Management of inbreeding in carp hatcheries in Myanmar

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2019

MYSAP
Myanmar Sustainable Aquaculture Programme

CGIAR
RESEARCH PROGRAM ON Fish
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Importance of seed quality

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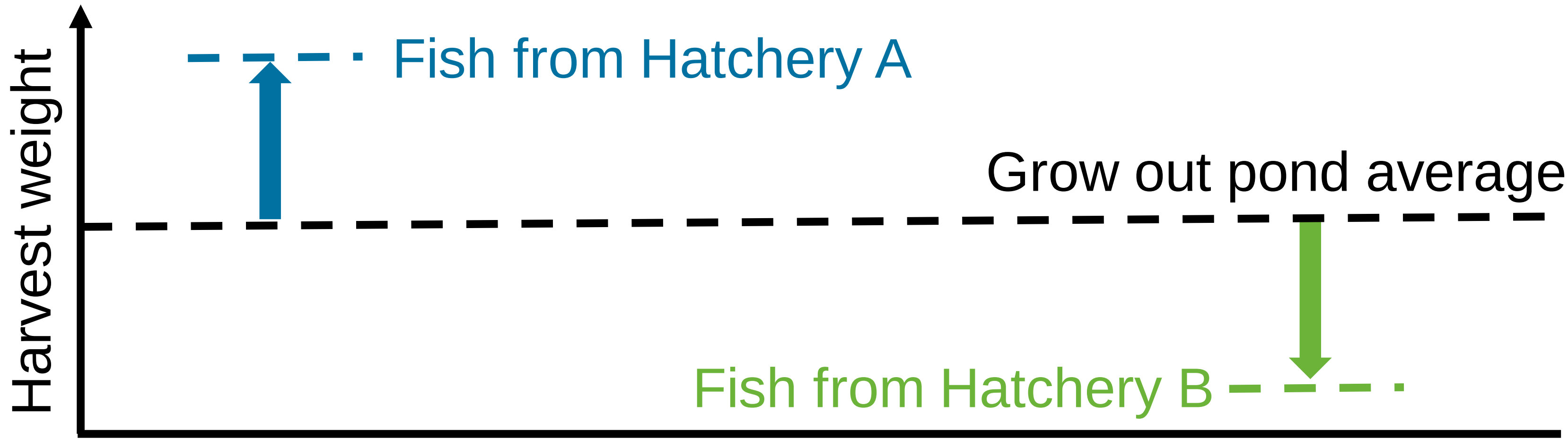
Scenario

- One grow out pond stocked with seed from two hatcheries



Factors affecting seed quality

Hatchery environment

- Hatchery rearing and handling practices

Disease status

- The movement of fish among rivers, hatcheries and farms represents a biosecurity risk
- Hatcheries have an important role in minimising risks

Genetic quality

- Minimise **inbreeding**
- Maximise the level of **genetic improvement**

Importance of seed quality

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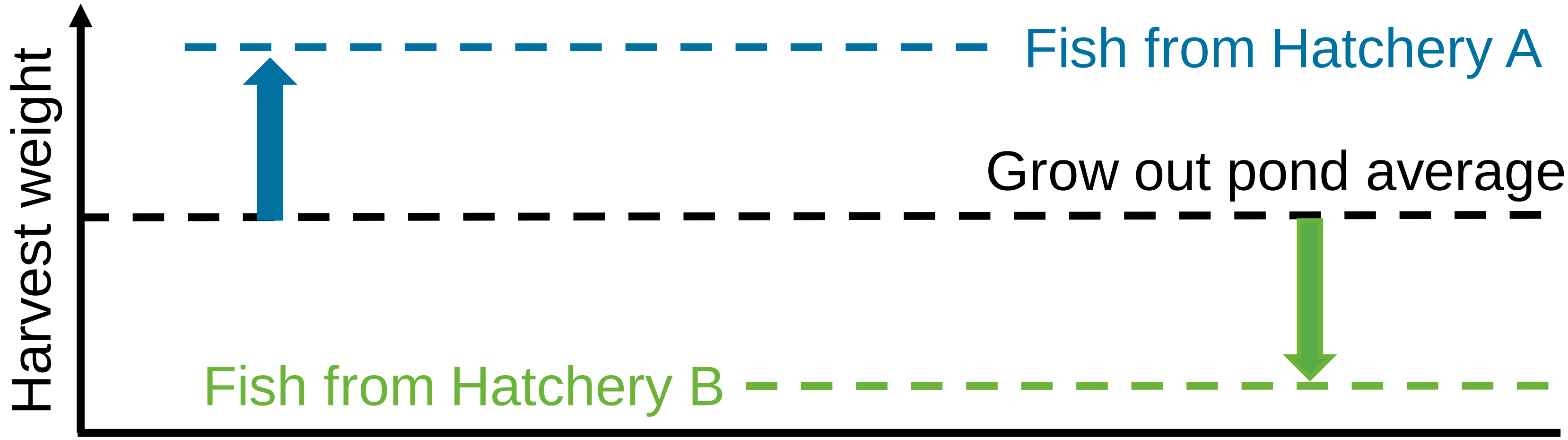
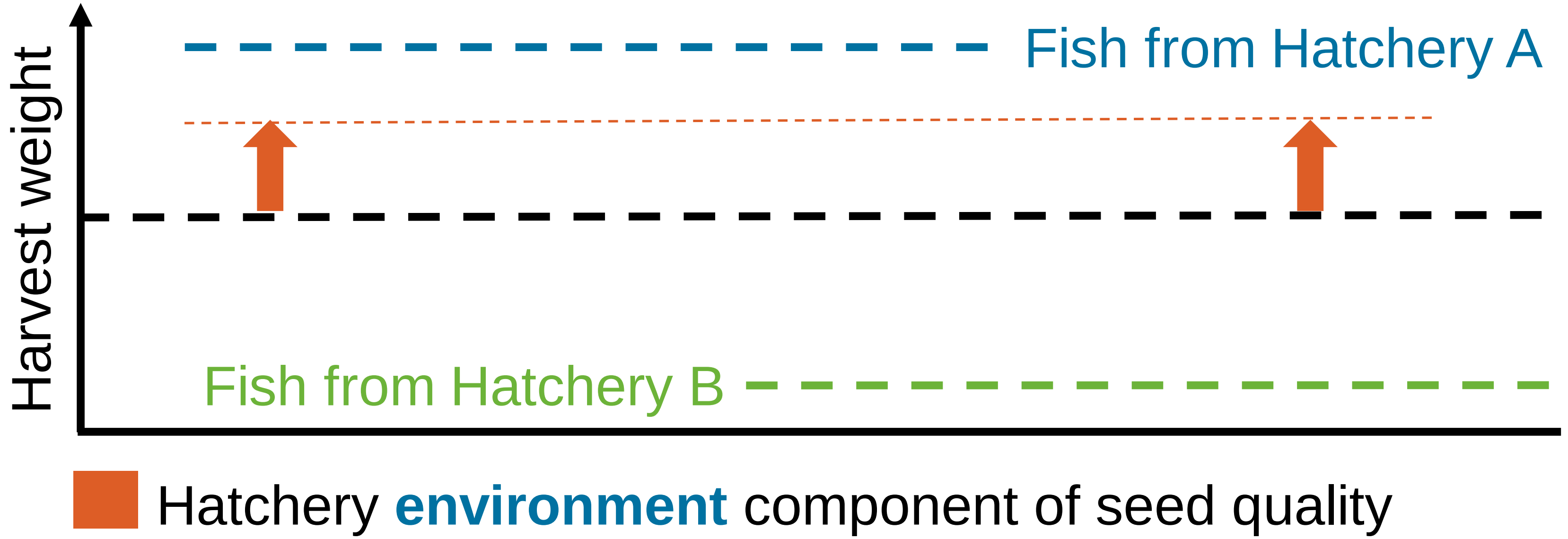


Importance of seed quality

Scenario

- One grow out pond stocked with seed from two hatcheries
- No biosecurity issues
- Both hatcheries adopting best-practice rearing and handling



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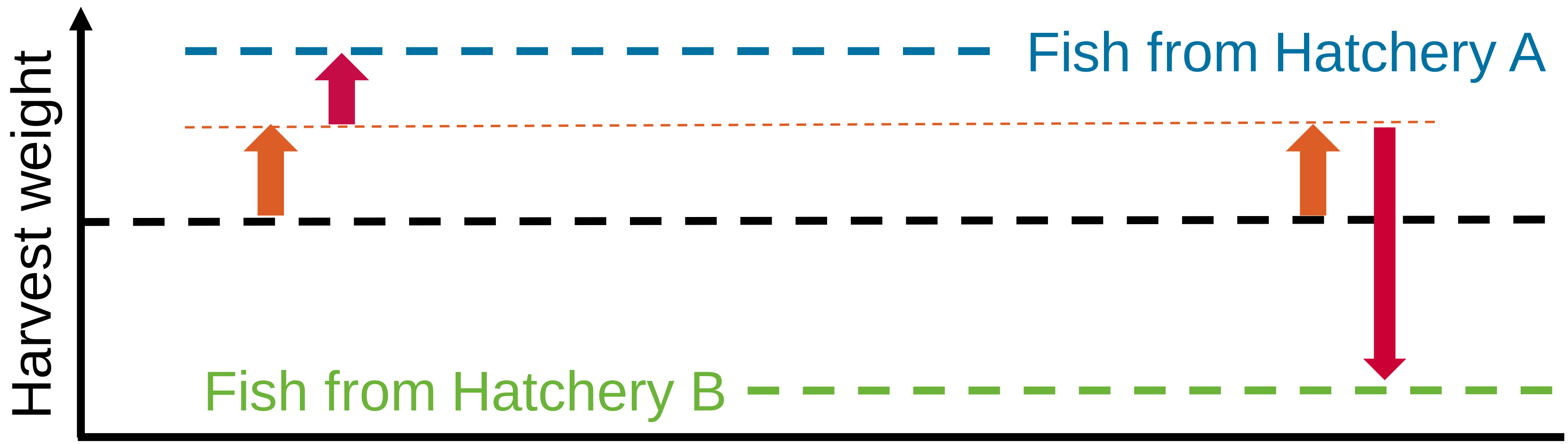


Hatchery **environment** component of seed quality

Genetic component of seed quality


Closed populations and strains

Closed populations and strains

A population descended from a finite number of founder individuals into which no subsequent introduction of individuals or genes has occurred.

There is no universally accepted definition of a strain but here it is considered synonymous with a closed population.

closed population = strain

Many hatcheries in Myanmar have maintained their own strains over multiple generations.

Closed populations and strains

Strains can be categorized as ‘wild’ or ‘hatchery’ strains.

Wild strains are comprised of animals that hatched in the wild.

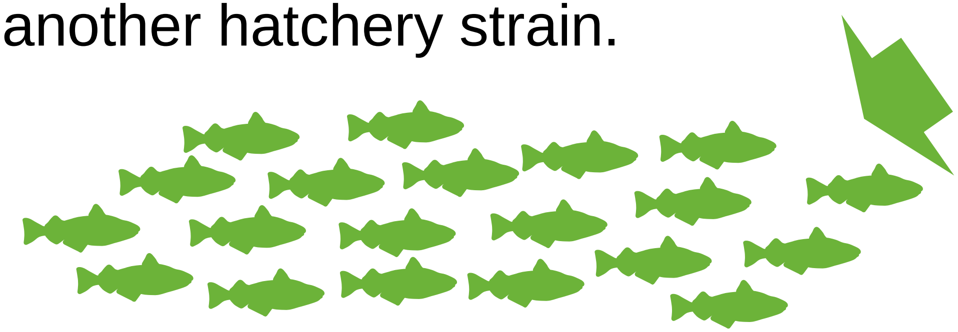
Hatchery strains are comprised of fish that hatched in captivity (i.e. hatcheries).

Closed populations and strains

Founders of a strain may be sourced from the wild and/or be members of another hatchery strain.

Sourced from wild strain

Founders



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Closed populations and strains

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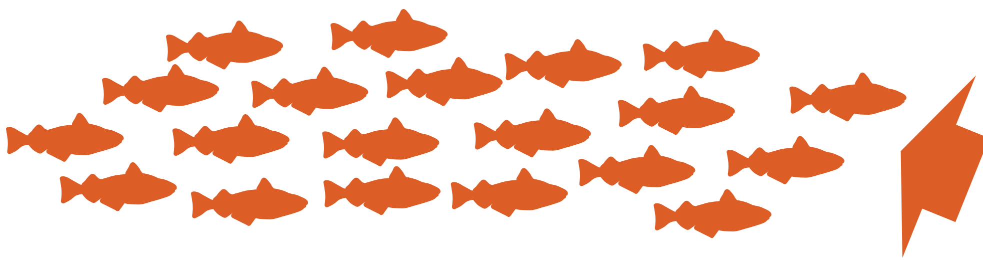

Sourced from hatchery strain

Closed populations and strains

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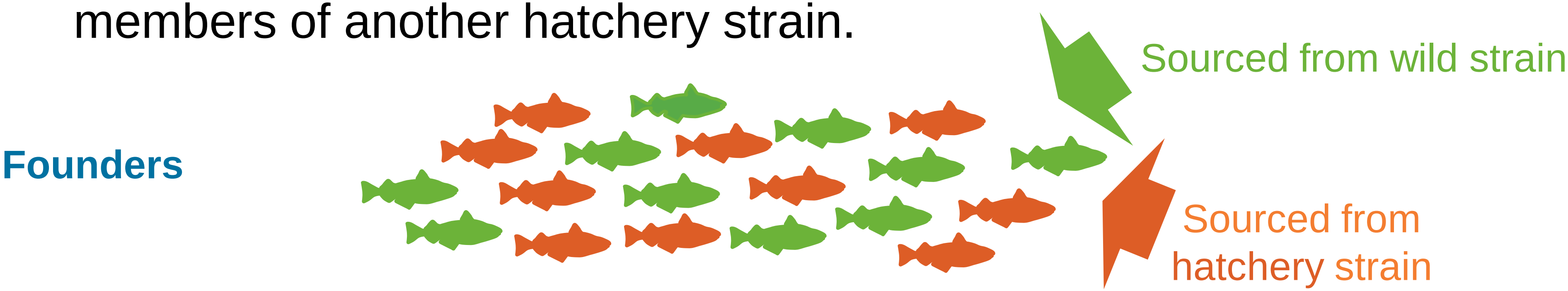

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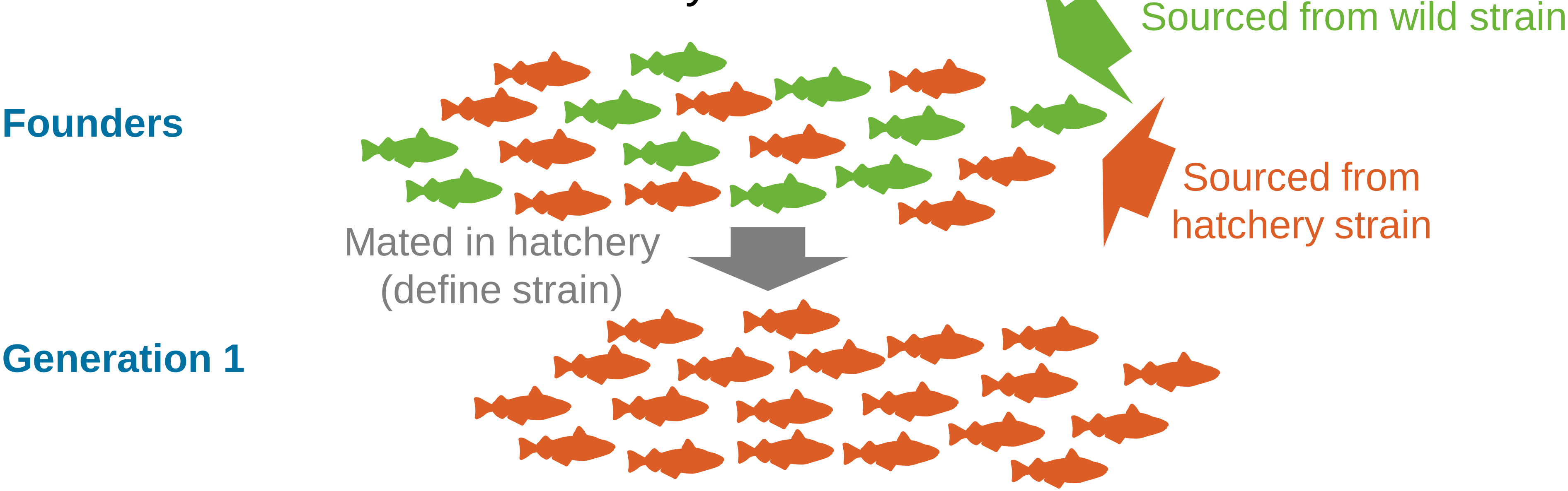

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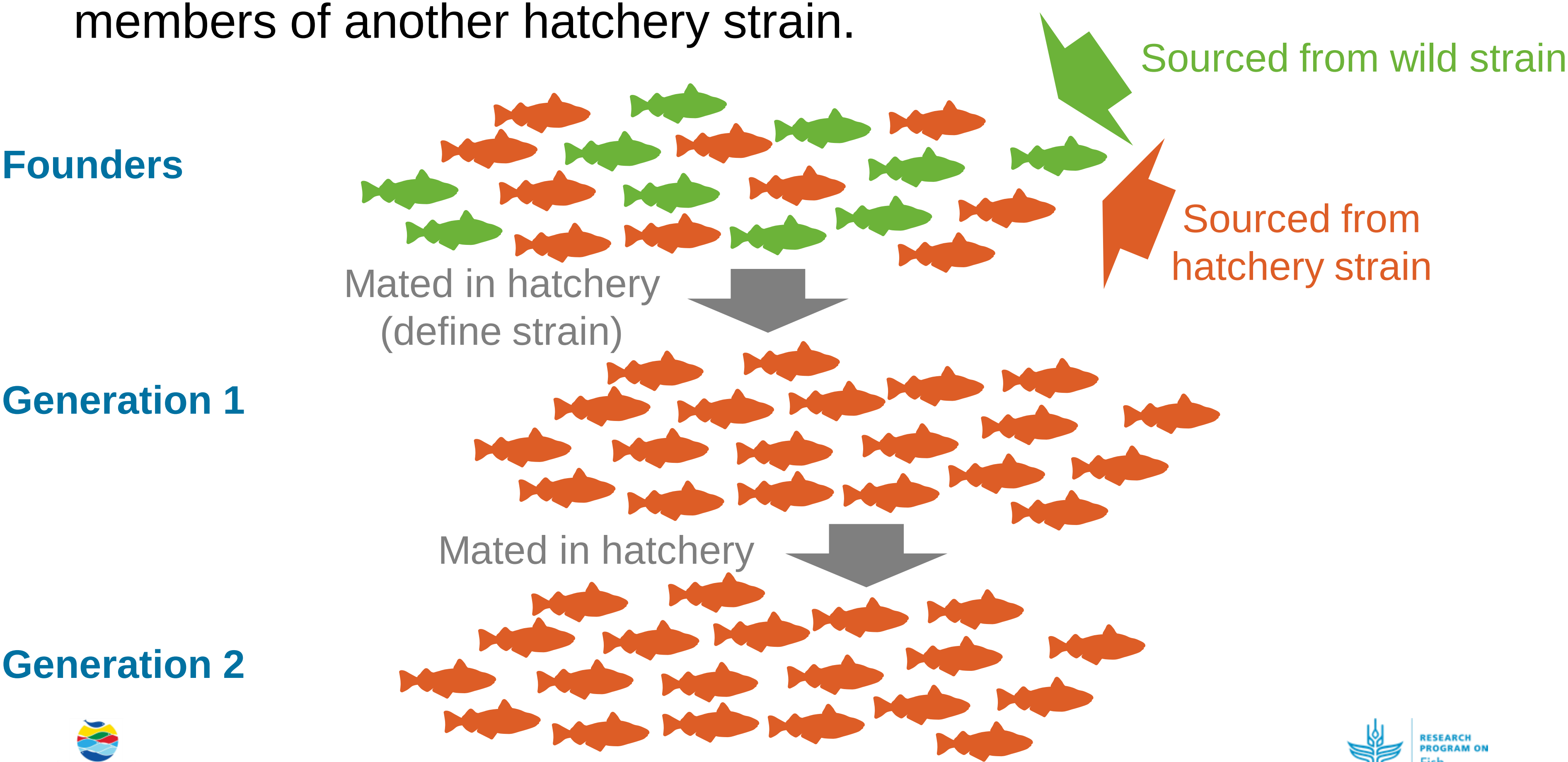

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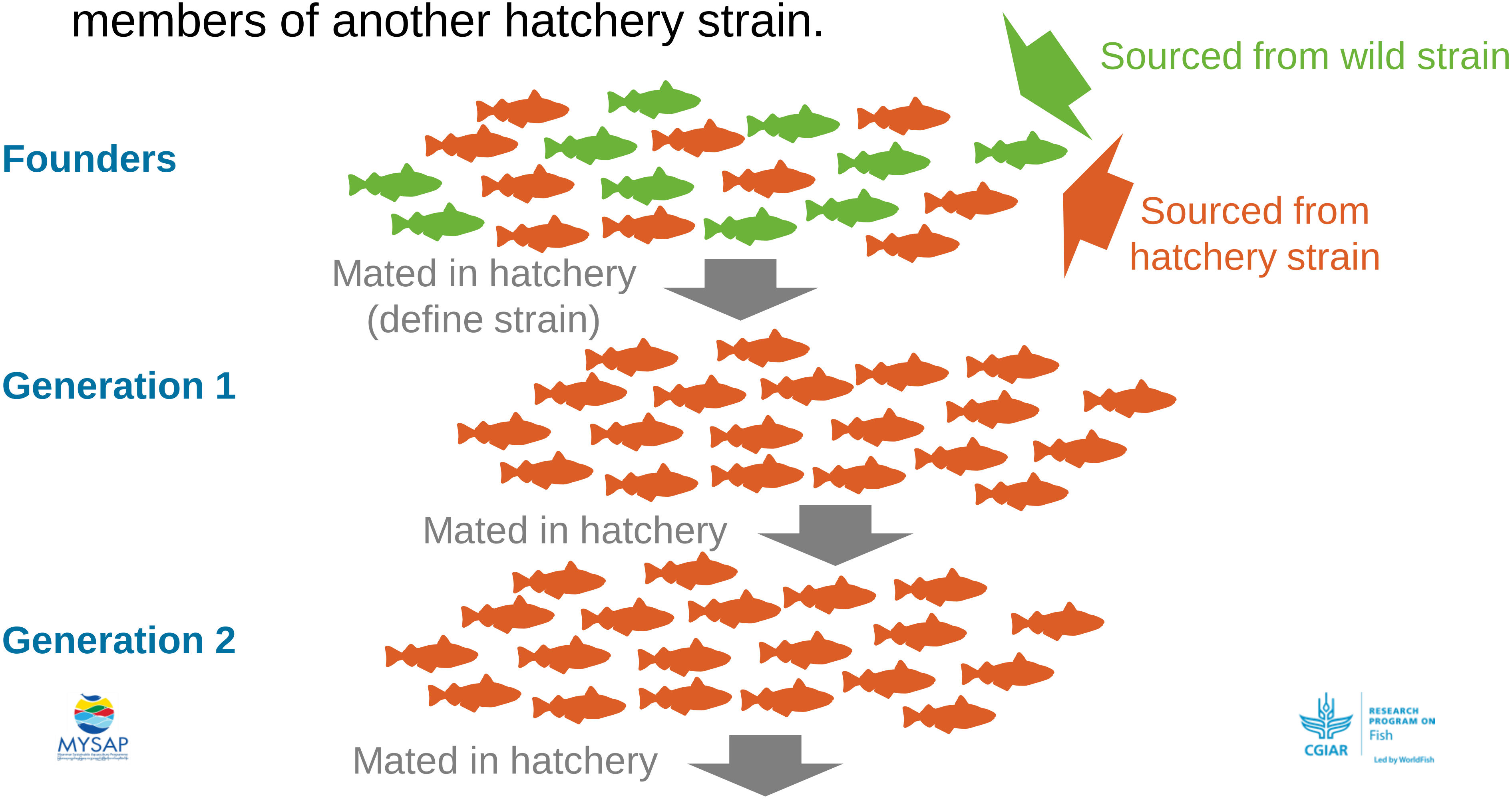

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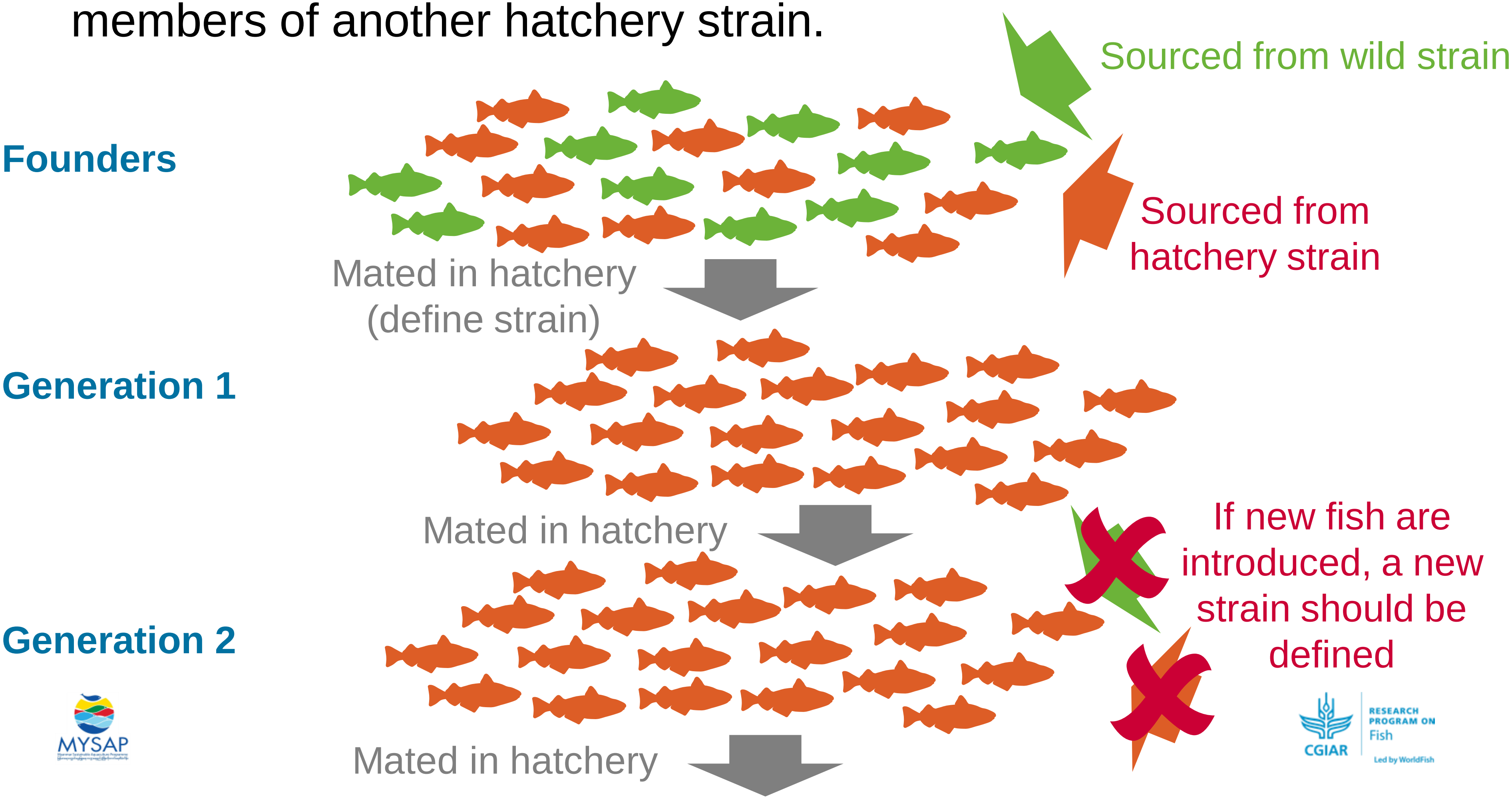
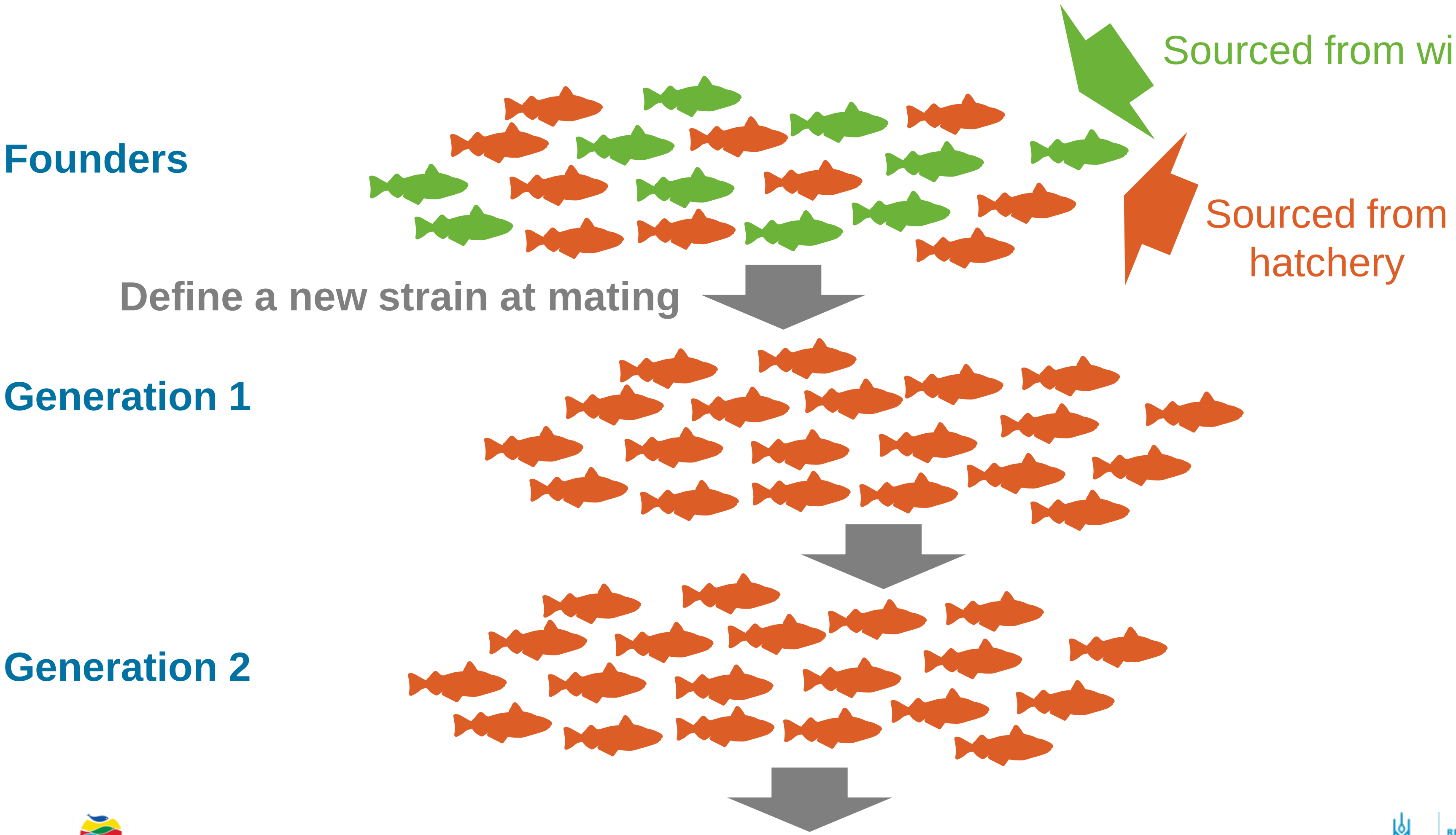


New strains

A new strain should be defined when.

- wild founders are collected
- strains are merged
- a strain is split
- a strain is moved to a new hatchery

Merging strains

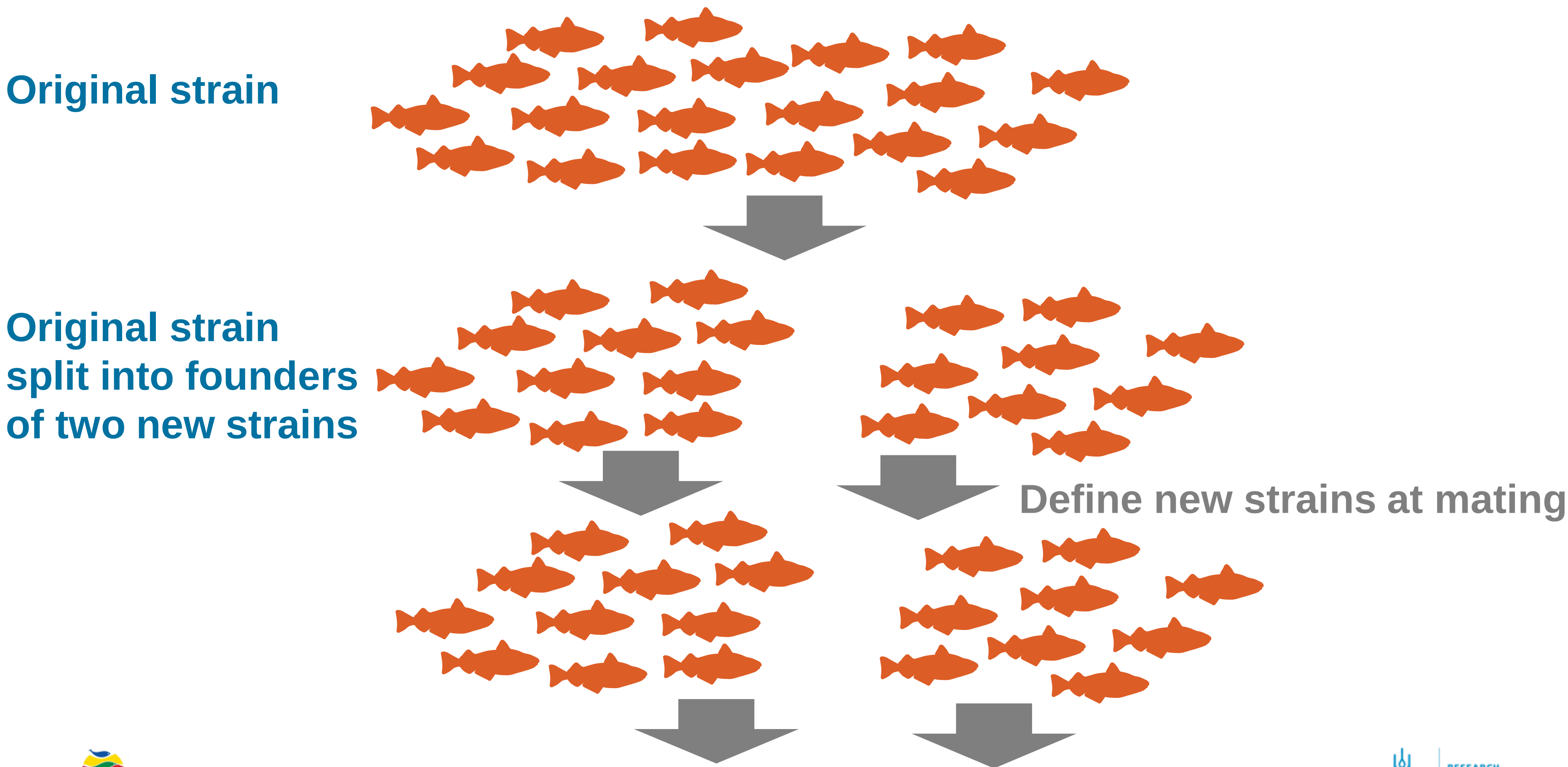


Merging strains

Generally, when merging strains it is best to

- merge only 2 strains at once
- use large numbers of each strain as parents (e.g. 50)
- mate males from one strains with females from the other to ensure that both strains are represented in all progeny

Splitting strains



Data to be recorded when creating a new strain

- Species scientific name (e.g. '*Labio rohita*').
- Strain type
  - Founders from a wild population
  - Founders from a hatchery population
- Date of capture or date of mating
- Place of collection or source hatchery
- Collector's name or strain identifier within hatchery
- Name under which the new strain is to be marketed
- Other relevant details depending on context and availability of information

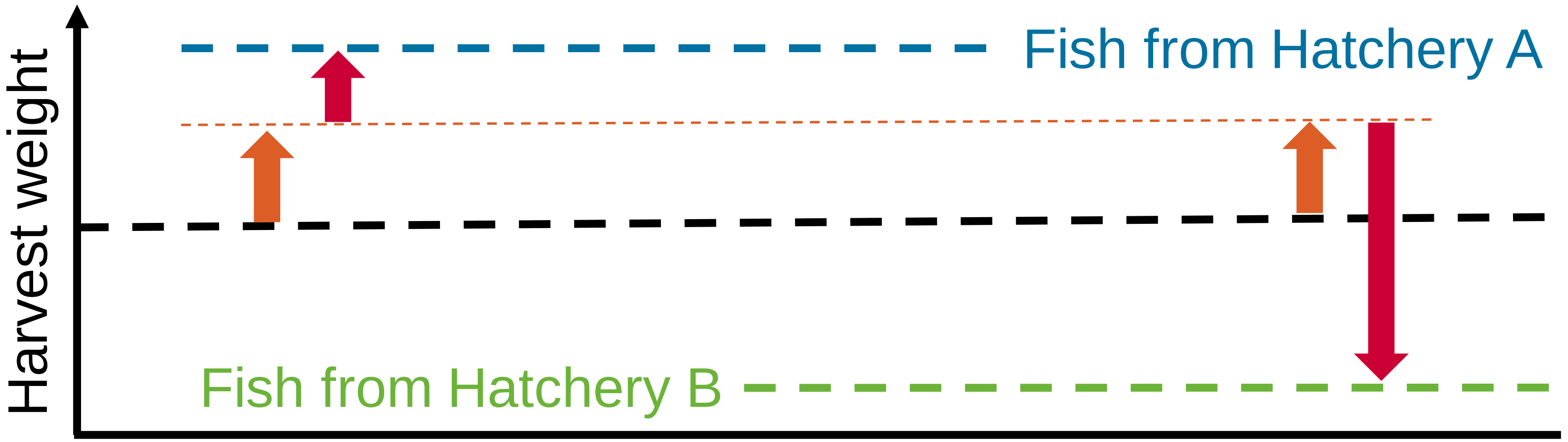
Naming and tracking strains

See Appendix 3 of Hamilton MG. 2019. Management of inbreeding in carp hatcheries in Myanmar. Inland Myanmar Sustainable Aquaculture Programme (INLAND MYSAP), Mandalay, Myanmar, p 31.

This has been translated into Myanmar.

Genetic theory

Importance of seed quality

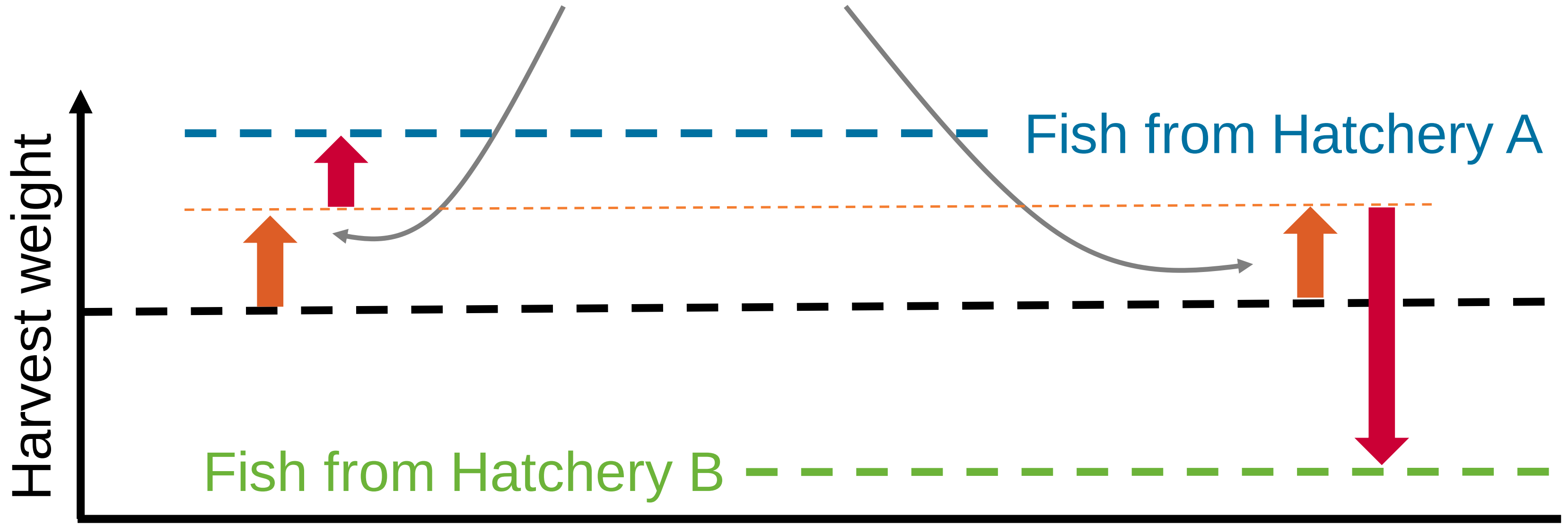


Hatchery **environment** component of seed quality

Genetic component of seed quality

Importance of seed quality

Same logic applies to individual fish as well as strains



Hatchery **environment** component of seed quality

Genetic component of seed quality

Genetic value of an individual fish for a given trait (e.g. weight at harvest)

Total genetic value

=

Additive genetic value

+

Non-additive genetic value

Genetic value of an individual fish for a given trait (e.g. weight at harvest)

Total genetic value

=

Additive genetic value

- transmitted from one generation to the next
- also called the **breeding value** of an individual

+

Non-additive genetic value

Genetic value of an individual fish for a given trait (e.g. weight at harvest)

Total genetic value

=

Additive genetic value

- transmitted from one generation to the next
- also called the **breeding value** of an individual

+

Non-additive genetic value

- not transmitted from one generation to the next
- **inbreeding depression** is a component of this

Genetic value of individual fish

Total genetic value

=

Breeding value

-

Inbreeding depression

+

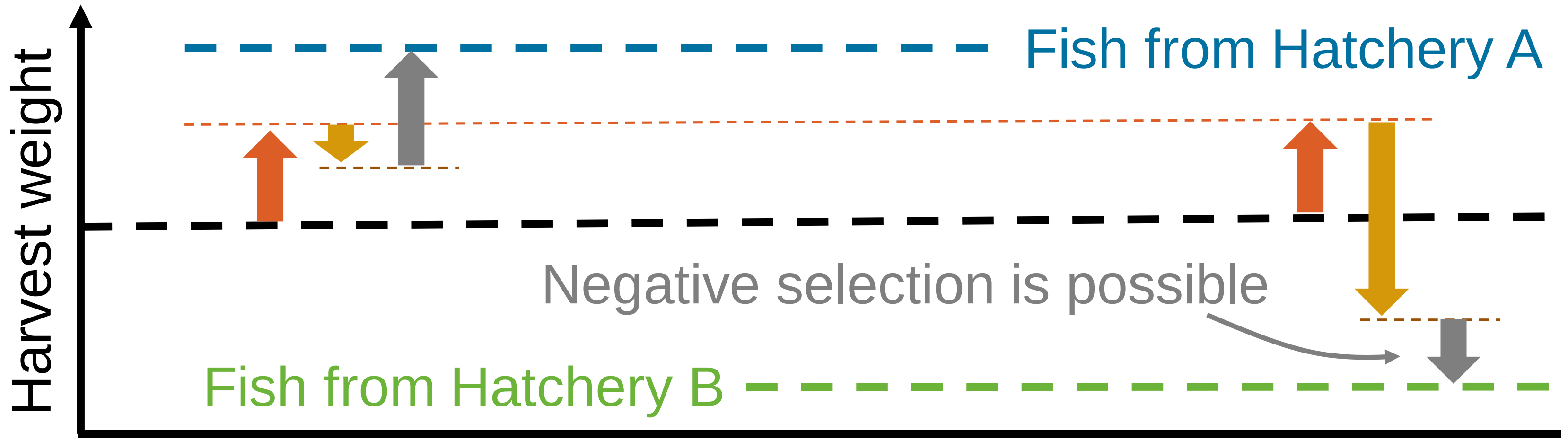
Other non-additive effects

Increased with artificial selection (i.e. a genetic improvement program)

Reduced with good broodstock management

Difficult to quantify and exploit (we will ignore this)

Importance of seed quality



Hatchery **environment** component of seed quality

Inbreeding depression component of seed quality

Breeding value component of seed quality

Inbreeding depression

Inbreeding depression can result in:

- poor growth
- poor survival
- poor reproductive performance
- disease susceptibility
- morphological deformities

What is inbreeding?

Inbreeding results from the mating of related parents.

Related parents have at least one common ancestor.

The more closely related parents are, the greater the level of inbreeding in the progeny.

What is inbreeding?

Inbreeding results from the mating of related parents.

Founders (assumed unrelated)

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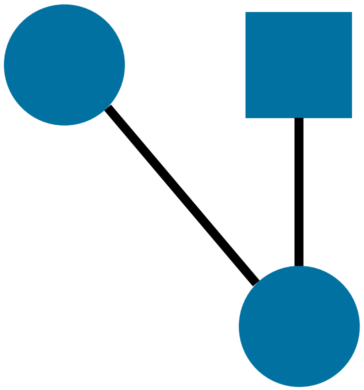

Generation 1

What is inbreeding?

Inbreeding results from the mating of related parents.

Founders
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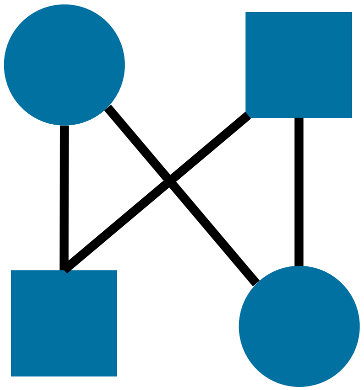
Generation 1 Full siblings



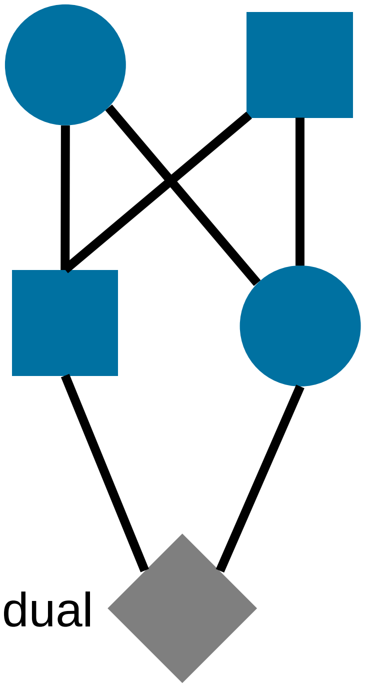
What is inbreeding?

Inbreeding results from the mating of related parents.

Founders
(assumed unrelated)

Generation 1 Full siblings

Generation 2 Inbred individual



What is inbreeding?

Path Analysis

Inbreeding results from the mating of related parents.

Founders
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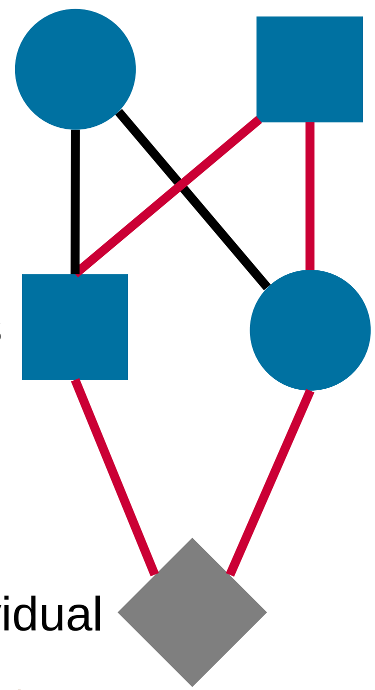

Generation 1 Full siblings

Generation 2 Inbred individual

See http://www.fao.org/3/x3840e/X3840E00.htm

What is inbreeding?

Path Analysis

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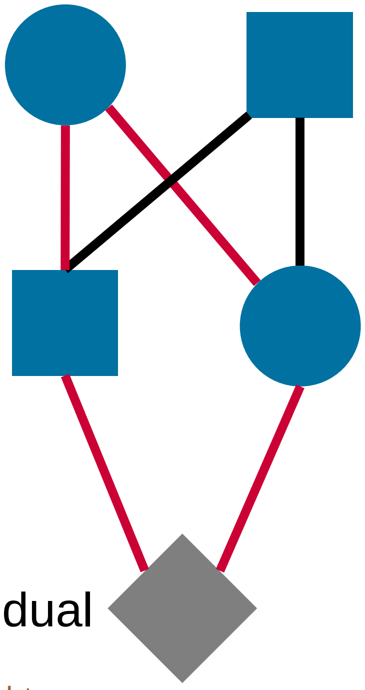
Founders (assumed unrelated)

Generation 1 Full siblings

Generation 2 Inbred individual



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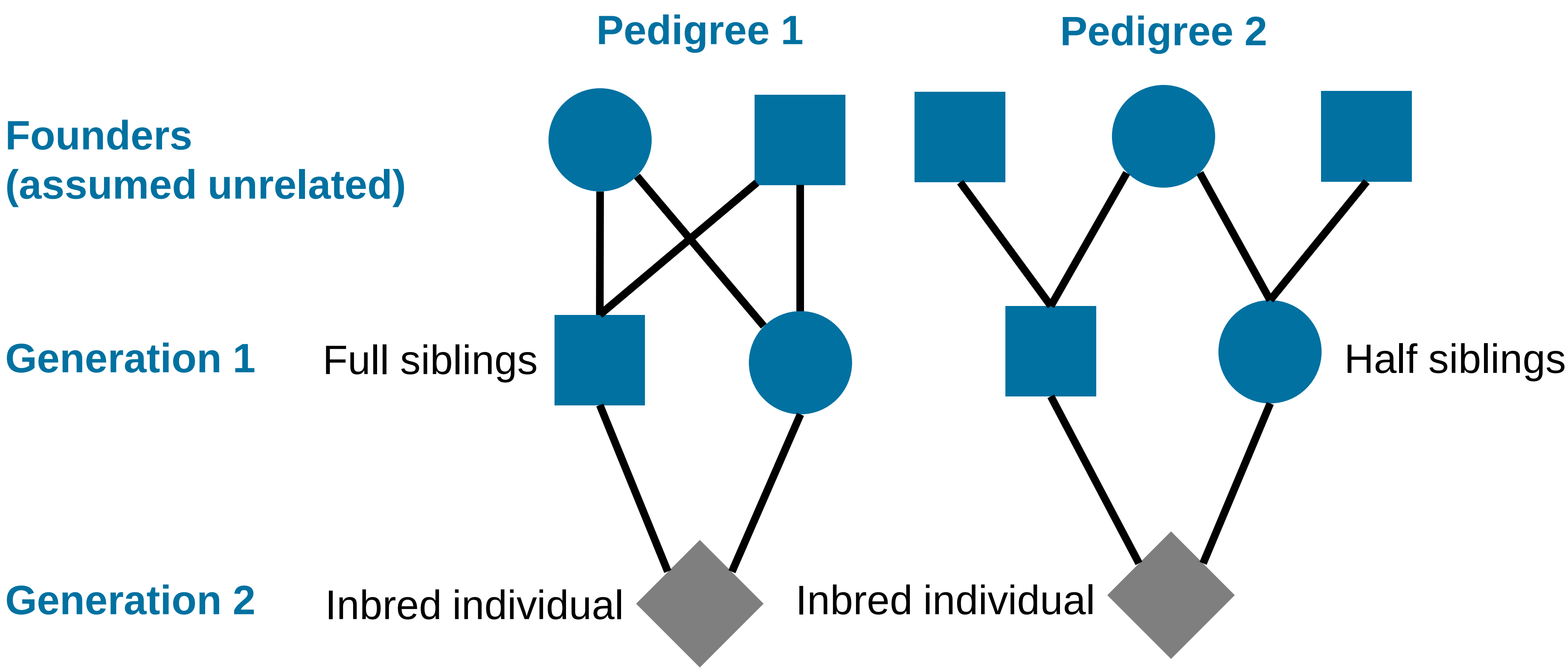

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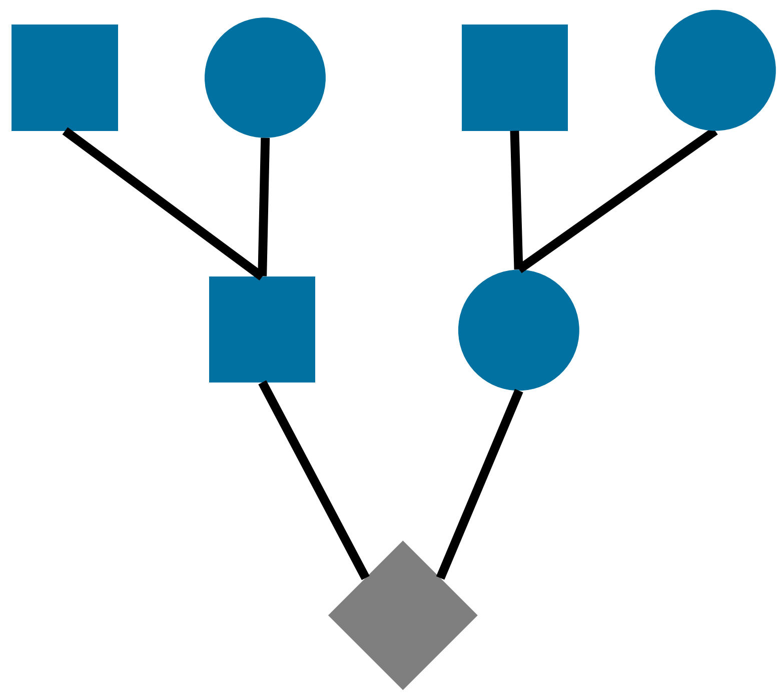
Founders (assumed unrelated)

Generation 1

Generation 2



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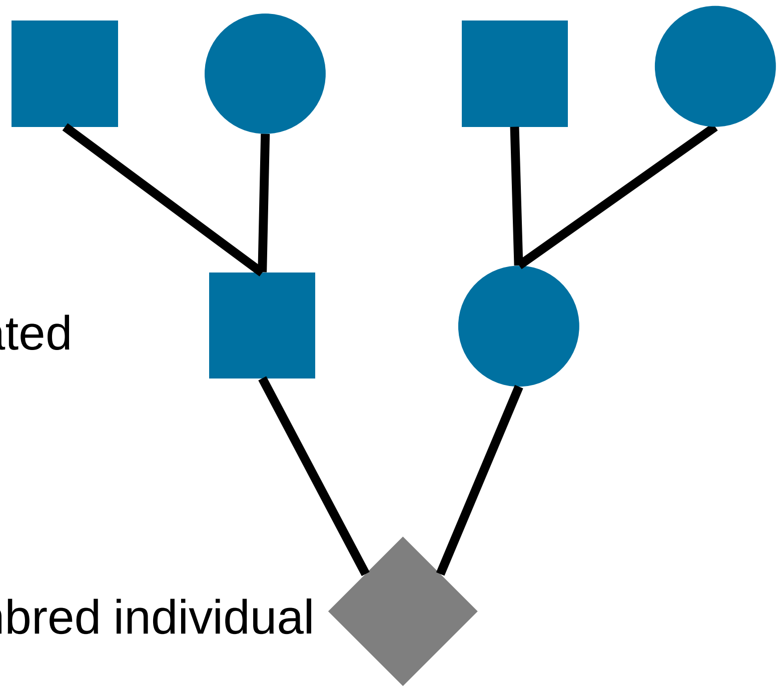


Founders (assumed unrelated)

Generation 1 Unrelated

Generation 2 Non-inbred individual

Quantifying inbreeding

Calculating the inbreeding coefficient (F)

Coefficient of relationship (r)

- a measure of relationship **between individuals**
- the proportion of genes shared by two individuals as a result of the transmission of genes from parents to offspring

Inbreeding coefficient (F)

- a measure of inbreeding **in an individual**
- half the coefficient of relationship between an individual’s parents

Quantifying inbreeding

Calculating the inbreeding coefficient (F)

Coefficient of inbreeding (F)

- F = 0 in individuals with no a common ancestor (no inbreeding)
- F > 0 in individuals with one or more common ancestors

Pedigree 1 **Pedigree 2**

Founders (assumed unrelated)

Generation 1

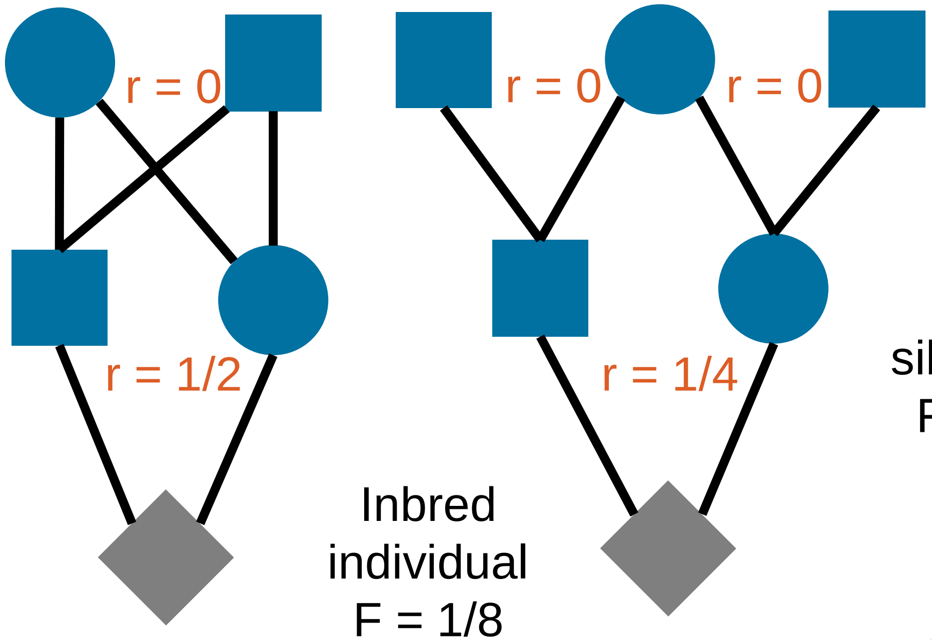
Full siblings
F = 0

Half siblings
F = 0

Generation 2

Inbred individual
F = 1/4

Inbred individual
F = 1/8



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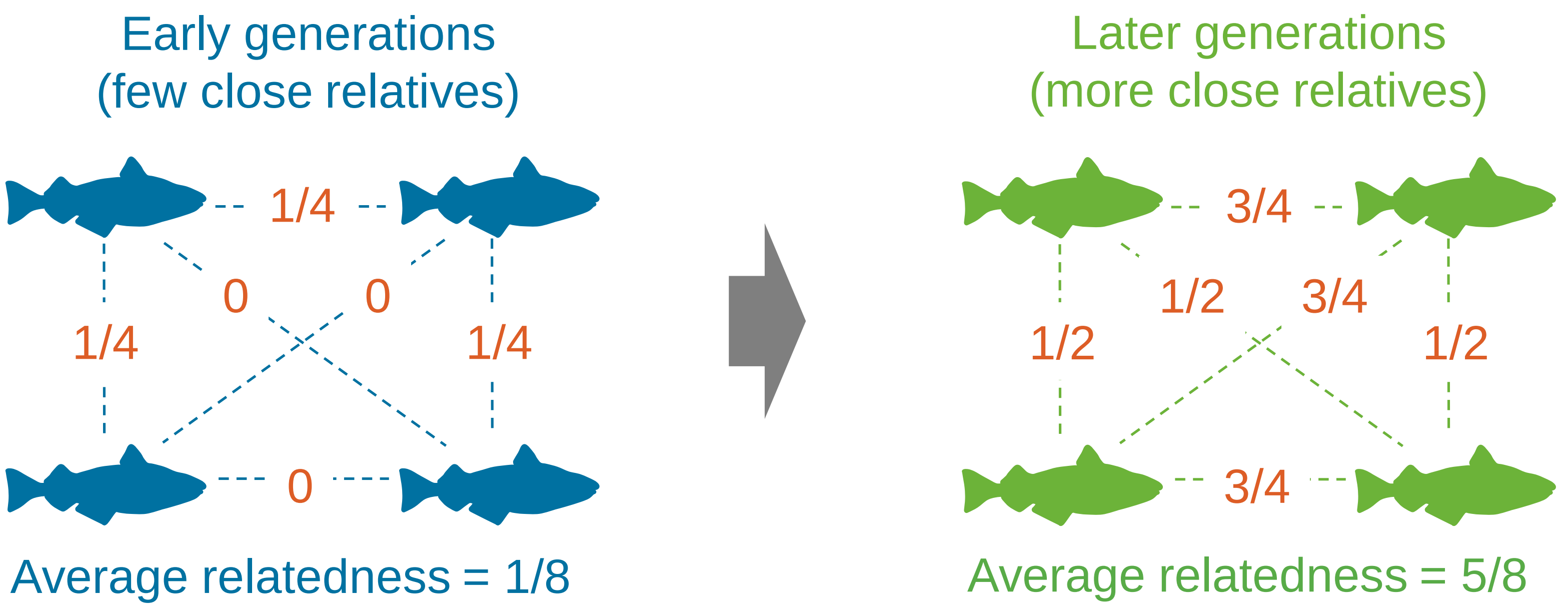
Inbreeding

Inbreeding increases in closed populations over generations because **average relatedness** among individuals increases.



Can implement broodstock management strategies to slow down the increase in average relatedness over generations.

Inbreeding increases over generations

An extreme example – many parents should be used

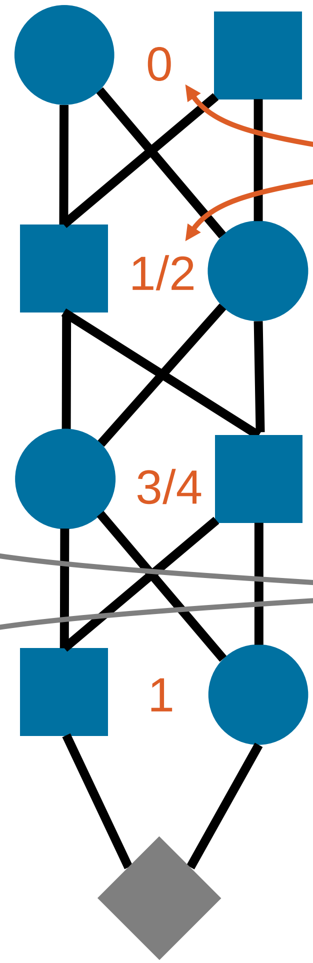
Founders (assumed unrelated)

Generation 1 F = 0

Generation 2 F = 1/4

Generation 3 F = 3/8

Generation 4 F = 1/2



Coefficient of relationship (r) **between** individuals

Coefficient of inbreeding (F) **within** individuals

Inbreeding increases over generations

An extreme example – many parents should be used

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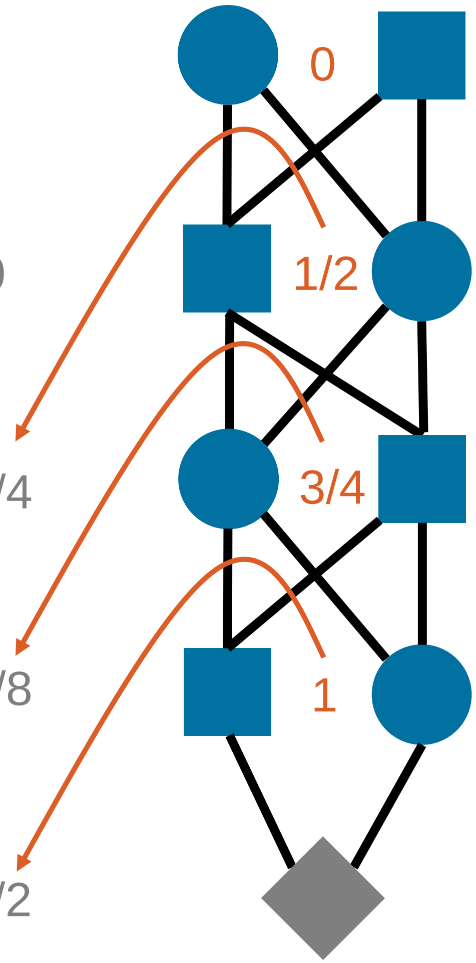

The inbreeding coefficient (F) of an individual is half the coefficient of relationship between its parents

Crossing unrelated strains

An extreme example – many parents should be used

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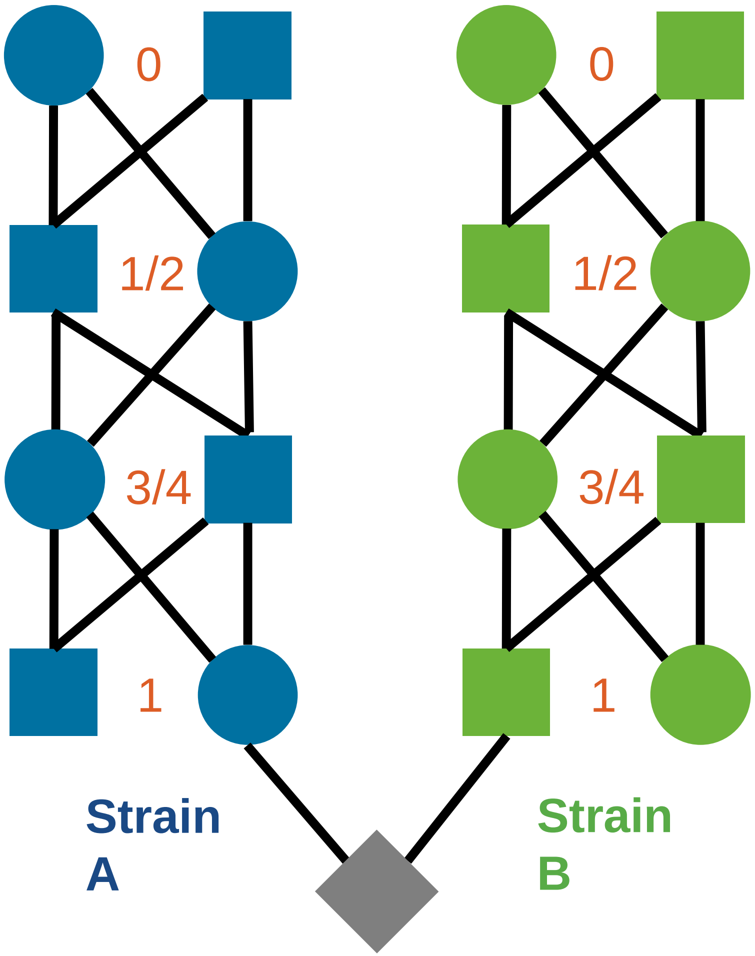
Generation 1 F = 0

Generation 2 F = 1/4

Generation 3 F = 3/8

Generation 4 F = ?



Crossing unrelated strains

An extreme example – many parents should be used

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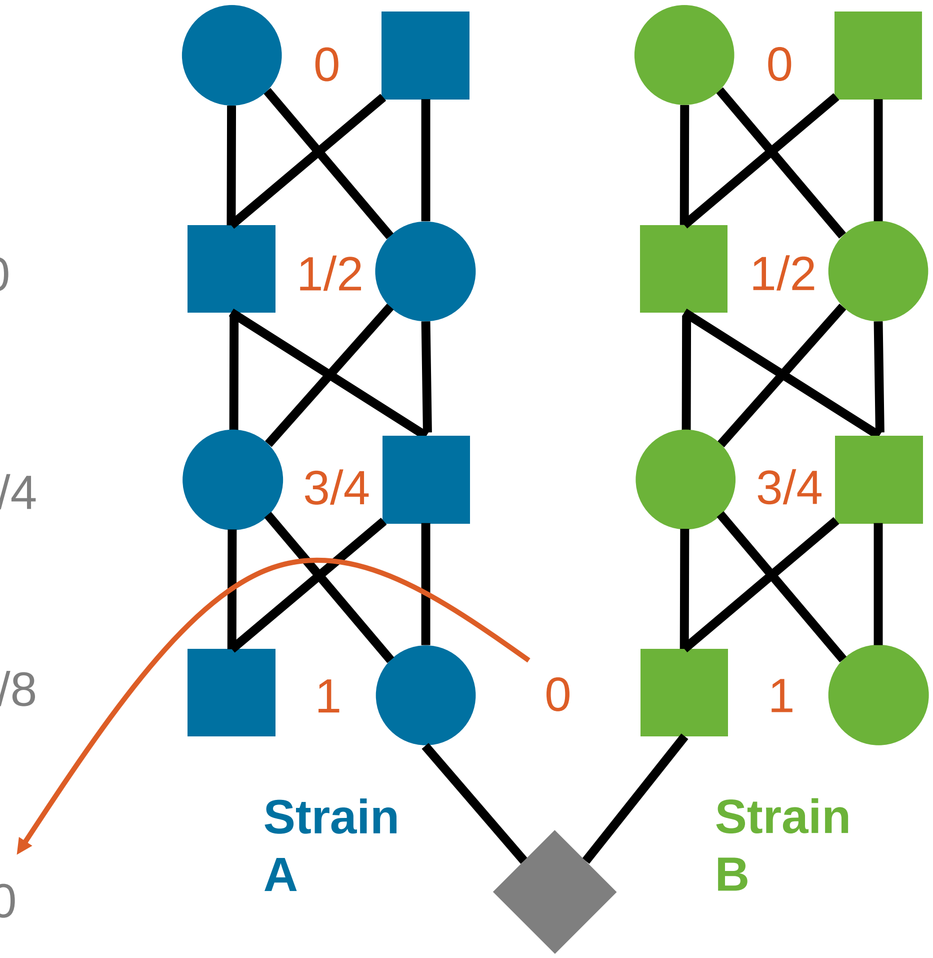


Inbreeding

If two highly inbred but unrelated parents are crossed their progeny will not be inbred.

Key points

Inbreeding results from the mating of related parents.

Inbreeding increases in closed populations over generations because **average relatedness** among individuals increases.

Can implement broodstock management strategies to slow down the increase in average relatedness over generations.

If two highly inbred but unrelated parents are crossed their progeny will not be inbred.

Inbreeding control

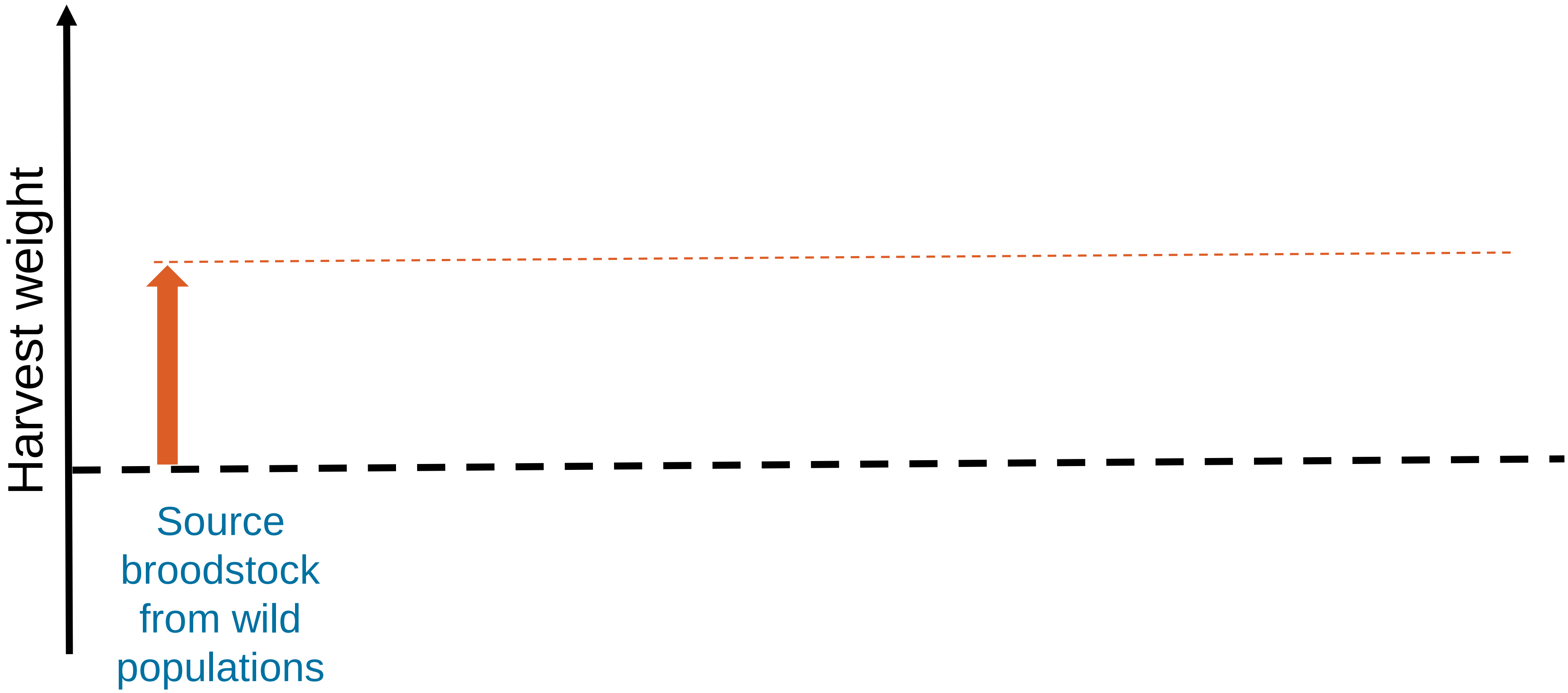
Inbreeding control

Methods to control inbreeding in hatcheries producing seed for aquaculture can be classified into two general approaches:

- Approach 1: Minimise average relatedness in a single strain
- Approach 2: Cross unrelated strains

Inbreeding control

True scale of environment, inbreeding and breeding value components of seed quality are unknown



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Inbreeding depression component of seed quality

Breeding value component of seed quality

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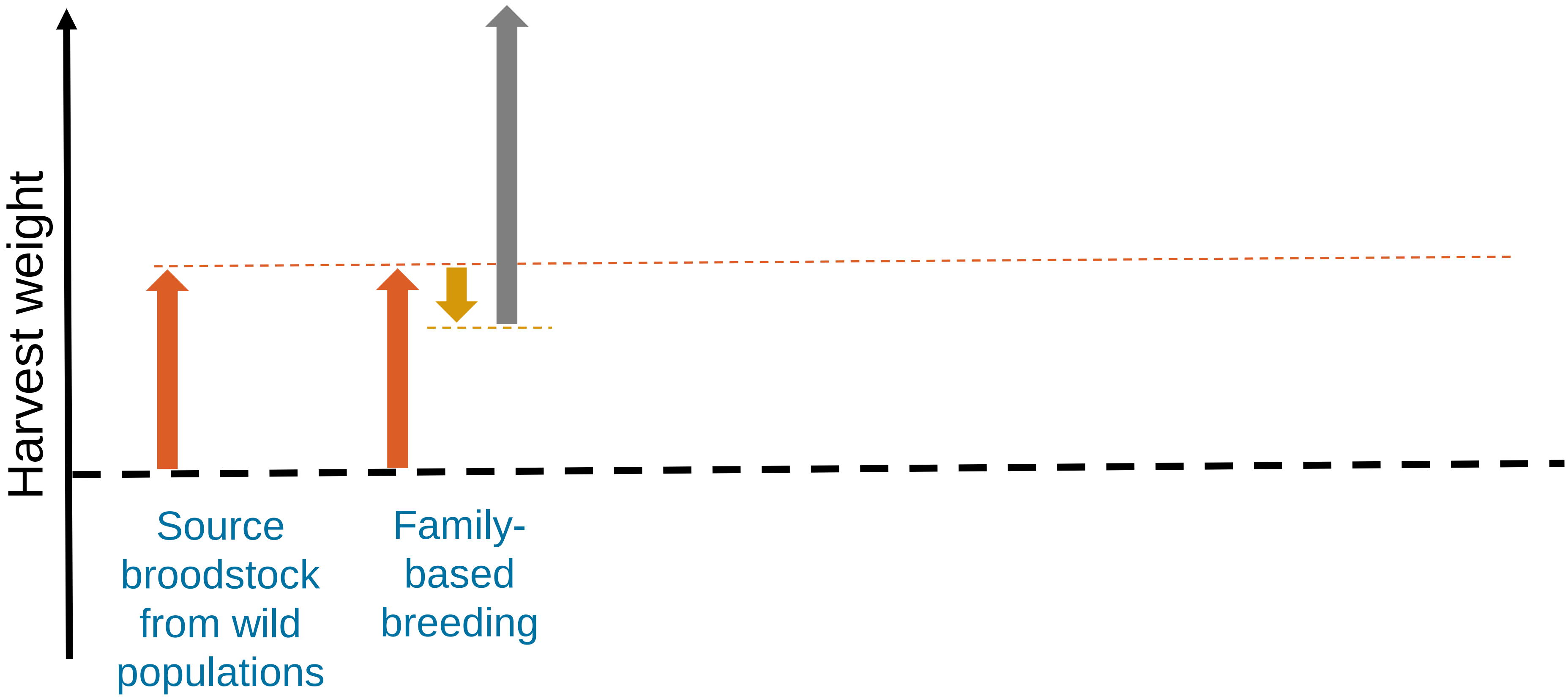

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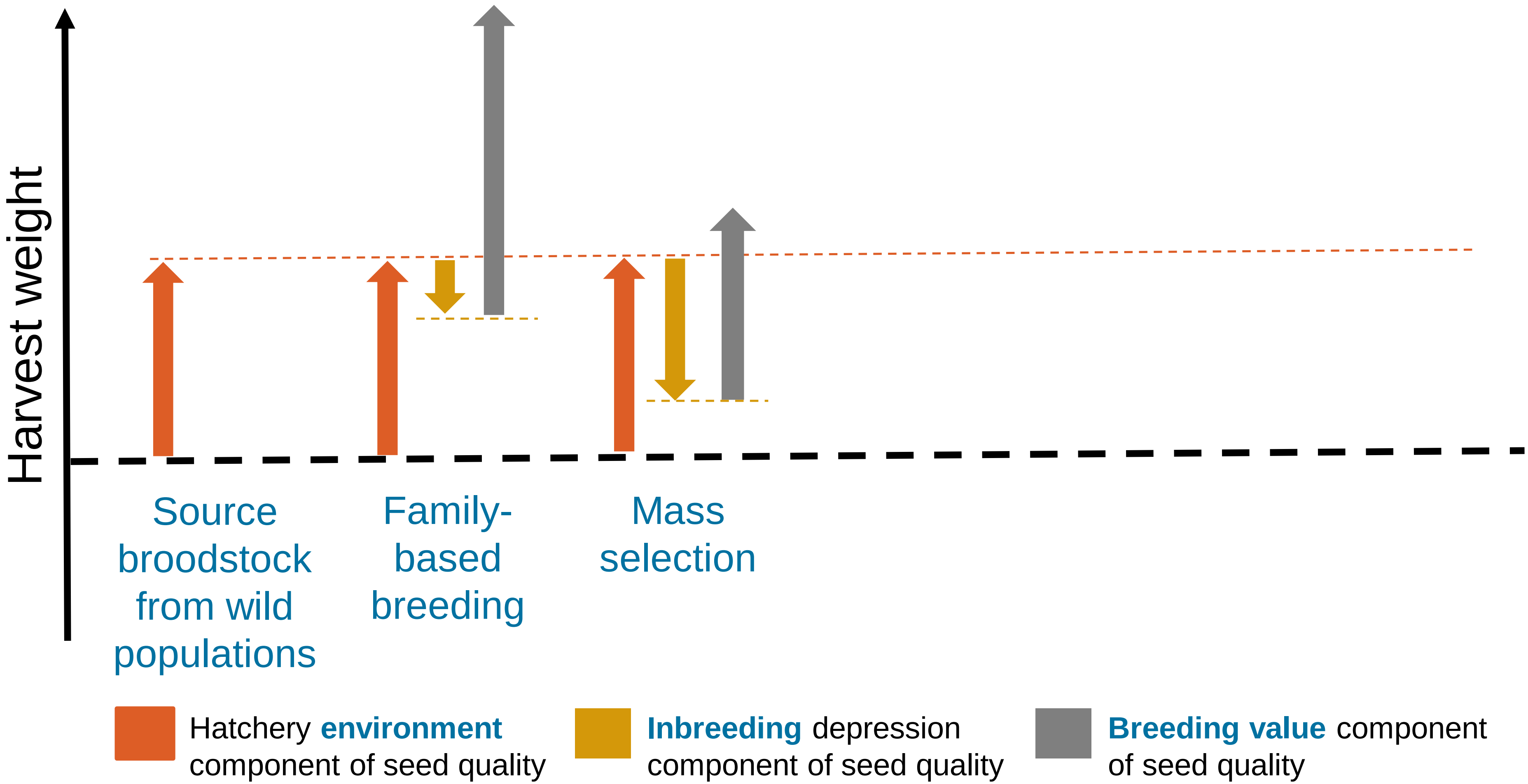

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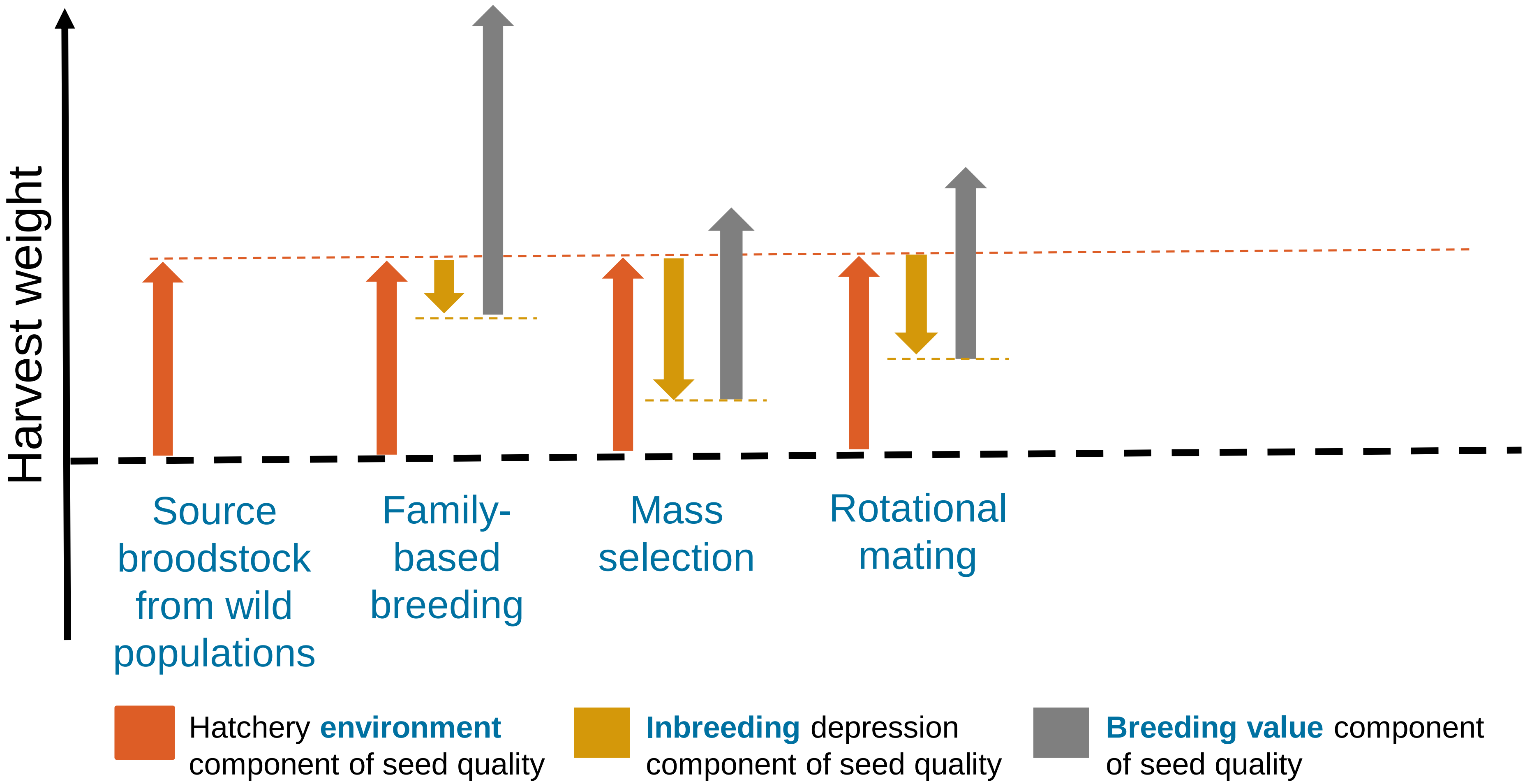

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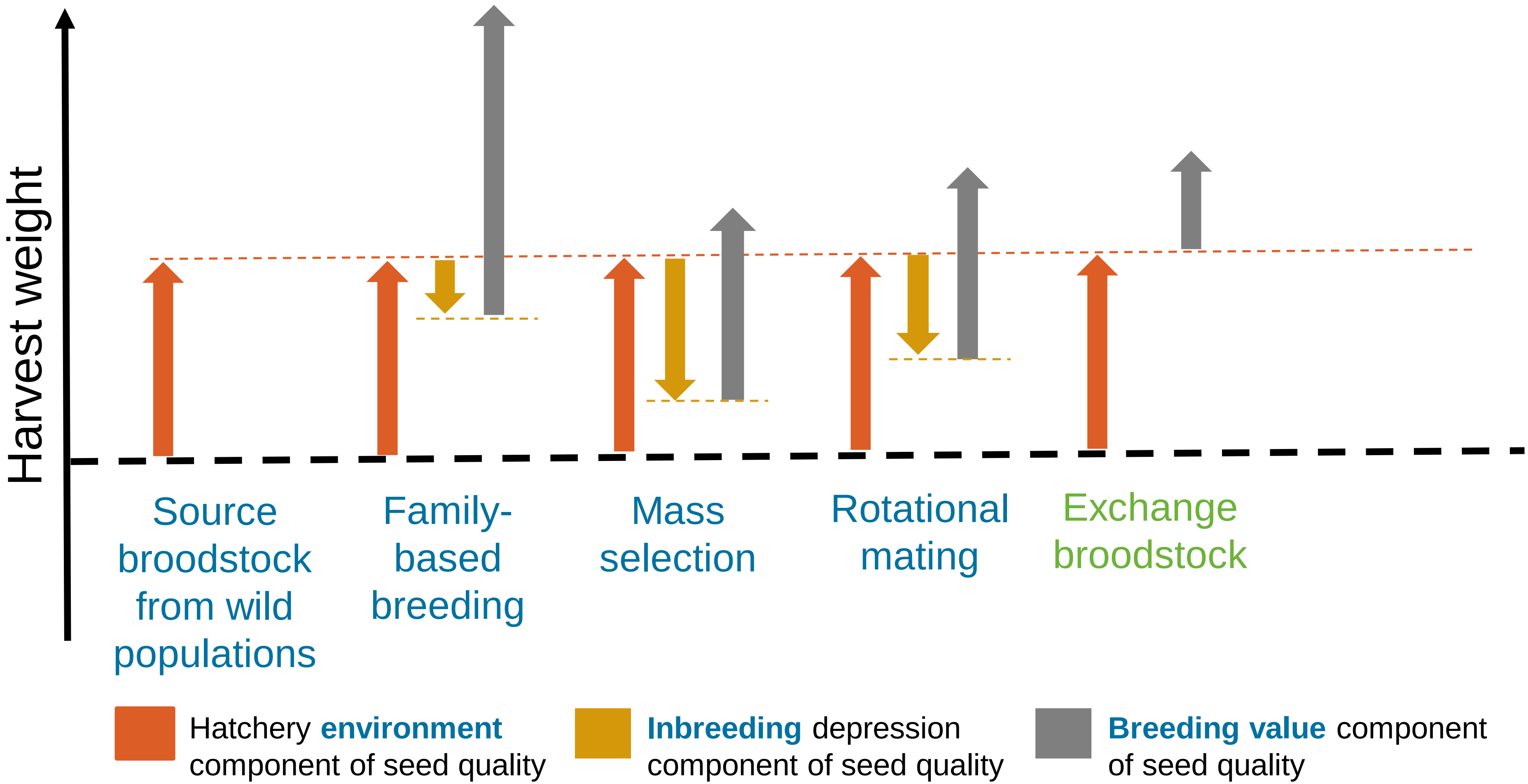

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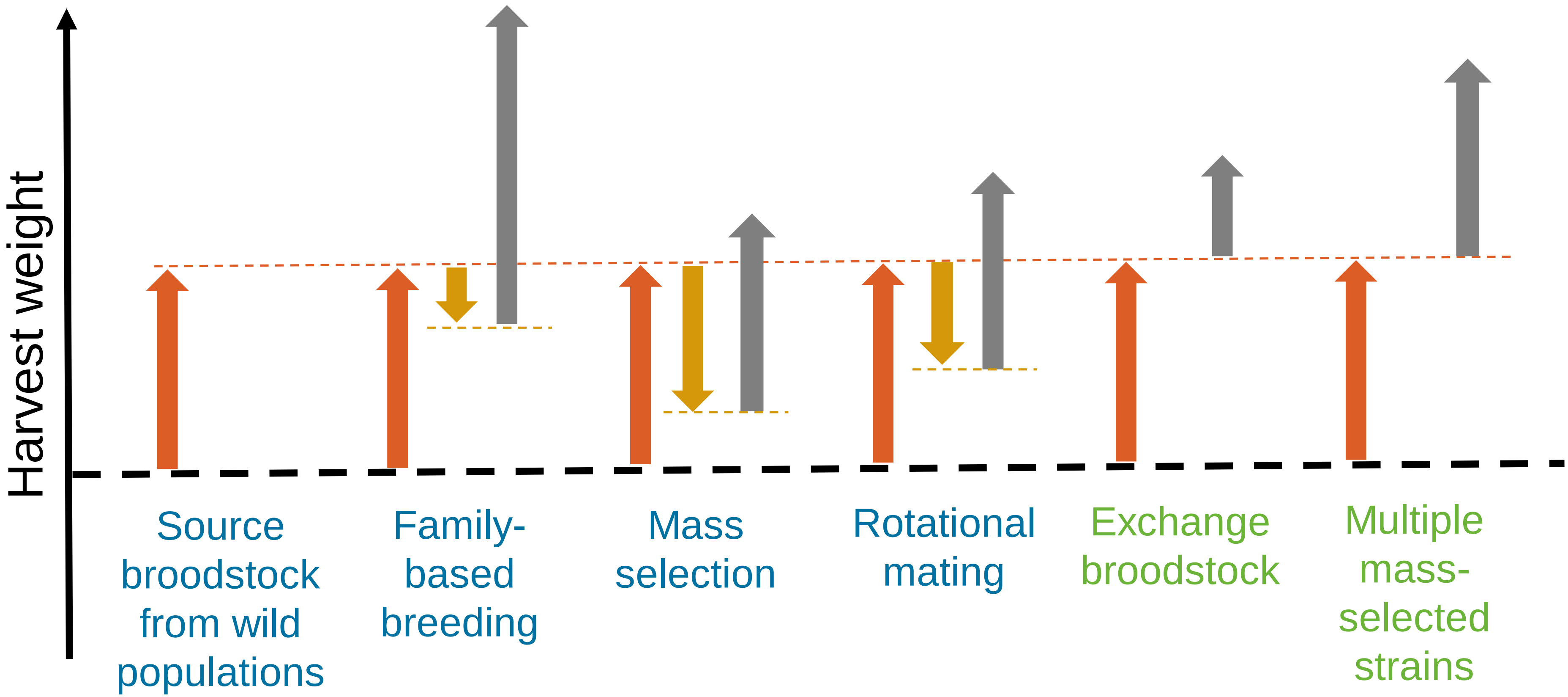

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Inbreeding control

	Source broodstock from wild populations	Family-based breeding	Mass selection	Rotational mating	Exchange broodstock	Multiple mass-selected strains
Low-moderate cost	✓	✗	✓	✓	✓	✓
Technically simple	✓	✗	✓	✓	✓	✓
Controls average relatedness in strains	✓	✓	✗	✓	✗	✗
Controls inbreeding in seed for grow out	✓	✓	✗	✓	✓	✓

Inbreeding control

	Source broodstock from wild populations	Family-based breeding	Mass selection	Rotational mating	Exchange broodstock	Multiple mass-selected strains
No need for partnerships or collaborations	✓	✓	✓	✓	✗	✓
No need for tags or marks	✓	✗	✓	✓	✗	✗
No need for ongoing access to wild-caught fish	✗	✓	✓	✓	✓	✓
Allows genetic improvement	✗	✓	✓	✓	✓	✓

Inbreeding control

	Source broodstock from wild populations	Family-based breeding	Mass selection	Rotational mating	Exchange broodstock	Multiple mass-selected strains
Allows estimation of genetic parameters	✘	✓	✘	✘	✘	✘
Uses genetic relationships to optimise genetic improvement	✘	✓	✘	✘	✘	✘
Suitable for introduced species	✘	✓	✓	✓	✓	✓
No biosecurity risk from external broodstock	✘	✓	✓	✓	✘	✓

Genetic improvement

Genetic improvement

Is the process of making cumulative desirable changes to the average **breeding value** of a strain, for one or more characteristics.

Genetic improvement is achieved by selecting the best individuals from each generation as parents of the next generation.

Select parents that are believed to have high breeding values:

- measured characteristics of an individual
- characteristics of relatives

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Select parents that are believed to have high breeding values:

- measured characteristics
- characteristics of relatives

Mass selection

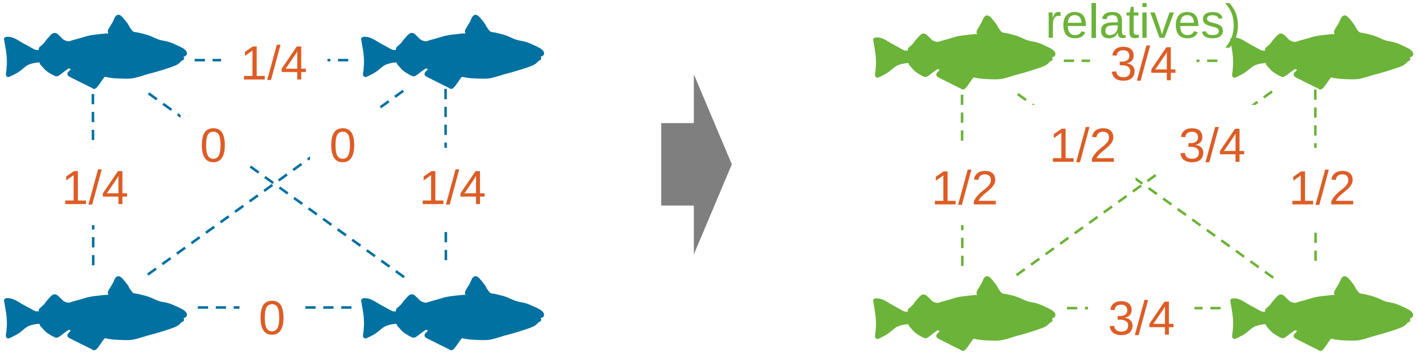
Family-based breeding (expensive and complex)

Genetic improvement

Ongoing genetic improvement requires the retention of additive genetic diversity in a strain.

A high **average relatedness** in a closed population is an indicator of low additive genetic diversity.

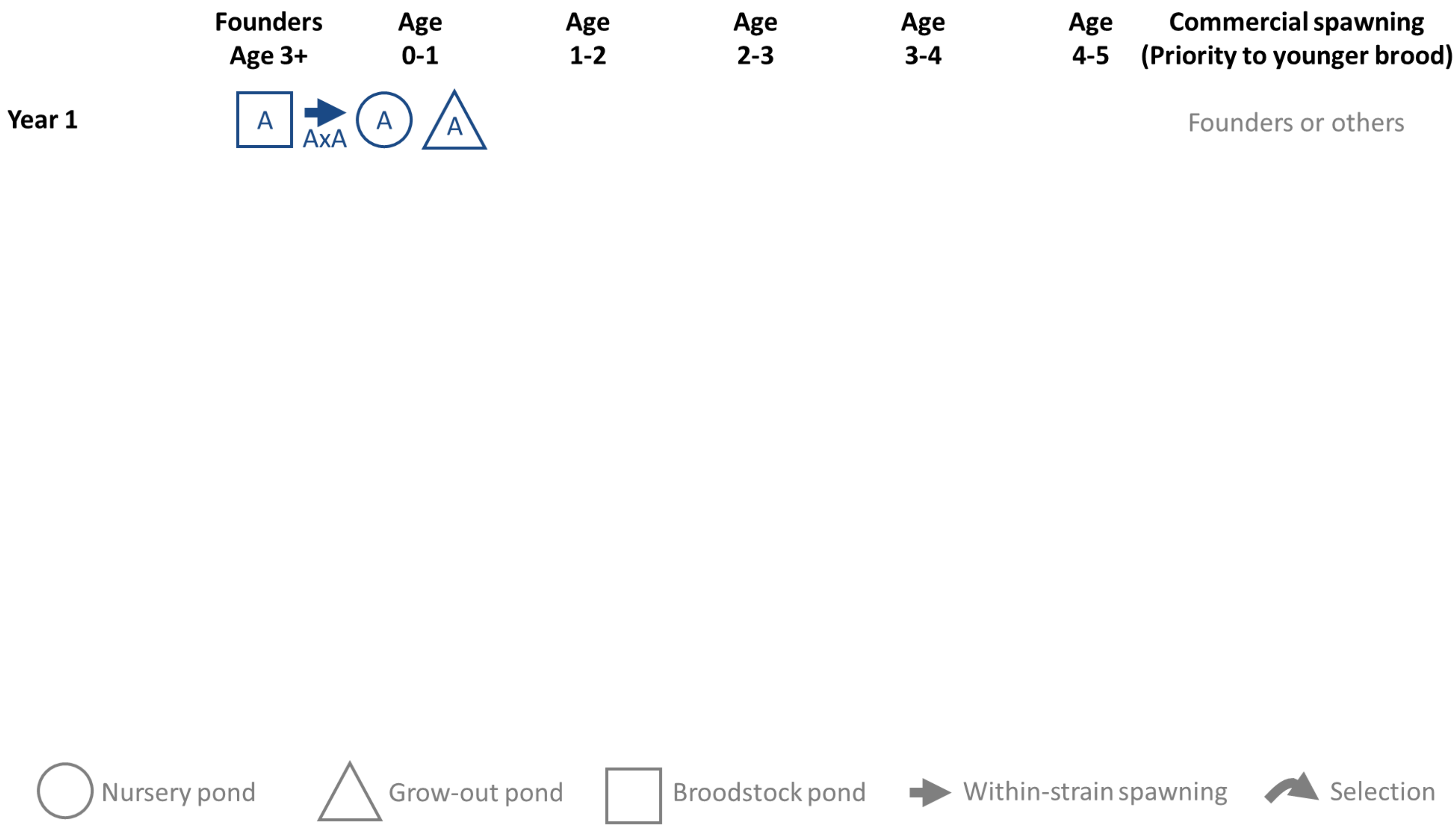
Early generations (few close relatives) | Later generations (more close relatives)



Average relatedness = 1/8 | Average relatedness = 5/8

Broodstock management strategies that reduce inbreeding also retain additive genetic diversity allowing long term genetic improvement.

Mass selection



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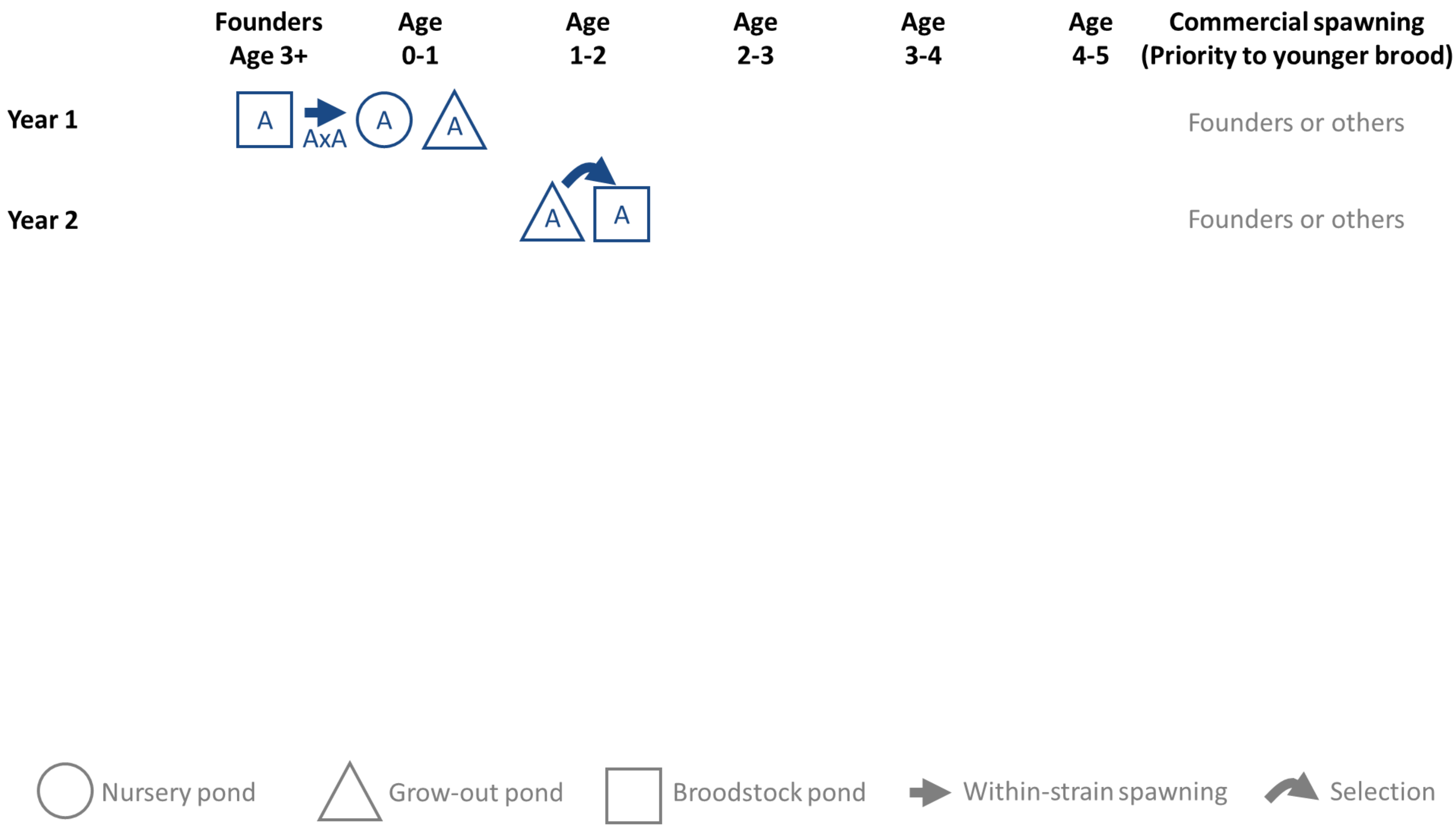

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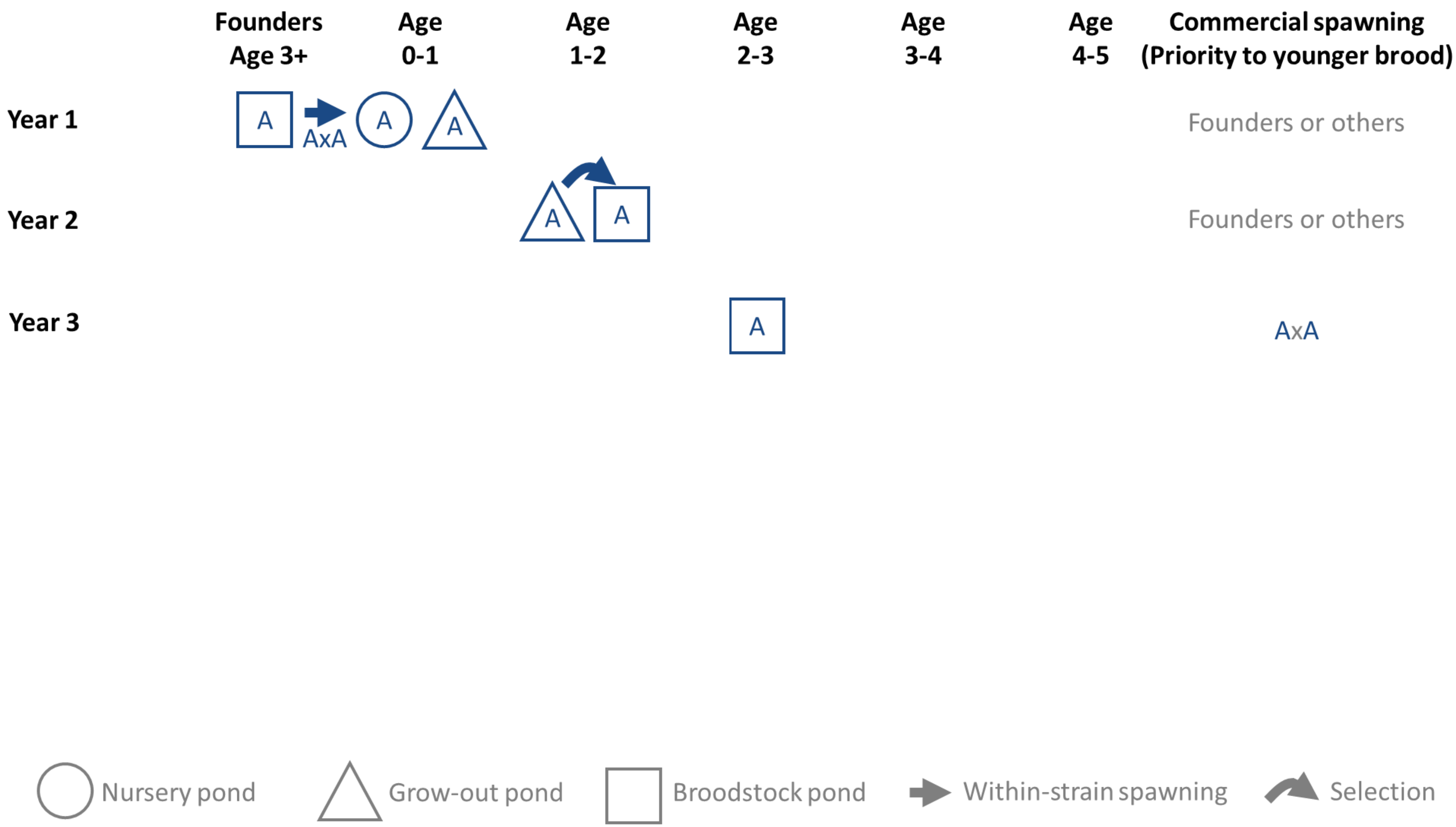

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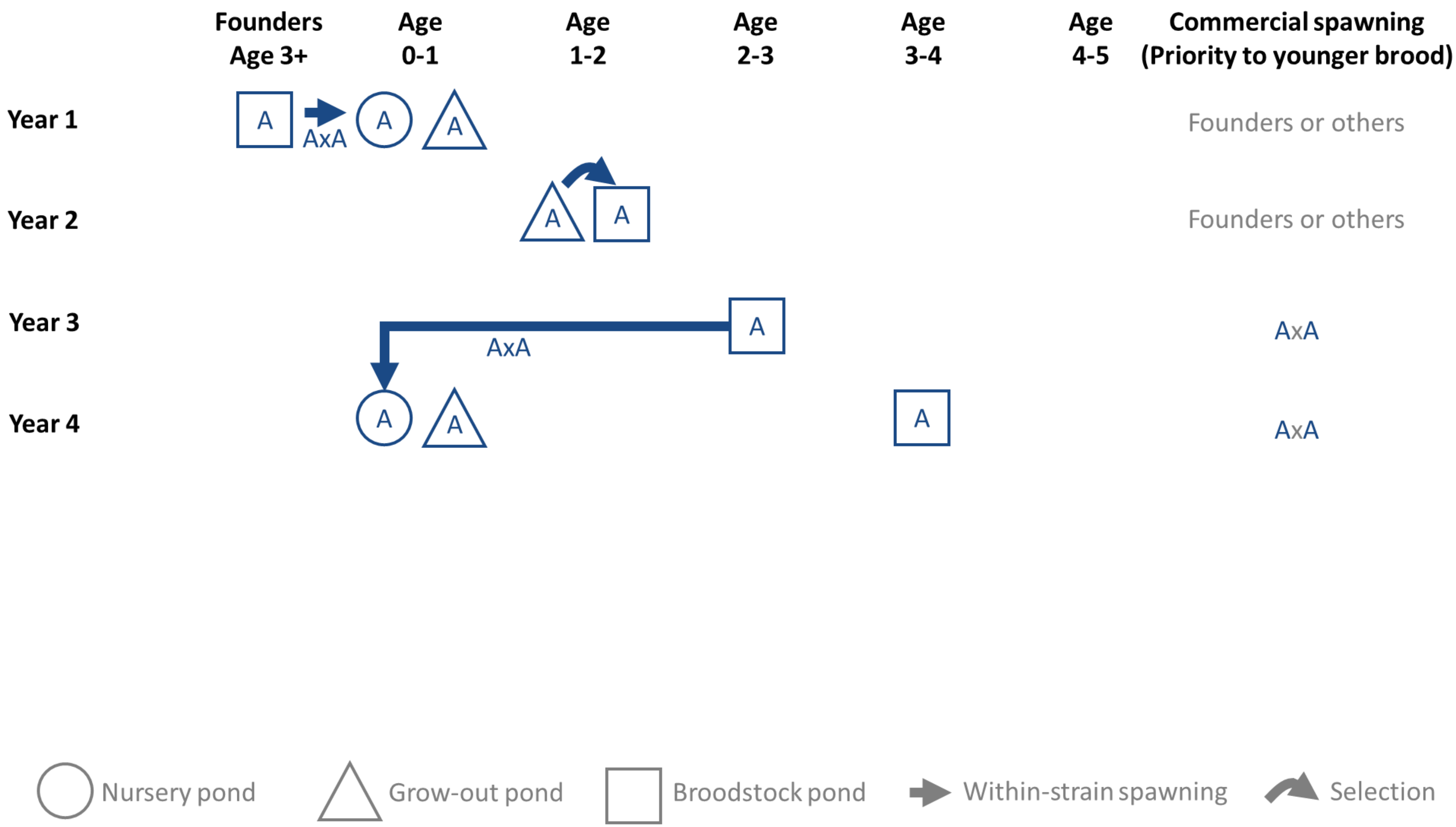
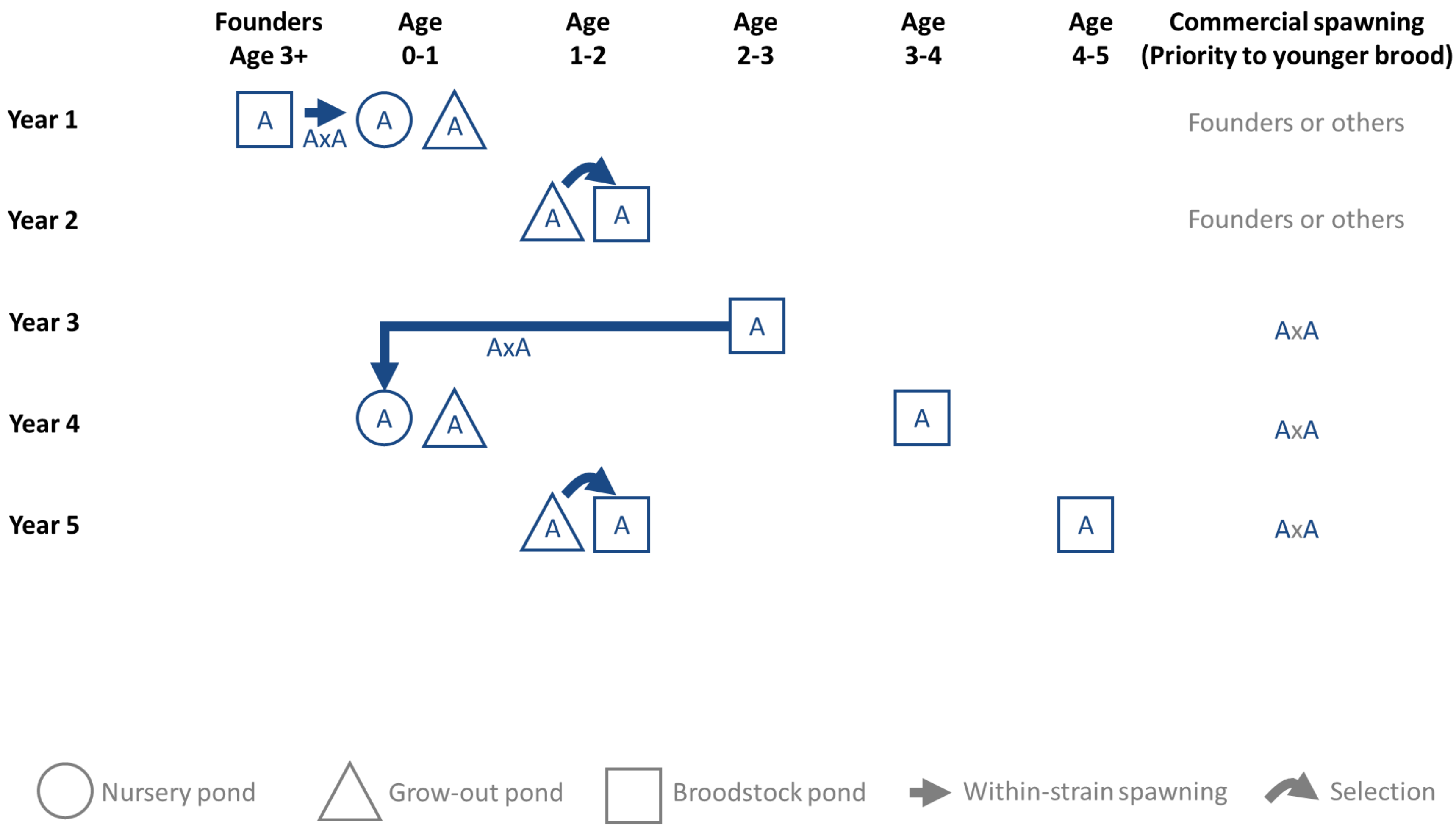
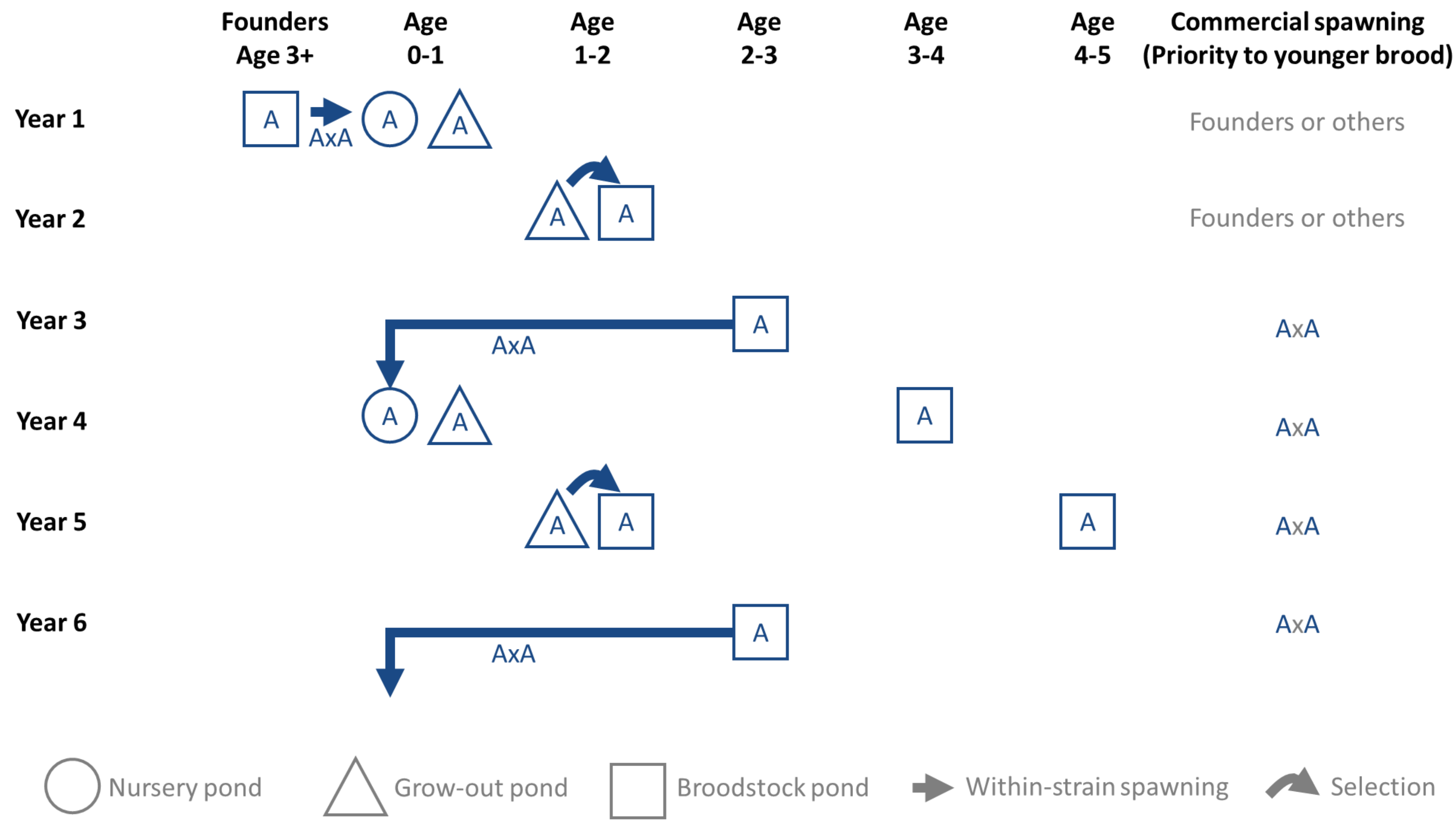


Mass selection

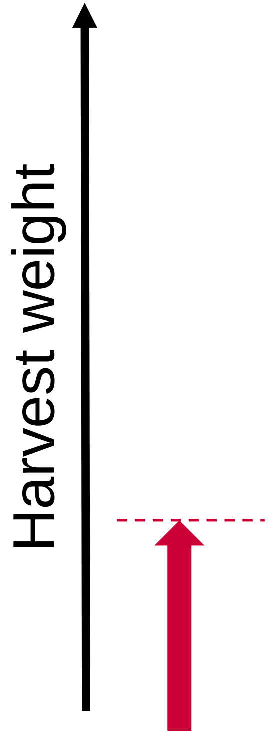


Mass selection



Mass selection

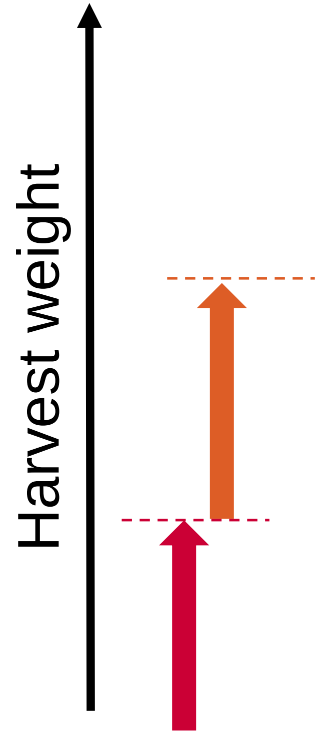
Measured value of each individual is assumed to be proportional to its breeding value



Pond **environment** component of harvest weight

Mass selection

Measured value of each individual is assumed to be proportional to its breeding value

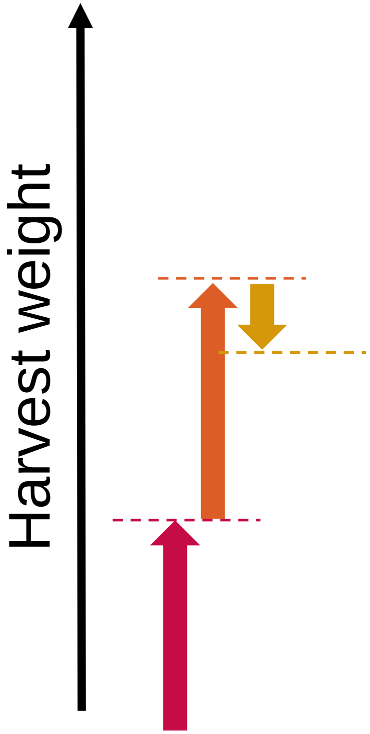


Pond **environment** component of harvest weight

Hatchery **environment** component of harvest weight

Mass selection

Measured value of each individual is assumed to be proportional to its breeding value



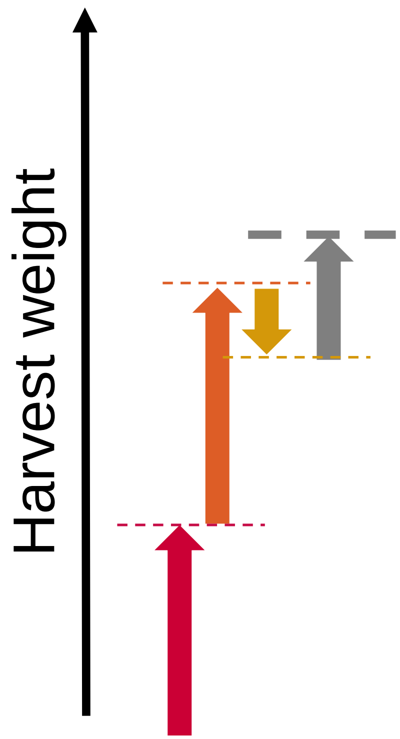
Pond **environment** component of harvest weight

Hatchery **environment** component of harvest weight

Inbreeding depression component of harvest weight

Mass selection

Measured value of each individual is assumed to be proportional to its breeding value



Pond **environment** component of harvest weight

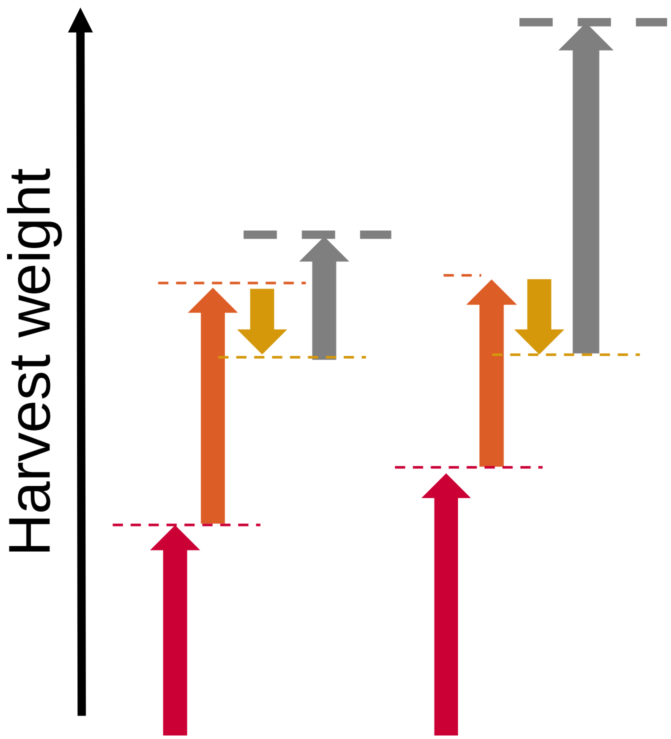
Hatchery **environment** component of harvest weight

Inbreeding depression component of harvest weight

Breeding value component of harvest weight

Mass selection

Measured value of each individual is assumed to be proportional to its breeding value



Pond environment component of harvest weight

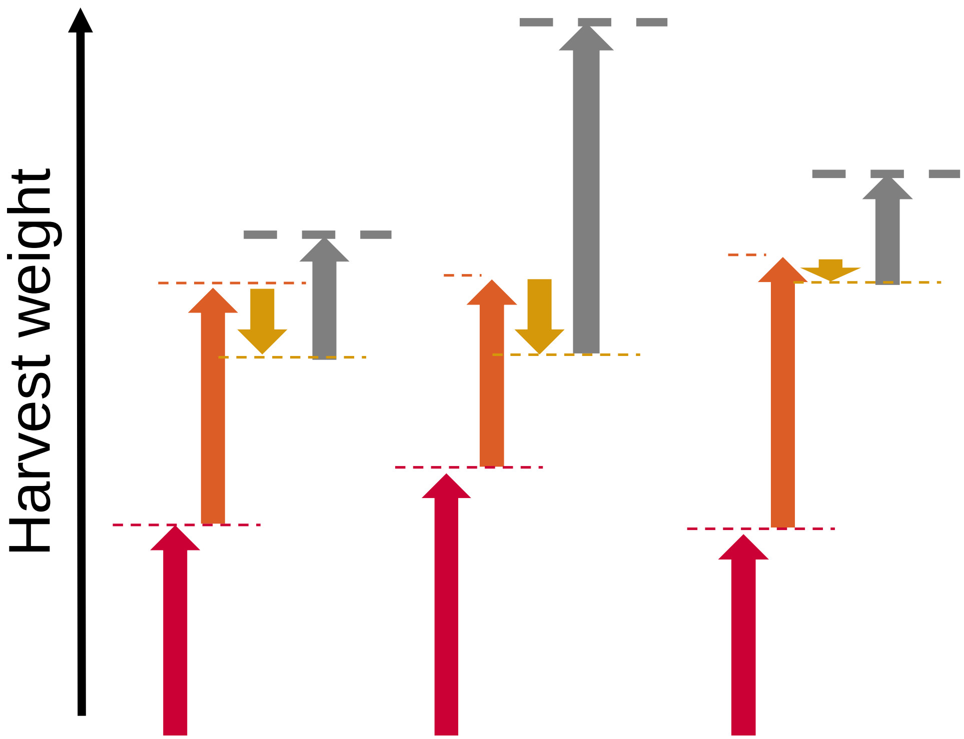
Hatchery **environment** component of harvest weight

Inbreeding depression component of harvest weight

Breeding value component of harvest weight

Mass selection

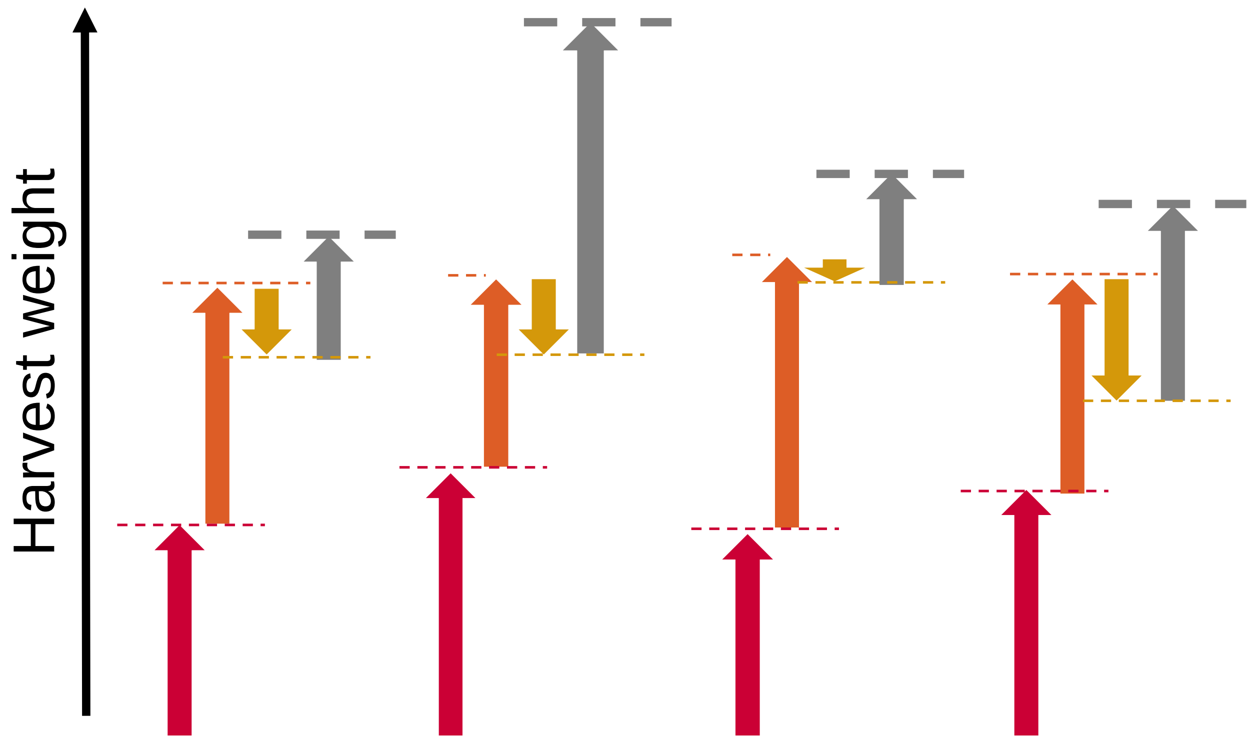
Measured value of each individual is assumed to be proportional to its breeding value



- Pond **environment** component of harvest weight
- Hatchery **environment** component of harvest weight
- **Inbreeding depression** component of harvest weight
- **Breeding value** component of harvest weight

Mass selection

Measured value of each individual is assumed to be proportional to its breeding value



Pond **environment** component of harvest weight

Hatchery **environment** component of harvest weight

Inbreeding depression component of harvest weight

Breeding value component of harvest weight

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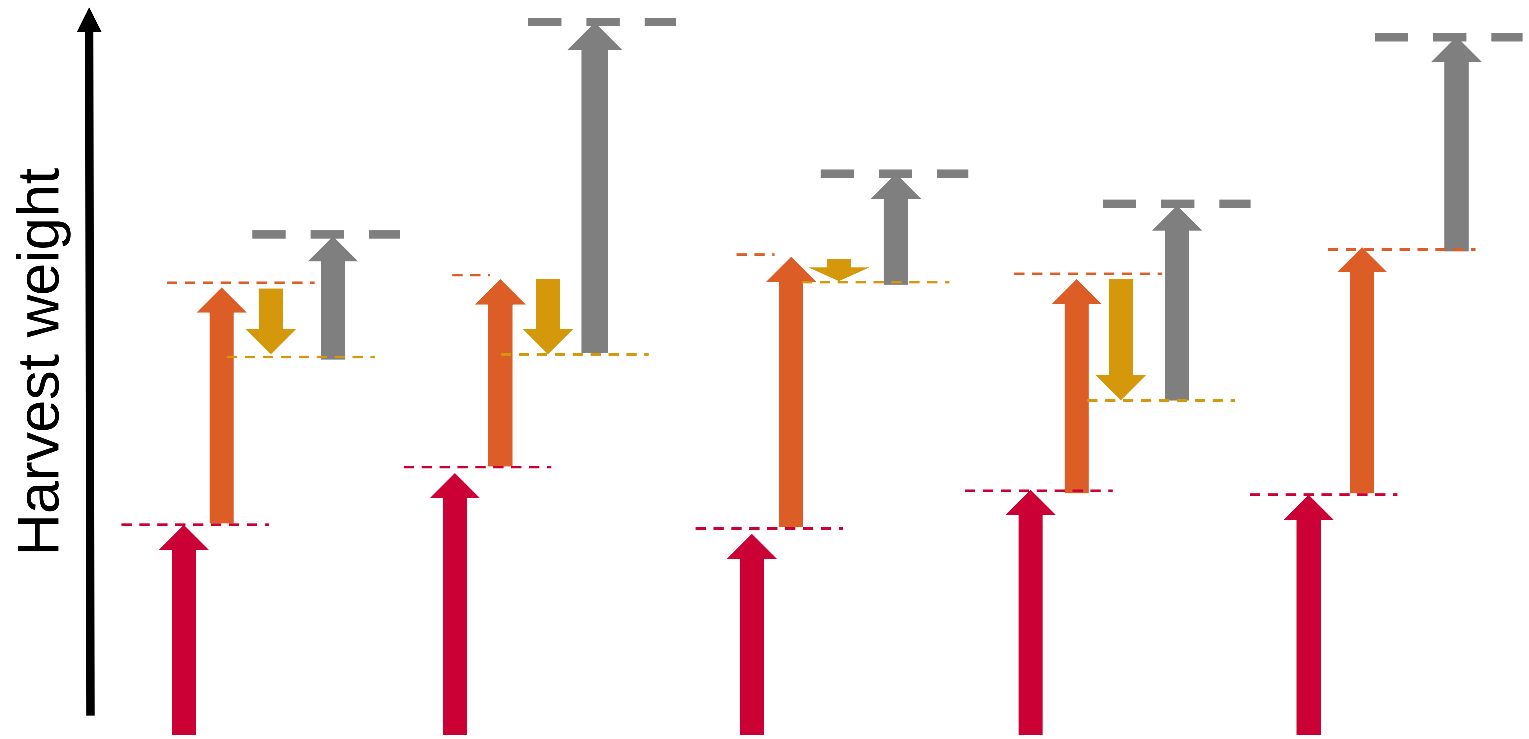
Mass selection

Measured value of each individual is assumed to be proportional to its breeding value



Pond **environment** component of harvest weight

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Mass selection

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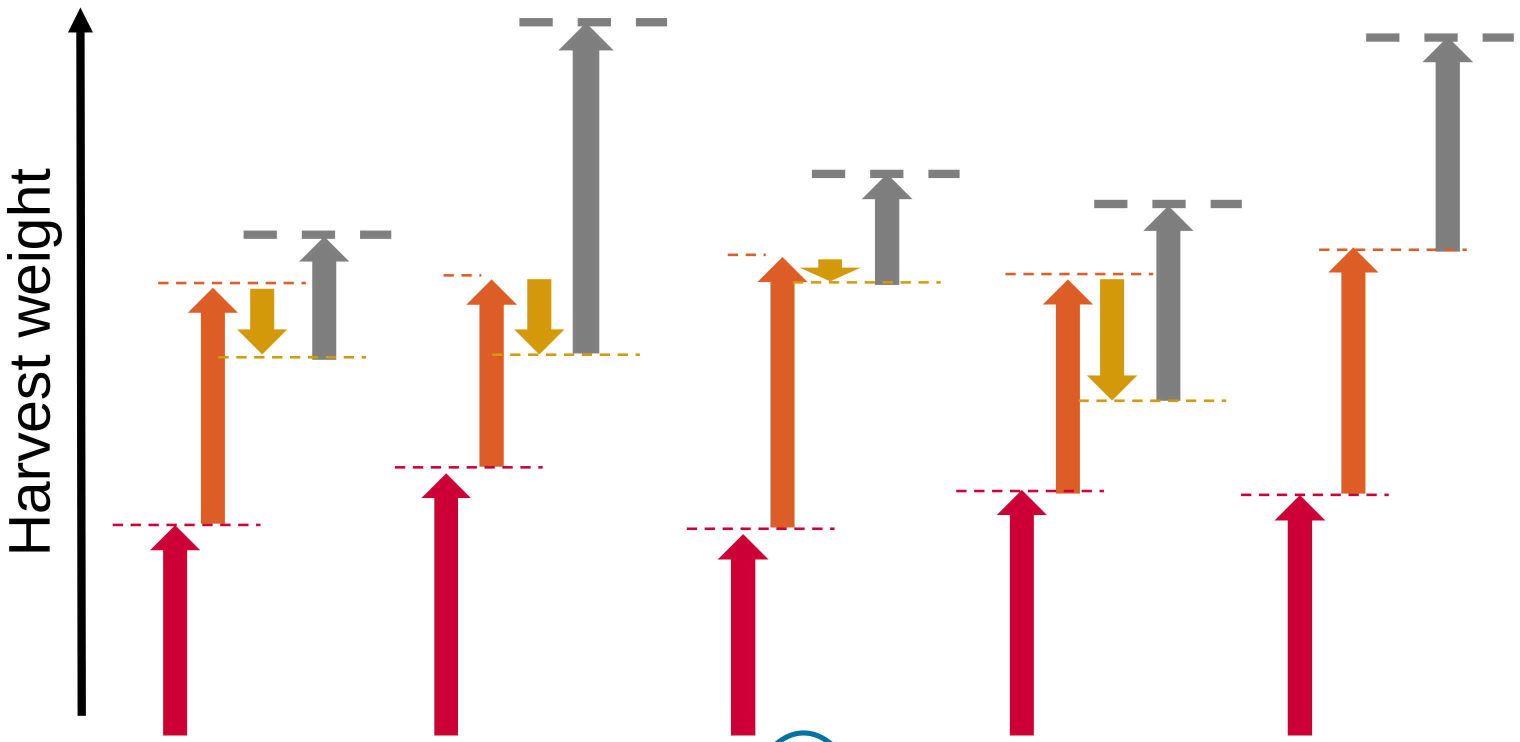
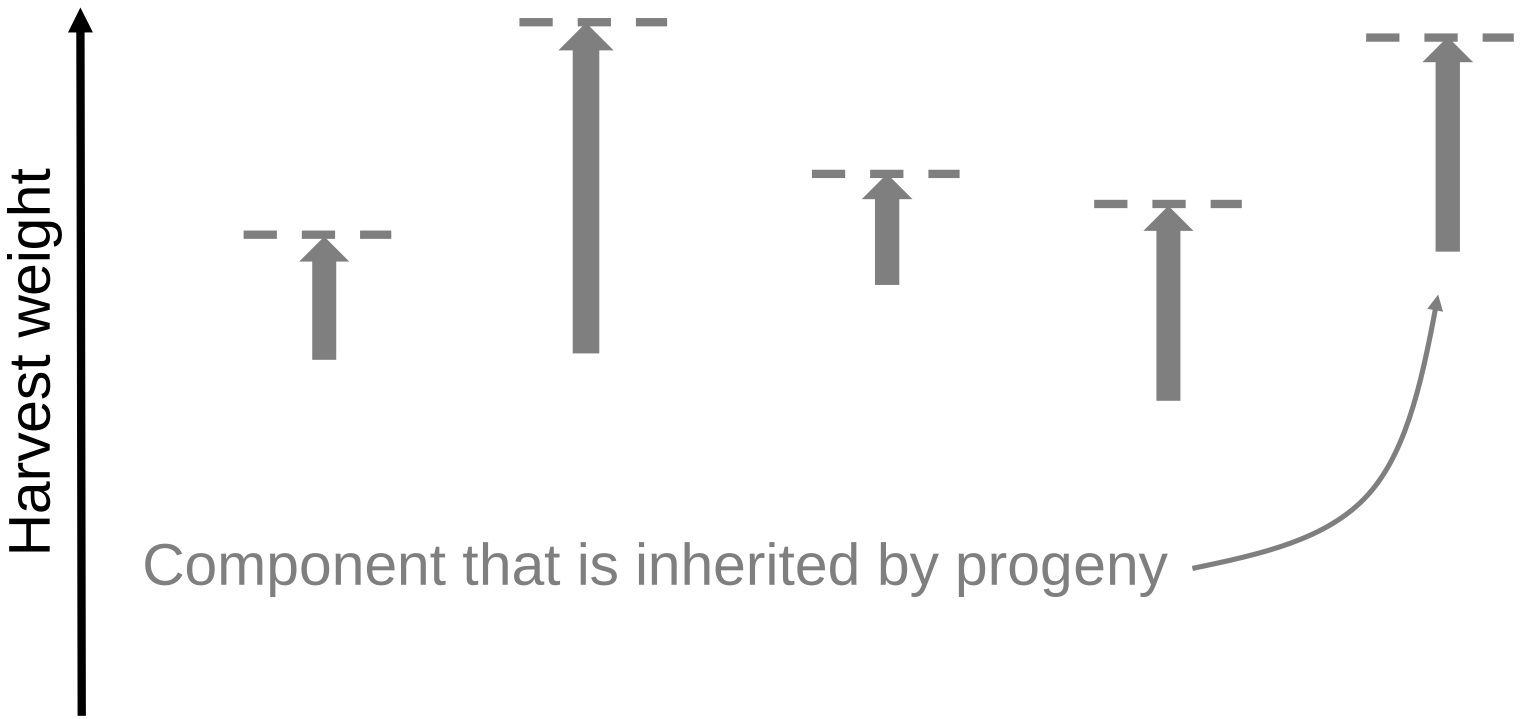


Weight rank	5	1	3	4	2
Breeding value rank	4	1	5	3	2

Mass selection

Measured value of each individual is assumed to be proportional to its breeding value



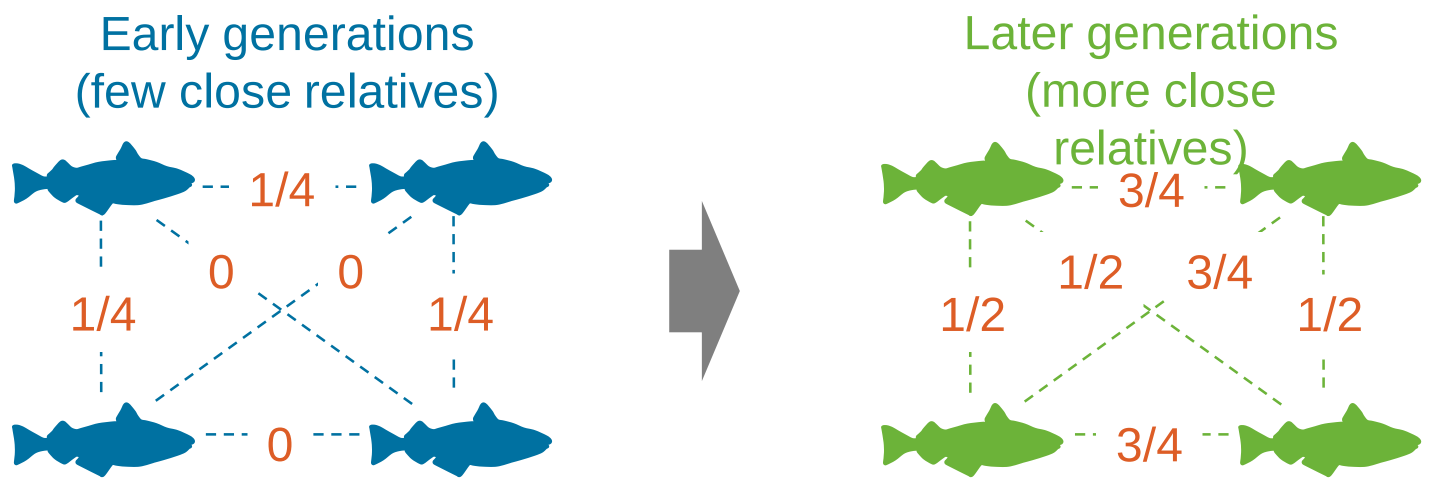
Weight rank	5	1	3	4	2
Breeding value rank	4	1	5	3	2

Breeding value component of harvest weight

Mass selection

With mass selection the rate at which average relatedness increases in a strain is difficult to control

Can implement strategies to reduce the risk of a rapid increase in average relatedness



Average relatedness = 1/8

Average relatedness = 5/8

Mass selection – Selecting founders

Strategies to reduce average relatedness

Avoid genetic relationships among founders.

No less than 50 male and 50 female founders.

Founders obtained from wild populations:

- should be from large water bodies with large populations
- if collected as fertilised eggs, should be obtained at the peak of the spawning season from areas in which the species is prevalent

Biosecurity must be considered.

Mass selection – Spawning new broodstock

Strategies to reduce average relatedness

Maximise the number of parents that contribute to the next generation (e.g. 50 dams and 50 sires).

Maximise the number of full-sibling families to which each parent contributes.

Ideally contributions to the next generation should be equal from each parent.

If possible, avoid mass spawning (e.g. Chinese style spawning tanks) due to the associated uncertainty of parental contributions.

Mass selection – Spawning new broodstock

Strategies to reduce average relatedness

Ideally each sire would be mated with each female and equal numbers of progeny from each full-sibling family retained. This could be achieved by:

1. inducing and strip spawning each of the males
2. obtaining equal quantities of milt from each male – excess milt could be used for commercial seed production by crossing with an unrelated strain
3. using milt-extenders to allow short-term milt storage
4. pooling milt from all sires and mixing
5. inducing and strip spawning each of the females

Mass selection – Spawning new broodstock

Strategies to reduce average relatedness

6. obtaining equal volumes of eggs from each female – excess eggs could be used for commercial seed production by crossing with an unrelated strain
7. separately fertilising the eggs of each female with equal volumes of the pooled milt
8. pooling fertilised eggs and rearing according to normal procedures

Mass selection – Grow out

Strategies to reduce average relatedness

No less than an average of 25 progeny per parent should be grown out.

Future broodstock requirements also need to be considered when determining the number of individuals to be grown out.

Fish spawned at different times should be grown out separately up to the point of selection.

If different aged fish are grown out together it is not possible to determine if differences in performance at the time of selection are the result of differences in age or genetics.

Mass selection – Selection

Strategies to reduce average relatedness

Large and healthy fish should be selected as parents but other traits may also be selected for (e.g. shape and colour).

The more traits that are selected for, the less genetic improvement achieved in any one trait.

The very best individuals should be retained to produce new broodstock. Additional fish may need to be retained for commercial production.

Practical management of inbreeding

Practical management of inbreeding

Remember the basic principles and determine what is affordable and practical.

1. Inbreeding results from the mating of related parents
2. Average relatedness within strains increases with each generation
   - Minimising this increases reduces inbreeding and allows within-strain genetic improvement over the long term
3. If two highly inbred but unrelated parents (or strains) are crossed, their progeny will not be inbred
4. Genetic improvement is achieved by selecting the best individuals from each generation as parents of the next generation
5. Biosecurity issues must be considered when moving fish to and from hatcheries

Practical management of inbreeding

Without industry-wide collaboration

Remember the basic principles and determine what is affordable and practical.

Possible approaches:

- Routinely source broodstock from wild populations
- Exchange broodstock
- Maintain multiple unrelated strains

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} Biosecurity risks

Practical management of inbreeding

Without industry-wide collaboration

Remember the basic principles and determine what is affordable and practical.

Possible approaches:

- Routinely source broodstock from wild populations
- Exchange broodstock
- Maintain multiple unrelated strains

Biosecurity risks

Genetic improvement with mass selection possible

Exchange broodstock

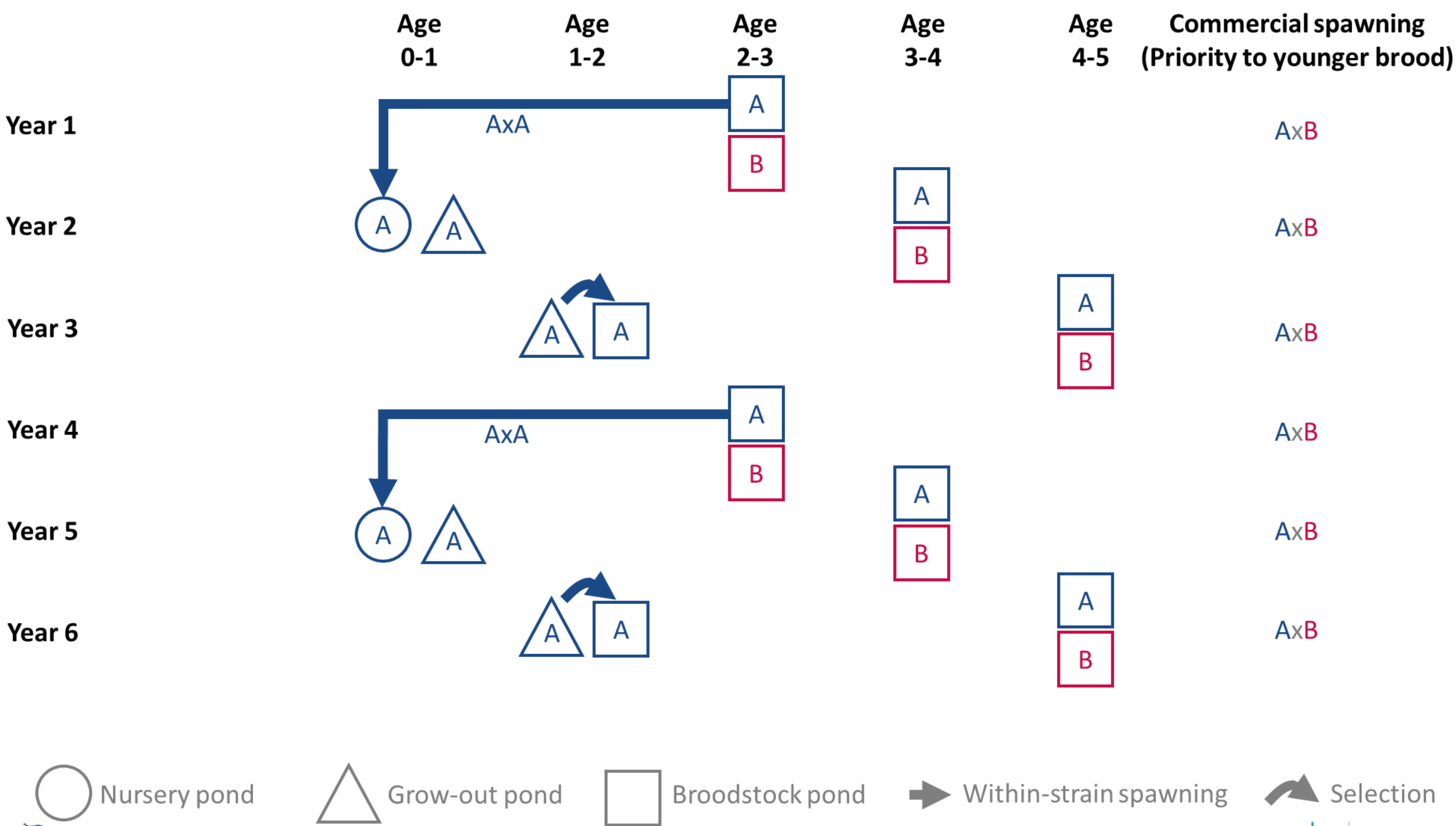
Many hatcheries maintain their own strains:

- average relatedness may be high if strains have been maintained for multiple generations
- strains may have undergone some degree of genetic improvement through deliberate or inadvertent selection

To overcome inbreeding in seed sold for grow out, such strains can be mated with an external **unrelated** wild or hatchery strain.

Still need to regenerate and maintain the ‘purity’ of the hatchery’s own strain.

Exchange broodstock



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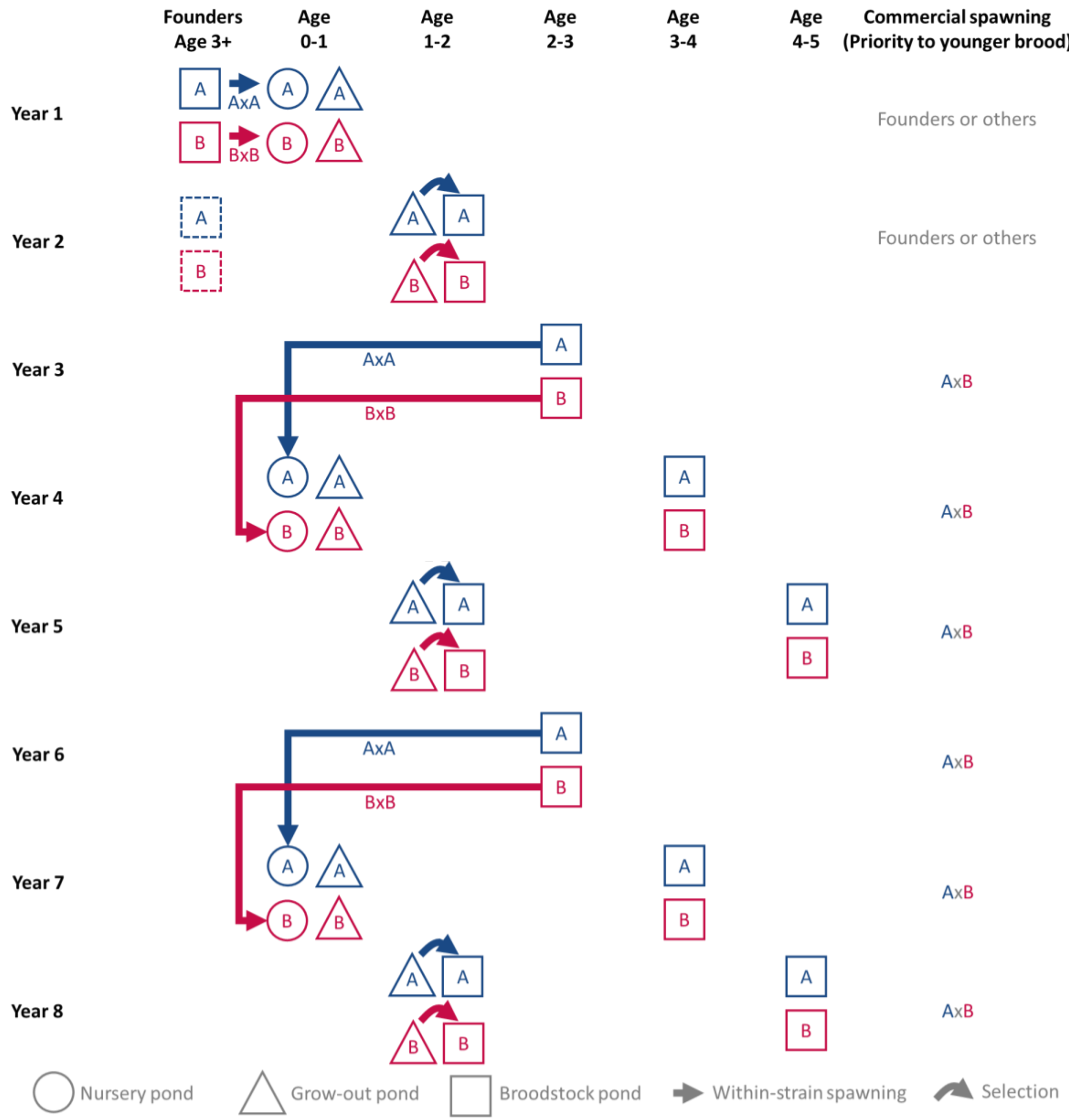
Maintain multiple strains

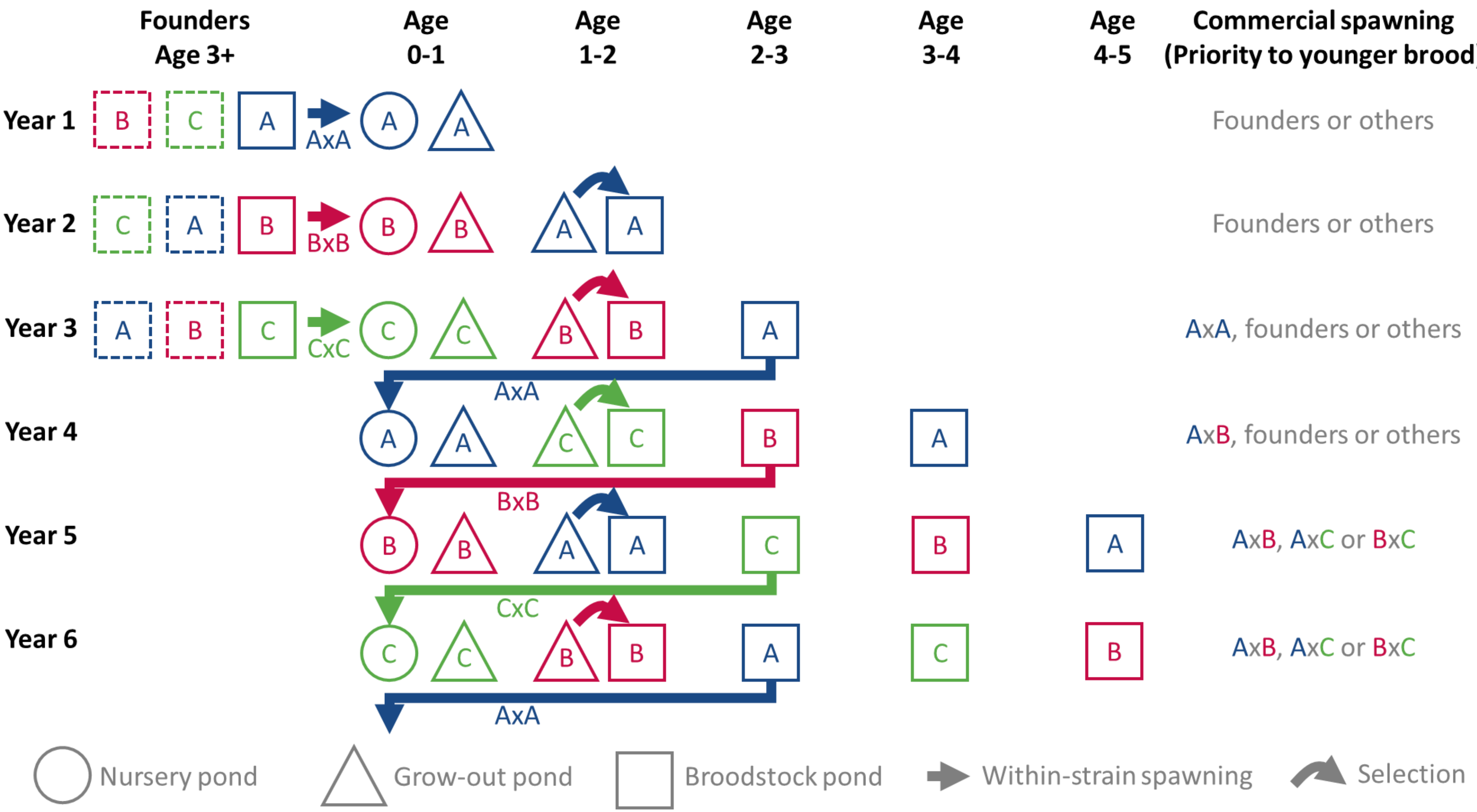
Produce non-inbred seed for grow out by crossing unrelated strains.

Two main approaches:

- discrete-generations
    - all strains spawned in the same year
- rolling-front
    - each strain spawned in a different year



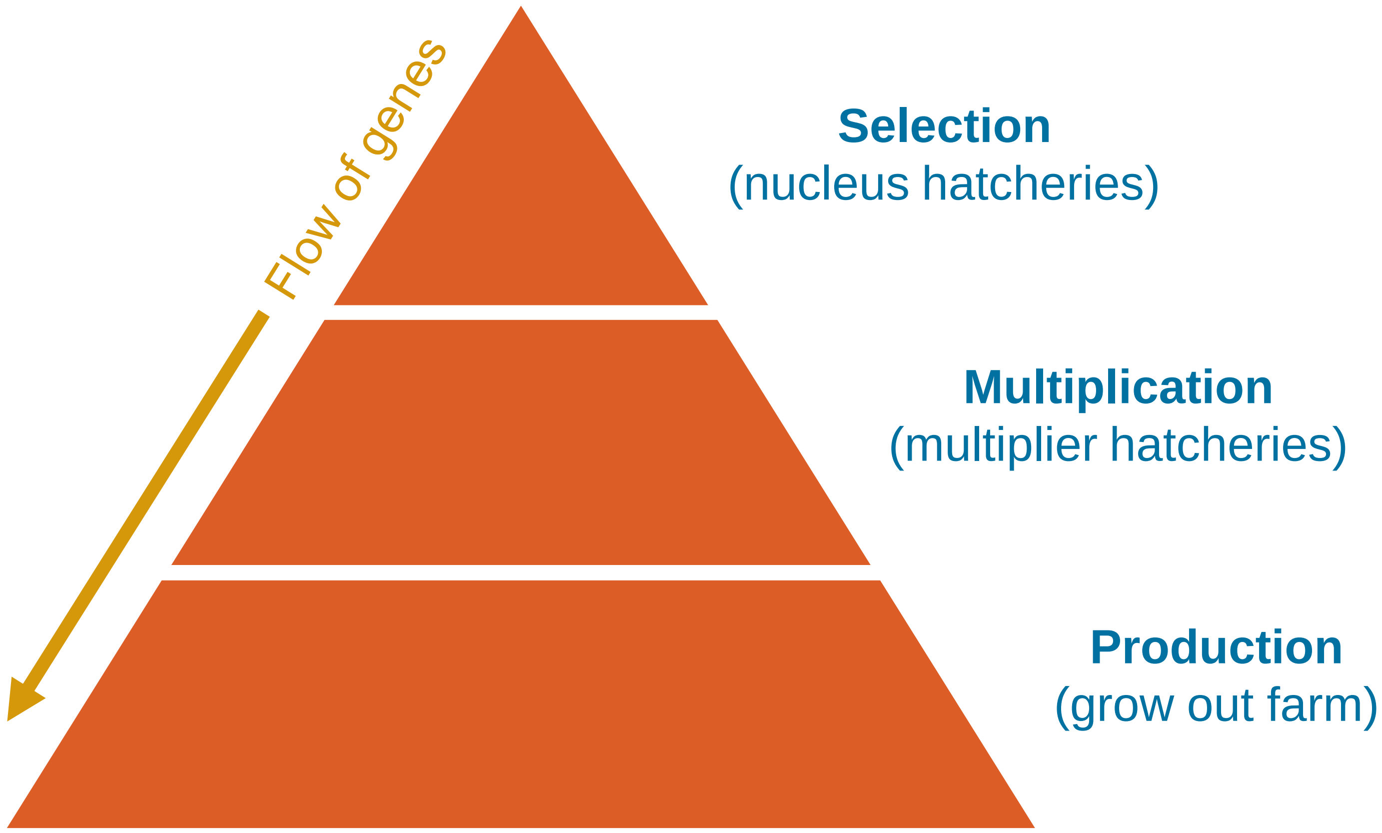
Two strains managed using a ‘discrete generations’ approach



Three strains managed using a 'rolling front' approach. Note that Strain C is not strictly necessary

Practical management of inbreeding

With industry-wide collaboration



Maintain multiple strains

Benefits of the rolling front approach:

- smooths peaks and troughs in activity across years
- better utilises infrastructure – all ponds are used every year
- skills retained – all skills are practiced each year

Maintaining broodstock in ponds according to age class may further simplify management.

Practical management of inbreeding

With industry-wide collaboration

Remember the basic principles and determine what is affordable and practical.

Biosecurity risks must be considered.

Implement a genetic improvement program at one or more ‘breeding centres’ (i.e. **nucleus hatcheries**):

- Family-based breeding
- Rotational mating
- Multiple mass-selected strains

Nucleus hatcheries distribute genetically improved broodstock to **multiplier hatcheries**.

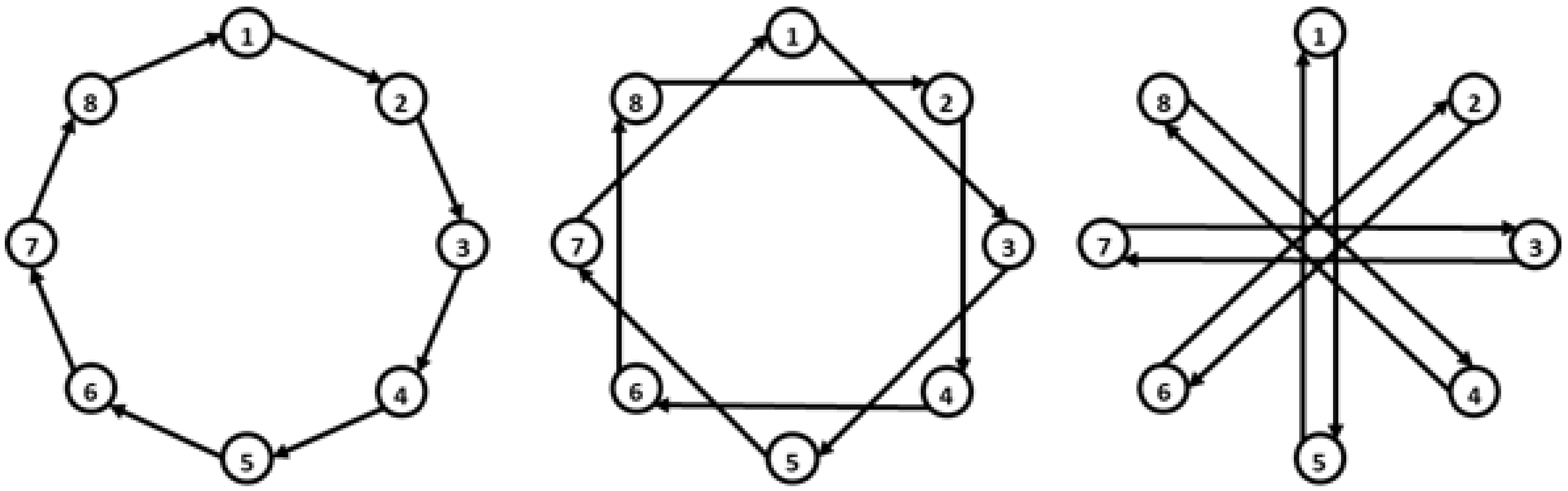
Family-based breeding

Recommended only if funds and technical expertise are available over the long-term.

Rotational mating

A form of mass selection in which inbreeding is minimised:

- Figure shows the movement of males between cohorts (indicated by arrows)
- The three cycles should be repeated in sequence indefinitely



Rotational mating

Only recommended if sufficient ponds are available, and human error and accidental mixing of cohorts (e.g. due to flooding) can be avoided.

Maintain multiple mass-selected strains

Genetically improve of two or more unrelated strains with mass selection.

Distribute unrelated strains to multiplier hatcheries each generation.

Produce non-inbred seed for grow out in multiplier hatcheries by crossing unrelated strains.

Arguably the best approach in the absence of funding for a family-based breeding program.

Management of multiple strains in a multiplier hatchery

Conclusion

Remember the basic principles and determine what is affordable and practical.

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2. Average relatedness within strains increases with each generation
    - Minimising this increases reduces inbreeding and allows within-strain genetic improvement over the long term
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Further information

Hamilton MG. 2019. Management of inbreeding in carp hatcheries in Myanmar. Inland Myanmar Sustainable Aquaculture Programme (INLAND MYSAP), Mandalay, Myanmar, p 31.

This has been translated into Myanmar.

Thank You

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