2. Commonly used mating designs in tree breeding

Mating design is used to generate genetic pedigrees, genetic information and materials that can be used in a breeding program.

Objectives of mating designs:

1) Provide information for evaluating parents
2) Provide estimates of genetic parameters
3) Provide estimates of genetic gains
4) Provide a base population for selection

A single mating design may not be the best (efficient) for all objectives. A complementary design with several simple designs may be used to achieve several objectives.

Commonly used mating designs:

1) Open-pollinated
2) Polycross
3) Single-pair mating
4) Nested mating
5) Factorial mating & tester design
6) Diallel mating (full, half, partial & disconnected)

Single-pair mating

Parents are mated only once by pairs
P parents generate ½ P full-sib families

- Provide good information for full-sib family performance
- Provide estimates of some genetic parameters
- Not for estimating genetic gains from \( V_A \)
- Maximum unrelated ness but not optimum for selection
- Low cost

\[
1 \times 2 \\
3 \times 4 \\
5 \times 6 \\
7 \times 8 \\
\ldots \times \ldots
\]

\[\text{COV}_{FS} = \frac{1}{2} V_A + \frac{1}{4} V_D + \ldots\]
Nested mating (NC Design I)

Each of male parents is mated to a different subset of female parents

\[
\begin{array}{cccc}
1 & 2 & 3 \\
A & X & & \\
B & X & & \\
C & X & & \\
D & & X & \\
E & & X & \\
F & & X & \\
G & & X & \\
H & & X & \\
I & & X & \\
\end{array}
\]

\[
COV_{PHS}=\frac{1}{4} V_A
\]

\[
V_{\text{female/male}} = COV_{\text{FS}} - COV_{\text{HS}}
\]

\[
= \frac{1}{2} V_A + \frac{1}{4} V_D - \frac{1}{4} V_A
\]

\[
= \frac{1}{4} V_A + \frac{1}{4} V_D
\]

- Provide information for parents and full-sib families
- Provide estimates of both additive and dominance effects
- Provide estimates of genetic gains from both $V_A$ and $V_D$
- Not efficient for selection
- Low cost for controlled mating

Factorial mating (NC Design II)

Each member of a group of males is mated to each member of group of females

\[
\begin{array}{cccccc}
1 & 2 & 3 & 4 & 5 \\
A & X & X & X & X & \\
B & X & X & X & X & \\
C & X & X & X & X & \\
D & X & X & X & X & \\
E & X & X & X & X & \\
\end{array}
\]

\[
COV_{PHS}=\frac{1}{4} V_A
\]

\[
COV_{MHS}=\frac{1}{4} V_A
\]

\[
V_{\text{female} \times \text{male}} = COV_{\text{FS}} - COV_{\text{HSm}} - COV_{\text{HSf}}
\]

\[
= \frac{1}{4} V_D
\]
- Provide good information for parents and full-sib families
- Provide estimates of both additive and dominance effects
- Provide estimates of genetic gains from both $V_A$ and $V_D$
- Limited selection intensity
- High cost

**Tester mating design (Factorial)**

Each parent in a population is mated to each member of the testers that chosen for a particular reason

\[
\begin{array}{c|c|c|c|c|c|}
\hline
\text{♂} & 1 & 2 & 3 & 4 & 5 \\
\hline
A & X & X & X & X & X \\
B & X & X & X & X \\
C & X & X & X & X \\
D & X & X & X & X \\
E & X & X & X & X \\
\hline
\text{♀} & \ldots & \ldots & \ldots & \ldots & \ldots \\
\hline
n & X & X & X & X \\
\hline
\end{array}
\]

$COV_{PHS} = \frac{1}{4} V_A$
$COV_{MHS} = \frac{1}{4} V_A$

$V_{female \times male} = COV_{FS} - COV_{HSm} - COV_{HSf} = \frac{1}{4} V_D$

- Provide good information for parents and full-sib families
- Provide estimates of both additive and dominance effects
- Provide estimates of genetic gains from both $V_A$ and $V_D$
- Limited selection intensity
- High cost

**Diallel mating design**

**Full diallel** – each parent is mated with every other parent in the population, including selfs and reciprocal:

\[
\begin{array}{c|c|c|c|c|c|}
\hline
\text{♂} & 1 & 2 & 3 & 4 & 5 \\
\hline
1 & X & X & X & X \\
2 & X & X & X & X \\
3 & X & X & X & X \\
4 & X & X & X & X \\
5 & X & X & X & X \\
\hline
\text{♀} & \ldots & \ldots & \ldots & \ldots & \ldots \\
\hline
\end{array}
\]
**Half diallel** – each parent is mated with every other parent in the population, excluding selfs and reciprocal:

```
♂
1 2 3 4 5
1 X X X X X
2 X X X
3 X X X
4 X X
5
♀
```

**Partial Diallel** – selected subsets of full diallels:

```
♂
1 2 3 4 5 . n
1 X X X
2 X X X
3 X X X
4 X X X
5 X X X
♀
```

**Disconnected half diallel** – selected subsets of full diallels:

```
♂
1 2 3 4 5 . n
1 X X X
2 X X
3 X X
4 X
5 X X X
♀
```

**Diallel analysis**

\[
\text{COV}_{HS} = \frac{1}{4} V_A \\
\text{COV}_{FS} = \frac{1}{2} V_A + \frac{1}{4} V_D \\
\text{COV}_{FS} = \text{COV}_{FS} - 2\text{COV}_{HS} = \frac{1}{4} V_D
\]


- Provide good evaluation of parents and full-sib families
- Provide estimates of both additive and dominance effects
- Provide estimates of genetic gains from both $V_A$ and $V_D$
- High cost

**Complementary mating design**

Complementary mating designs are used to combine different natures of single matings. For example;
> use the Polycross for evaluating parents
> use a type of a controlled cross for generating a base population for selection