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Ph.D. (III Semester)

GPB-607 (Crop Evolution) 3 (3+0)

Topic: Concept of gene pools and Crop Evolution

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DEPARTMENT OF GENETICS AND PLANT BREEDING

Gene pool

The **gene pool** is the set of all genes, or genetic information, in any population, usually of a particular species.

History

The Russian geneticist **Aleksandr Sergeevich Serebrovskii** first formulated the concept in the 1920s as *genofond* (gene fund), This word that was imported to the United States from the Soviet Union by **Theodosius Dobzhansky**, who translated it into English as “gene pool.”

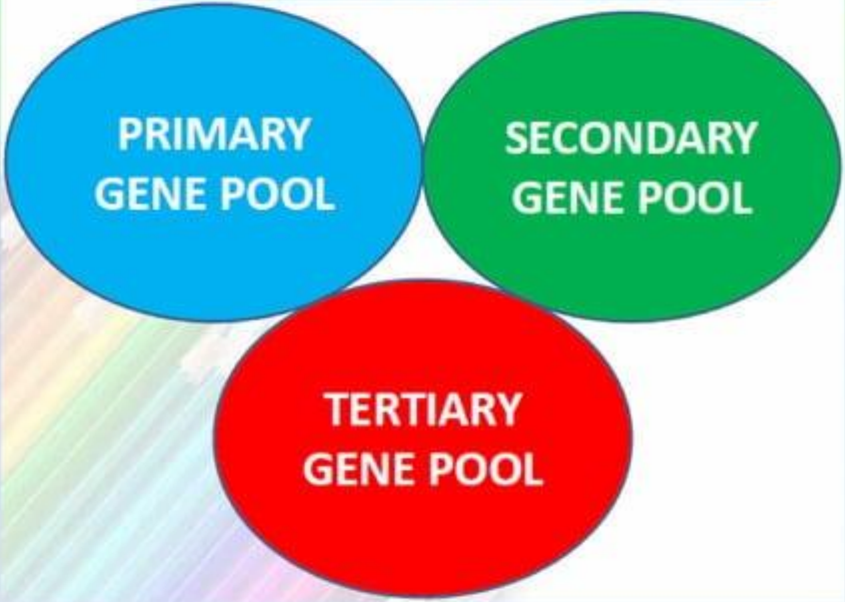
Rational behind 'Gene Pool'

✓A large gene pool indicates extensive genetic diversity, which is associated with robust populations that can survive bouts of intense selection.

✓Meanwhile, low genetic diversity (inbreeding and population bottlenecks) can cause reduced biological fitness and an increased chance of extinction, although as explained by genetic drift new genetic variants, that may cause an increase in the fitness of organisms, are more likely to fix in the population if it is rather small.

✓When all individuals in a population are identical with regard to a particular phenotypic trait, the population is said to be 'monomorphic. *When the individuals show several variants of a particular trait they are said to be polymorphic.*

TYPES OF GENE POOL



Gene pool concept in crop breeding
or
The Gene Pool System of Classification

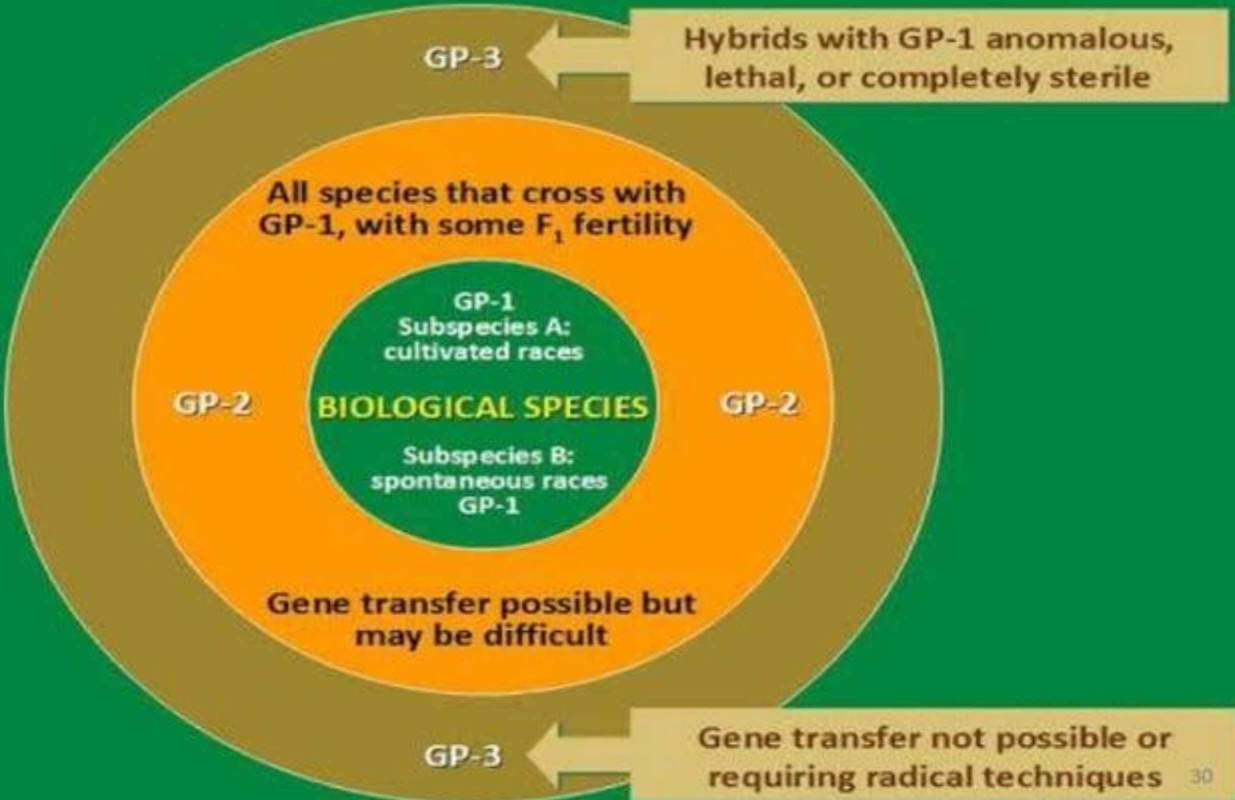
[Harlan and de Wet (1971)]

Gene pool of a crop included all cultivars (Obsolete and current) , wild species and wild relatives containing all the genes available for breeding use.

Based on degree of relationship, the gene pool of a crop can be divided into three groups, viz.

1) Primary gene pool,
2) Secondary gene pool,
3) Tertiary gene pool

The genepool concept
Harlan & de Wet 1971



1. Primary Gene Pool (GP1):

- Members of this gene pool are in the same "species" (in conventional biological usage) and can intermate freely and leads to production of fertile hybrids.
- It includes plants of the same species or of closely related species which produce completely fertile offspring's on inter-mating.
- Hybrids have good chromosome pairing; gene segregation is approximately normal and gene transfer is generally easy.
- In such gene pool, genes can be exchanged between lines simply by making normal crosses. This is also known as gene pool one (GP1).
- This is the material of prime breeding importance and each crop gene pool can be subdivided into two:

  Subspecies A: Cultivated races

  Subspecies B: Spontaneous races (wild or weedy)

Example of primary gene pool

- The primary gene pool of both cultivated and wild varieties of sunflower(*Helianthus annus*) .
- A winter's sunflower (*H.winterii)* a perennial grass in south Siberia whose genes are easy to be bought in cultivated ones.
- So both constitute members of gene pool 1.

2. Secondary Gene Pool (GP2):

- Members of **Secondary Gene Pool** are normally classified as different species than the crop species under consideration (the primary gene pool).
- These species are closely related to species of GP1 and can cross to produce fertile or partially fertile hybrids with them.
- Transfer of gene from such material to primary gene pool is possible but difficult.
- There is some reproductive barrier between members of the primary and secondary gene pools and leads to:
  i. Partially sterile, weak Hybrids.
  ii. Chromosomes may pair poorly or not at all.
  iii. Recovery of desired phenotypes may be difficult in subsequent generations.
  iv. The gene pool is available to be utilized by plant breeder or geneticist with due effort required."

Example of secondary gene pool

- *Aegilops tauschii* AND *Aegilopes speltoides,* two wild relatives in secondary gene pool of bread wheat (*Triticum aestivum*)are diploid. That means that they have paired chromosomes whereas **bread wheat** is hexaploid(six copies).
- So, some crosses if result from this would be partially sterile or weak.
- THESE CONSTITUTE SECONDARY GENE POOL

3. Tertiary Gene Pool (GP3):

- The genetic material which leads to production of sterile hybrids on crossing with primary gene pool is termed as tertiary gene pool or gene pool three (GP3).
- It includes material which can be crossed with GP1, but the hybrids are sterile.
- Members of this gene pool are more distantly related to the members of the primary gene pool.
- Transfer of gene from such material to primary gene pool is possible.
- The primary and tertiary gene pools can be intermated, but gene transfer between them is impossible without the use of special techniques "rather extreme or radical measures" such as:
    i. Embryo rescue (or embryo culture, a form of plant organ culture)
    ii. Induced polyploidy (chromosome doubling)
    iii. Bridging crosses (*e.g.*, With members of the secondary gene pool).

Example of tertiary gene pool

- *Triticum turgidum* (AABB, 2n=28) and
- *Aegilops speltoides*(BB,2n=14)

produce amphdipoid hybrid (INTERGENERIC CROSS).

This can be made fertile using various techniques like colchicine treatment.

EXAMPLE OF A SUCESSFUL CROSS BEING *Triticale* DEVELOPED BY RIMPAU.

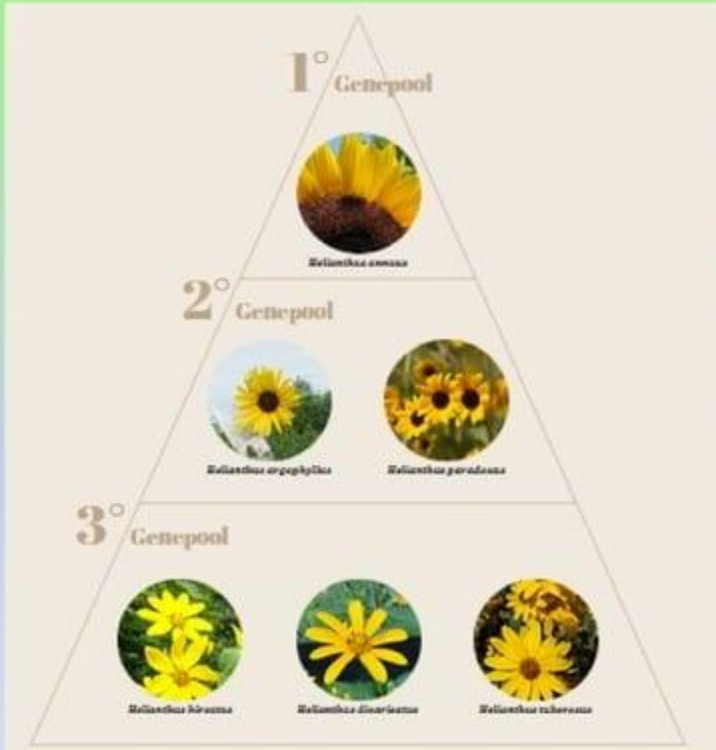
Gene pool centers

- Gene pool centers are areas on the earth where important crop plants and domestic animals originated.
- They have an extraordinary range of the wild counterparts of cultivated plant species and useful tropical plants.
- They also contain different sub tropical and temperate region species.
- They represent a reservoir of diversity that can be tapped into by organisms to adapt to a changing environment, and by scientists for plant breeding and crop improvement.
- In the system of Jack Harlan and Jan de Wet, Crossable Wild Relatives species are classified into groups based on how easy it is for them to exchange genes with the cultivated species to which they are related.
- In this system, wild relatives are said to be in the crop's primary, secondary or tertiary genepools.

1° Genepool
Helianthus annuus

2° Genepool
Helianthus argophyllus
Helianthus paradoxus

3° Genepool
Helianthus hirsutus
Helianthus divaricatus
Helianthus tuberosus



Evolutionary closeness is correlated with ease of crossing. Developed by Maxted *et al.* (2006), the "taxon group" concept uses existing taxonomic classifications, based on evolutionary relatedness, to predict which species will be easiest to use.

Why study of Gene Pool Concept is Important

- In the past huge gene pools of various wild and indigenous breeds have collapsed causing widespread genetic erosion and genetic pollution. This has resulted in loss of genetic diversity and biodiversity as a whole.
- Immigration may also result in the addition of new genetic variants to the established gene pool of a particular species or population. High rates of gene flow can reduce the genetic differentiation between the two groups, increasing homogeneity.
- For this reason,gene flow has been thought to constrain speciation by combining the gene pools of the groups, and thus, preventing the development of differences in genetic variation that would have led to full speciation.
- Endemic species can be threatened with extinction through the process of genetic pollution, i.e. uncontrolled hybridization, introgression and genetic swamping. The abundant species can interbreed with the rare species, swamping its gene pool.

Genecology

Genecology is a branch of ecology which studies genetic variation of species and communities compared to their population distribution in a particular environment. It is closely related to ecogenetics, but genecology focuses primarily on an ecological perspective, looking at changes and interactions between species, while eco-genetics focuses more on species' genetic responses to the environment.

VARIATION

Variation is the differences that exist between individuals… each individual organism is unique, even clones show some variation. It can occur within or between species and can be continuous or discontinuous…

- Continuous Variation ? the individuals within a population vary within a range, there are no distinct categories. (e.g. height weight)
- Discontinuous Variation ? each individual falls into only one of the two or more distinct categories, there are no intermediates. (e.g. blood group, gender)

Variation can be influenced by…

- Your genes
- The environment
- Both

EFFECT OF GENES

Different species have different genes and individuals of the same species have the same genes but have different versions of them (alleles). The difference in the genotype of an organism results in phenotypic variation. For example, there are three different blood group alleles which result in four different blood groups. Inherited characteristics that show continuous variation are polygenic (influenced by many genes). For example, human skin colour.

Inherited characteristics that show discontinuous variation are usually monogenic (influenced by only one gene). For example, violet flower colour.

THE ENVIRONMENT

Variation can also be caused by differences in the environment such as climate, food and lifestyle. Characteristics influenced by the environment can change over an organisms life…

For example, accent is determined by where you grew up, where you live now and the accents of people around you. Similarly, pierced ears is only determined by environmental factors such as fashion or peer pressure.

BOTH

Genetic factors determine genotype and the characteristics an organism’s born with, but environmental factors can influence how some characteristics develop. Most phenotypic variation is caused by the combination of genotype and environmental factors. Phenotypic variation influenced by both usually shows continuous variation.

For example, human body mass is partly genetic but it is also strongly influenced by environmental factors like diet and exercise.

Also, pea plants come in tall and dwarf forms which is determined by genotype. However, the exact height varies because of environmental factors such as light intensity and water availability.

EVOLUTION

The complete range of alleles present in a population is called the gene pool and new alleles are usually generated by mutations in genes. Evolution is a change in allele frequency (how often an allele occurs). Variation is generated by meiosis and mutations and occurs by natural selection…

selection pressures (predation, disease, competition) create a struggle for survival and the ones who survive are those best adapted – these individuals have a beneficial allele and are most likely to reproduce and pass on the beneficial alleles to their offspring. As a result, a greater proportion of the next generation inherit the beneficial allele and so on... So, the frequency of the beneficial allele increases from generation to generation.

CHANGE IN ENVIRONMENT

The environment affects which characteristics become more common via natural selection. When the environment isn't changing much, individuals with alleles for characteristics towards the middle of the range are more likely to survive and reproduce. This is called stabilising selection and it reduces the range of possible phenotypes. For example, in any mammal populations there's a range of fur lengths. In a stable climate, having fur at the extremes of this range reduces the chance of surviving as it's harder to maintain the right body temperature. Animals with alleles for average length fur are most likely to survive, reproduce and pass on their alleles to their offspring. When there's a change in the environment, individuals for alleles for characteristics of an extreme type are more likely to survive and reproduce. This is called directional selection. For example, if the environment becomes very cold, individual mammals with alleles for long fur will find it easier to maintain the right body temperature and survive and reproduce.

GENETIC DRIFT

Evolution also occurs due to genetic drift – instead of environmental factors, chance dictates which alleles are passed on. By chance, the allele for one genotype is passed on to the offspring more often than others. So, the number of individuals with the allele increases and if by chance the same allele is passed on more often again and again, it can lead to evolution as the allele becomes more common in the population.

Natural selection and genetic drift work alongside each other to drive evolution, but one process can drive evolution more than the other depending on the population size. Evolution by genetic drift usually has a greater effect in smaller populations where chance has a greater influence.

In larger populations, any chance factors tend to even out across the whole population.

ARTIFICIAL SELECTION

Artificial selection (selective breeding) is when humans select individuals in a population to breed together to get desirable traits. Important characteristics for these two cases include...

Modern Dairy Cattle

- High milk yield
- Large udders
- Long lactation period
- Docile/calm temperament
- Resistance to disease

Bread Wheat

- High wheat yield
- Resistant to disease
- Large ears

COMPARING

Natural Selection	Artificial Selection
The organisms that reproduce are selected by the environment	Humans select the organisms that reproduce
The result is unpredictable	The result is predetermined
The species will be better adapted to the environment	The species will be more useful for humans

Similarities…

- Both change the allele frequencies in the next generation – the alleles that code for the beneficial/desirable characteristics will become more common in the next generation
- Both may make use of random mutations when they occur – if a random mutation produces an allele that gives a beneficial/desirable phenotype, it will be selected for in the next generation

SPECIATION

Speciation is the development of a new species. It occurs when populations of the same species become reproductively isolated – changes in allele frequencies cause changes in phenotype that mean they can no longer breed together to produce fertile offspring.

Reproductive isolation occurs in many ways…

- Seasonal Changes (different mating seasons)
- Mechanical Changes (changes in genitalia)
- Behavioural Changes (courtship rituals which aren't attractive to the main
population)

GEOGRAPHICAL ISOLATION

Geographical isolation happens when a physical barrier divides a population (e.g. floods, volcanic eruptions, earthquakes) and this is known as allopatric speciation. Conditions on either side of the barrier will be slightly different and this means different characteristics will become more common due to natural selection (because there are different selection pressures). Because different characteristics will be advantageous on each side, the allele frequencies will change in each population. They are also changed by mutations which will take place independently. These changes lead to changes in phenotypic frequencies. Eventually, individuals from different populations will have changed so much they won't be able to breed with one another to produce fertile offspring – they'll be reproductively isolated and the two groups will have become different species.

CLASSIFYING A SPECIES

A species is traditionally defined as a group of similar organisms that can reproduce to give fertile offspring. Scientists usually have problems when deciding which species an organism belongs to – it could be a new, distinct species. This is because you can't always see their reproductive behaviour. For example, they might be extinct, reproduce asexually or there could be practical or ethical issues involved. Because of these problems, scientists sometimes use the phylogenetic species concept to classify organisms instead of the biological species concept. Phylogenetics is the study of evolutionary history – all organisms have evolved from shared common ancestors so the more closely related two species are, the more recently their last common ancestor will be. Scientists can use this to decide which species an organism belongs to, or if it's a new species. But, there are problems with classifying organisms using this concept. There are no cut-offs to say how different two organisms have to be different species (e.g. chimpanzees and humans are different species but about 94% of our DNA is exactly the same)

Eco-phenotypic physiologies: a new kind of modeling for unifying evolution, ecology and cultural transmission

We propose a mathematical **framework of formal relations** general enough to be applicable in

- biology (ecology and evolutionary biology)
- cultural transmission (economics)

We are interested in modeling some biological concepts we will call "eco-phenotypic concepts"

Development, plasticity, reaction norm, phenotypic heritability, epigenetics, and niche construction.

Physiology

Consider a population composed at each time of N_t agents and a set of resources R_t

A Physiology is an algorithm that defines the resource management behavior of the agent.

- the resources needed by the agent for the basic survival $\tilde{M}^i$
- the efficiency is the resource extraction α^i
- the efficiency of their use β^i
- the agent's *resource intake target* G_t^i

$$\bar{P}_t^i = (\tilde{M}_t^i, \alpha^i, \beta^i, G_t^i) \quad (1)$$

Environment

All the elements of the world and of the population that are not part of the agent.

- the resources R_t that are available to the population.
- The number of agents N_t
- the vector of all the other agents' physiologies $\bar{P}_t^{-i}$

$$\bar{E}_t^i = (R_t, N_t, \bar{P}_t^{-i}) \quad (2)$$

Resource extraction

$$\sum_i R_t^i \leq R_t$$

- own resource intake target G_t^i,
- others' resource intake targets G_t^{-i}
- the vector of all extraction efficiencies $\bar{\alpha}$

$$\bar{R}_t^i = (R_t, G_t^i, G_t^{-i}, \bar{\alpha}) \quad (3)$$

Notice that if $R_t^i < \tilde{M}_t^i$ then the agent dies.

Matching Function and Reproduction

each male with physiology i, that extracted R_t^i is matched with a female of physiology j that extracted R_t^j

γ_t^{ij} the share of R_t^i that an agent of physiology i in a ij matching devotes to own subsistence and $(1-\gamma_t^{ij})$ the share devoted for offspring production.

$$N_{t+1}^{ij}(R_t^i, R_t^j, \gamma_t^{ij}, \gamma_t^{ji}) \tag{4}$$

Niche construction and Resource Regeneration

$$R_{t+1} = (R_t - \sum_i R_t^i)(1 + \lambda)$$

if individuals resource extraction and physiologies are *niche constructing* then $\lambda_t(\bar{R}_t)$ so that

$$R_{t+1} = (R_t - \sum_i R_t^i)(1 + \lambda_t(\bar{R}_t)) \tag{5}$$

Reaction Norms and the New Generation's Physiology (I)

Reaction norm: dictates how to use or not use information from the environment and from parental physiologies as cues to form a new physiology.

The reaction norm X^i_{t+1} accepts as inputs

- the resources the new generation faces R_{t+1}
- the parental physiologies P^i_t and P^j_t
- the physiologies agents in new generation meet during their formation process $\bar{P}_t$

$$P^i_{t+1} = X^i_{t+1}(R_t, P^i_t, P^j_t, \bar{P}_t) \tag{6}$$

Reaction Norms and the New Generation's Physiology (II)

$$P_{t+1}^{i} = X_{t+1}^{i}(R_t, P_t^i, P_t^j, \bar{P}_t)$$

- with probability p_t^{ij} the new individual born from matching ij takes i's reaction norm $X_{t+1}^{i} = X_t^i$
- with probability $1 - p_t^{ij}$ the new individual born from matching ij takes j's reaction norm $X_{t+1}^{i} = X_t^j$.

Summing up the framework

- Physiology: $\bar{P}_t^i = (\tilde{M}_t^i, \alpha^i, \beta^i, G_t^i)$
- Environment: $\bar{E}_t^i = (R_t, N_t, \bar{P}_t^{-i})$
- Resource Extraction: $\bar{R}_t^i = (R_t, G_t^i, G_t^{-i}, \bar{\alpha})$
- Matching and Reproduction: $N_{t+1}^{ij}(R_t^i, R_t^j, \gamma_t^{ij}, \gamma_t^{ji})$
- Niche construction and resource generation: $R_{t+1} = (R_t - \sum_i R_t^i)(1 + \lambda_t(\bar{R}_t))$
- Reaction Norms and new physiology: $P_{t+1}^i = X_{t+1}^i(R_t, P_t^i, P_t^j, \bar{P}_t)$

Next Steps

- Fixing one reaction norm, studying how the shape of the different elements impact the dynamics of the population
- Compare the patterns of different reaction norms (adaptive and forward looking reaction norms)
- Make reaction norms compete (plasticity in most successful population, necessary feature for a reaction norm to survive, ...)

GENE-ENVIRONMENT INTERACTION

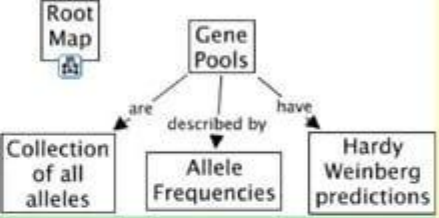
A change in how a particular allele is expressed that is caused by an environmental influence. Gene-environment interactions are an example of phenotypic plasticity.

FACULTATIVE TRAIT

A trait in which the phenotypic expression of the genotype has been shaped by natural selection such that environmental variation triggers the production of different adaptive phenotypes well-suited to that environment — i.e., a trait with adaptive phenotypic plasticity. For example, melanin level is a facultative trait. Humans that are exposed to higher levels of solar radiation produce more melanin, which provides protection from the sun. This response likely evolved through many generations of natural selection.

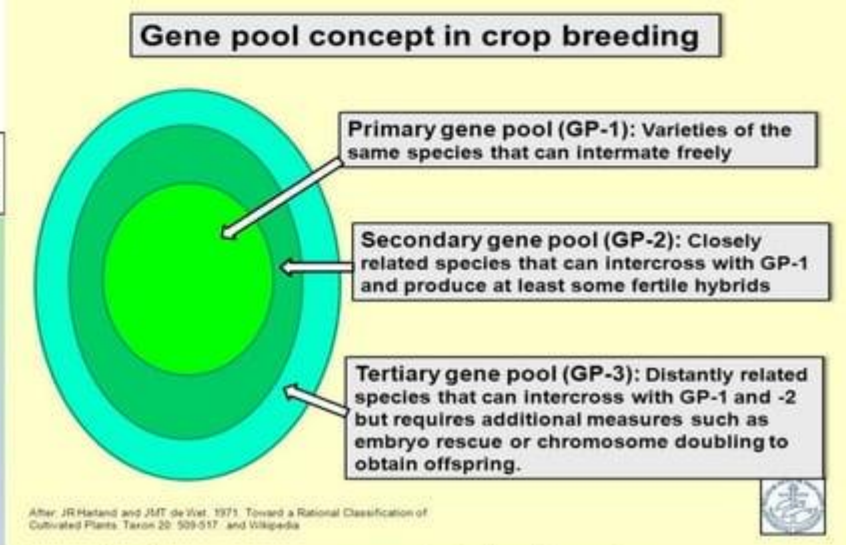
NORM OF REACTION

The pattern of phenotypic plasticity for a particular genotype. A norm of reaction describes the way in which a genotype is expressed as a trait under different environmental circumstances. For example, for a particular plant genotype that affects height, the norm of reaction in relation to watering level might look like a bell curve: very small and very large amounts of watering result in shorter plants and normal amounts of watering result in taller plants. For plant with a different genotype, the ideal amount of water to grow a tall plant might be different because this genotype might have a different norm of reaction.

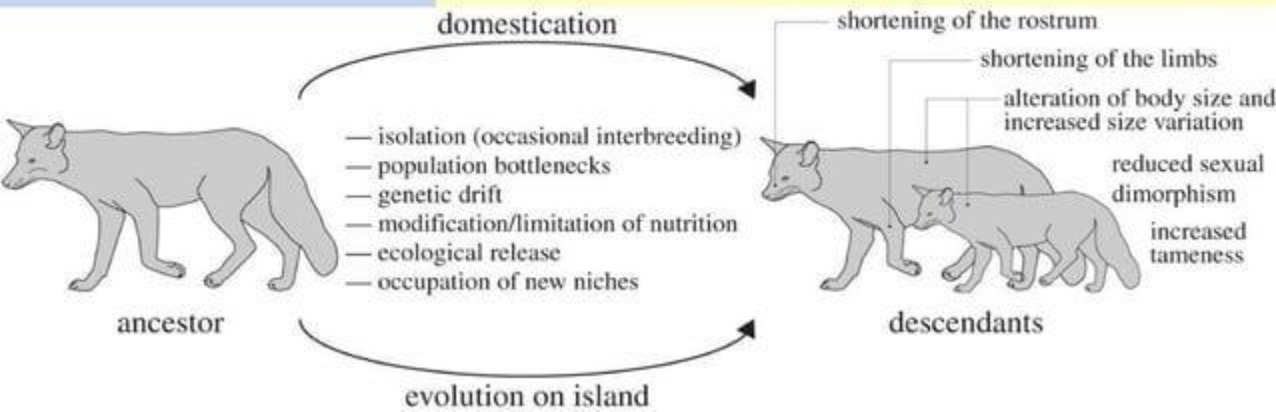


Root Map
Gene Pools
are
described by
have
Collection of all alleles
Allele Frequencies
Hardy Weinberg predictions

Thank You



Gene pool concept in crop breeding
Primary gene pool (GP-1): Varieties of the same species that can intermate freely
Secondary gene pool (GP-2): Closely related species that can intercross with GP-1 and produce at least some fertile hybrids
Tertiary gene pool (GP-3): Distantly related species that can intercross with GP-1 and -2 but requires additional measures such as embryo rescue or chromosome doubling to obtain offspring.
After: JR Harland and JMT de Wet. 1971. Toward a Rational Classification of Cultivated Plants. Taxon 20: 509-517. and Wikipedia



domestication
ancestor
— isolation (occasional interbreeding)
— population bottlenecks
— genetic drift
— modification/limitation of nutrition
— ecological release
— occupation of new niches
shortening of the rostrum
shortening of the limbs
alteration of body size and increased size variation
reduced sexual dimorphism
increased tameness
descendants
evolution on island

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