 0.059 | 0.003         | 0.174 | 0.006 |

Mateus et al. (2004), Anim. Genet.

## Illustrations: National vs. International

|                      | Porto    | Core sets     |              | AD( <i>i</i> ) |
|----------------------|----------|---------------|--------------|----------------|
|                      |          | Incl. exotics | S + <i>i</i> |                |
| <i>Mertolenga</i>    | 0.238(1) | 0.310(1)      | 0.463        | 0.021(1)       |
| <i>Cachena</i>       | 0.220(2) | 0.215(2)      | 0.399        | 0.018(2)       |
| <i>Arouquesa</i>     | 0.027(9) | 0.034(7)      | 0.392        | 0.014(3)       |
| <i>Maronesa</i>      | 0.136(5) | 0.136(3)      | 0.329        | 0.014(4)       |
| <i>Marinhao</i>      | 0.000    | 0.008(8)      | 0.319        | 0.013(5)       |
| <i>Barrosa</i>       | 0.000    | 0.000         | 0.283        | 0.012(6)       |
| <i>Garvonesa</i>     | 0.146(4) | 0.131(4)      | 0.277        | 0.011(7)       |
| <i>Alentejana</i>    | 0.000    | 0.000         | 0.261        | 0.011(8)       |
| <i>Minhota</i>       | 0.152(3) | 0.108(5)      | 0.258        | 0.010(9)       |
| <i>Mirandesa</i>     | 0.023(8) | 0.053(6)      | 0.190        | 0.009(10)      |
| <i>Brava de lide</i> | 0.059(6) | 0.003(9)      | 0.174        | 0.006(11)      |

Mateus et al. (2004), Anim. Genet.

## Conclusion

- Special breeds get same priority national and international
  - Different from other breeds
  - High within variation
- Changes in priority in next breeds
  - Risk of priority to exotic diversity influences
- Safe set analysis
  - Tests individual breeds for added diversity
  - Added diversity assessed on strictly own merit
  - Exotics accounted for through inclusion in Safe set

## Recommendations + discussion

- Think globally
  - Gather data of all populations possibly influencing national genetic resources
- Construct benchmark “safe” set
- Test each national genetic resource in safe + 1 set
  - Unique diversity determines priority
- Global safe set needed?
- Who conserves genetic variation in safe set?
- What to do with transboundary breeds?

Thank you