# Parentage verification
## Technote # 1

**HIGHLIGHTS**

- Parentage verification is a standard inclusion with Australian genomic reports.
- Most herds have parentage errors automatically corrected as part of the genomic testing process.
- Parentage verification increases the reliability of Australian Breeding Values (ABVs) for bulls and females.
- Correct pedigree data adds value to surplus stock and improves culling and selective breeding decisions.
- Correct parentage is critical for managing inbreeding.

Parentage verification involves cross checking an animal's recorded pedigree with its genomic pedigree to confirm its sire and dam. It is included with genomic results for animals tested through the Australian system.

Parentage verification can be used to correct errors and/or fill gaps in records where data is unknown, uncertain or has been lost.

## Parentage errors

Parentage misidentification occurs even under the most astute management. The error level varies across farms with up to 20% of Australian dairy cattle recorded with incorrect parentage.

There are many reasons why an animal's recorded parentage may be incorrect. The challenges of correctly identifying a calf's parents are greater with larger herd sizes, intensive calving periods, large herd AI synchronisation programs and multiple staff.

The most common parentage data errors occur at calving and at mating (see table 1).

## Benefits

Parentage verification can establish pedigrees in herds that do not have adequate records or have lost calving or mating records or have purchased animals without records.

Improved accuracy of on-farm records and pedigree data can add value to surplus stock through export and/or herdbook registration eligibility.

Corrective mating programs benefit from accurate pedigrees by combining performance data (phenotypes) of the animal with the correct genotypic data to make better breeding combinations for the future.

Farmers can use correct pedigree data and reliable genomic breeding values to aid in their culling decisions and selective breeding decisions – ie. selective use of sexed semen or dairy beef.

Correct parentage is critical for managing inbreeding as inbreeding calculations rely on accurate pedigree records.

## Table 1: Common causes of parentage errors

| Errors at mating | Misidentified calves |
|---|---|
| <ul><li>Semen handling errors or incorrect semen straw used</li><li>Errors in data entry</li><li>Lost AI dockets or mating records</li><li>Cow IDs misidentified when mated (misread freeze brand/tag)</li><li>Errors in heat detection - cow mated multiple times within a cycle period</li><li>Calves born in 'cross-over' period between AI mating and paddock mating, or between natural bull rotations</li><li>Multiple natural bulls run simultaneously</li><li>Natural bulls 'jumping the fence'</li></ul>**Embryo transfer**<ul><li>Multiple sires used over donor animal</li><li>Incorrect embryo implanted</li><li>Recipient IDs misidentified</li><li>Incorrect embryo identification</li><li>Lost ET transfer records</li></ul> | <ul><li>Mismothering of calves</li><li>Calf tagging errors</li><li>Calves transported or penned in batches before they are tagged</li><li>Misidentified dam IDs (misread freeze brand/tag)</li><li>Calving data entry errors</li><li>Lost calving books</li></ul>**Errors at sampling**<ul><li>Incorrect recording of calf ID against the sample ID during sampling</li></ul> |

At an industry level, parentage verification increases the accuracy and reliability of all breeding values by ensuring accurate progeny data is submitted for more reliable bull breeding values.

The accuracy and ease of parentage verification improves as more animals are genotyped, adding to the data available to search to correct errors.

## Parentage verification process

Parentage verification is a standard inclusion with DataGene's genomic reports. Parentage is routinely calculated with every genomics run and reported to customers via their genomic service provider and through DataVat.

When an animal is recorded at a herd recording centre or breed association, it is allocated with a National ID (this is different to a Herd Recording ID or Herdbook ID). The sire and dam on these records is referred to as '**nominated** parentage.'

Once a hair or tissue sample has been submitted for genomic testing, the genotype is sent to DataGene to link the results to a National ID and verify the parentage.

If the **nominated** parents match the parents identified by the genotype (**identified** or discovered parentage), the pedigree is verified and a genomic evaluation can be reported.

In most cases, if a parentage error is detected and an alternative parent is identified, it will be updated automatically. In a small number of cases* the genomic evaluation will be withheld until the error is resolved. (see table 2).

> **Terms**
>
> **Nominated** parent: a sire/dam nominated from mating and calving records that has not been genomically verified.
>
> **Identified** parent: a sire/dam that has been identified and genomically verified. The terms identified and **discovered** parent are used interchangeably.
>
> **Geno-inconsistency**: a report showing parentage errors where the nominated parent does not match the identified / discovered parent.

The sample is automatically checked against genotyped animals in DataGene's genetic evaluation system to find an alternative.

If an alternative cannot be detected, the genomic service provider notifies the breeder and attempts to correct the error to ensure a genomic result.

The animal may be resampled to eliminate sampling errors. Otherwise, the breeder can review calving records and mating records to look for alternatives. Parents and/or siblings may be tested to eliminate inconsistencies in parent samples.

If an alternative parent is identified, the correction is made, and a genomic report is generated. This information is automatically sent to the relevant herd test centre.

If an alternative parent cannot be identified, the parentage is left blank. A genomic breeding value can be generated – with a lower reliability.

## Table 2: Resolving parentage issues/errors

| Issue | Cause | Action |
|---|---|---|
| 1. The sire/dam identified is different to the sire/dam nominated. | An incorrect sire/dam was nominated. An alternative sire/dam that has been genotyped is identified. | The nominated sire/dam is automatically updated to the identified sire/dam and a genomic result can be created*. |
| 2. Nominated parent sire/dam is not discovered, but the nominated sire/dam has been genotyped. | The nominated sire/dam is incorrect. The correct sire/dam is not on the genomic database. | The genomic results are withheld pending approval from breeder.<br>• The sire/dam can be left blank. A genomic breeding value can be created, with a lower reliability.<br>• The breeder can nominate an alternative sire/dam that has not been genotyped. |
| 3. The nominated sire/dam is not discovered, and the nominated sire/dam has not been genotyped. | The nominated parent has not been genotyped, therefore is not on the genomic database. | No action required. The system automatically assumes the nominated parent is correct and a genomic result can be created. |
| 4. No sire/dam nominated, but a genotyped parent is identified. | No sire/dam was nominated. A sire/dam was identified through the genomic database. | The sire/dam is automatically updated. A genomic breeding value can be created. |
| 5. No sire/dam discovered | No sire/dam was nominated, and no sire/dam could be identified through the genomic database. | The sire/dam will be left blank. A genomic breeding value can be created, with a lower reliability. |

*Holstein Australia and Jersey Australia customers and Ginfo herds: the genomic results are not updated automatically. A request is sent to the breeder for authorisation to change the record.

## Reliability improvements

Correcting parentage errors will improve the reliability of an animal's breeding values. For example, providing the correct sire can improve the reliability of an animals Balanced Performance Index (BPI) by up to about 15%.

## Accurate record keeping

Parentage verification can be used to correct errors in records, and fill gaps in records where data is unknown or has been lost. However, it is still important genomic tests are supported by accurate record keeping.

Data collected on-farm is used to:

- Provide mating records to identify potential semen handling errors - ie. match the sire to another sire used on a given joining day.

- Provide natural bull rotation dates so alternative sires can be nominated/identified for calves born during cross-over periods.

- Provide calving records to identify potential dam ID or calf mismothering errors – i.e. match the animal with an alternative dam that calved at the same time.

- Cross-check animal IDs to ensure the sampling collection process was correct and accurate.

## Parentage verification services

Genomic service providers currently operating in Australia include:

- Holstein Australia

- Jersey Australia

- ABS Global Australia

- Zoetis

- Total Livestock Genetics (TLG)

- Semex

- Neogen

- ST Genetics Australia

- Weatherbys Scientific Australia

- Viking Genetics

## More information

Predicting heifer performance with genomic testing

Genomic Testing Calves: Standard Operating Procedure

Datagene Technote - Female ABVs

## Contact DataGene

Ph 1800 841 848
E: abv@datagene.com.au
www.datagene.com.au

July 2021