



Estimated output from assisted reproductive techniques (OPU/IVF) in Holstein cattle associated with the genetic background

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Introduction

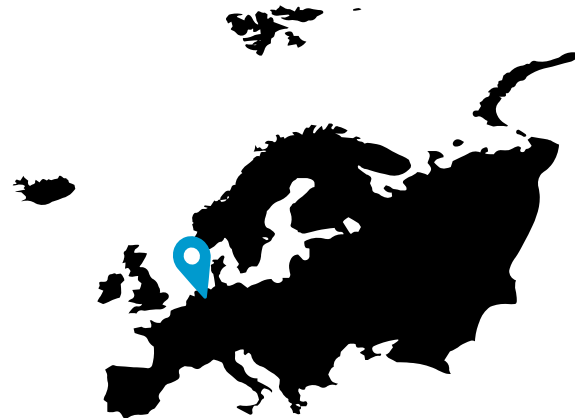
- Reproduction technologies are a central element of breeding scheme efficiency.
- Since 2015 **gEBV** (and candidate gene information) are used within our breeding scheme to assess **MOET productivity** of donors.
- Over the last years, **OPU/IFV** became the **predominant** reproduction technology.
- **Objective:** Assess the genetic contribution to productivity in order to adapt consequently the breeding scheme decision and improve our production process.



Material & Methods

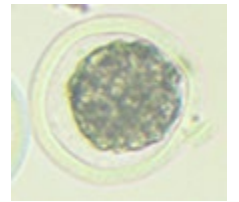
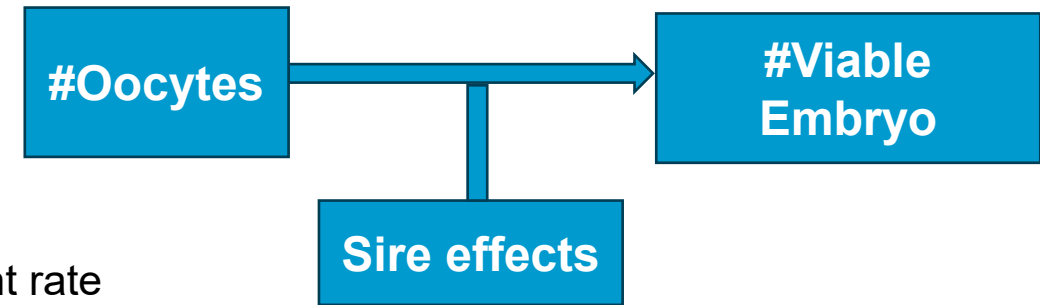
Data

- SYNETICS **donor stud Nückel**, Northwest Germany
- OPU/IVF results from April 2018 – August 2023
- **9,099** sessions performed
- **1,596** Holstein donors originating from 254 farms
- 336 different sires of sons used for fertilization



Model building

- Phenotypes
 - Number of oocytes, number of viable embryos, development rate
 - Transformation of the traits or not?
- Effects taken into account
 - Season, Year, Age Group, OPU Rank, Day of production, Semen sexed or not, HH1 risk mating, Donor, Sire of embryo...
 - Type of the effect fix, Random, genetic?
- Model
 - Linear model
 - Threshold model



Assess the model that best fit data at hand while being sound

Results 1: Model

- Final models

#Oocyte = $\mu + \text{year} + \text{season} + \text{age group} + \text{env}_{\text{perm}} + \text{animal} + \text{day} + \text{OPU rank}$

#Viable Embryo = $\mu + \text{year} + \text{season} + \text{age group} + \text{env}_{\text{perm}} + \text{animal} + \text{day} + \text{embryo sire} + \text{semen type}$

Devpt Rate = $\mu + \text{year} + \text{season} + \text{age group} + \text{env}_{\text{perm}} + \text{animal} + \text{day} + \text{embryo sire} + \text{semen type} + \text{NRH}_{\text{GEBV}}$

- Similar effects retained within traits, among which donor's genetic effects
- Expected effect of the semen for traits related to embryo
- Some effects needing more investigations



Results 2: Genetic parameters

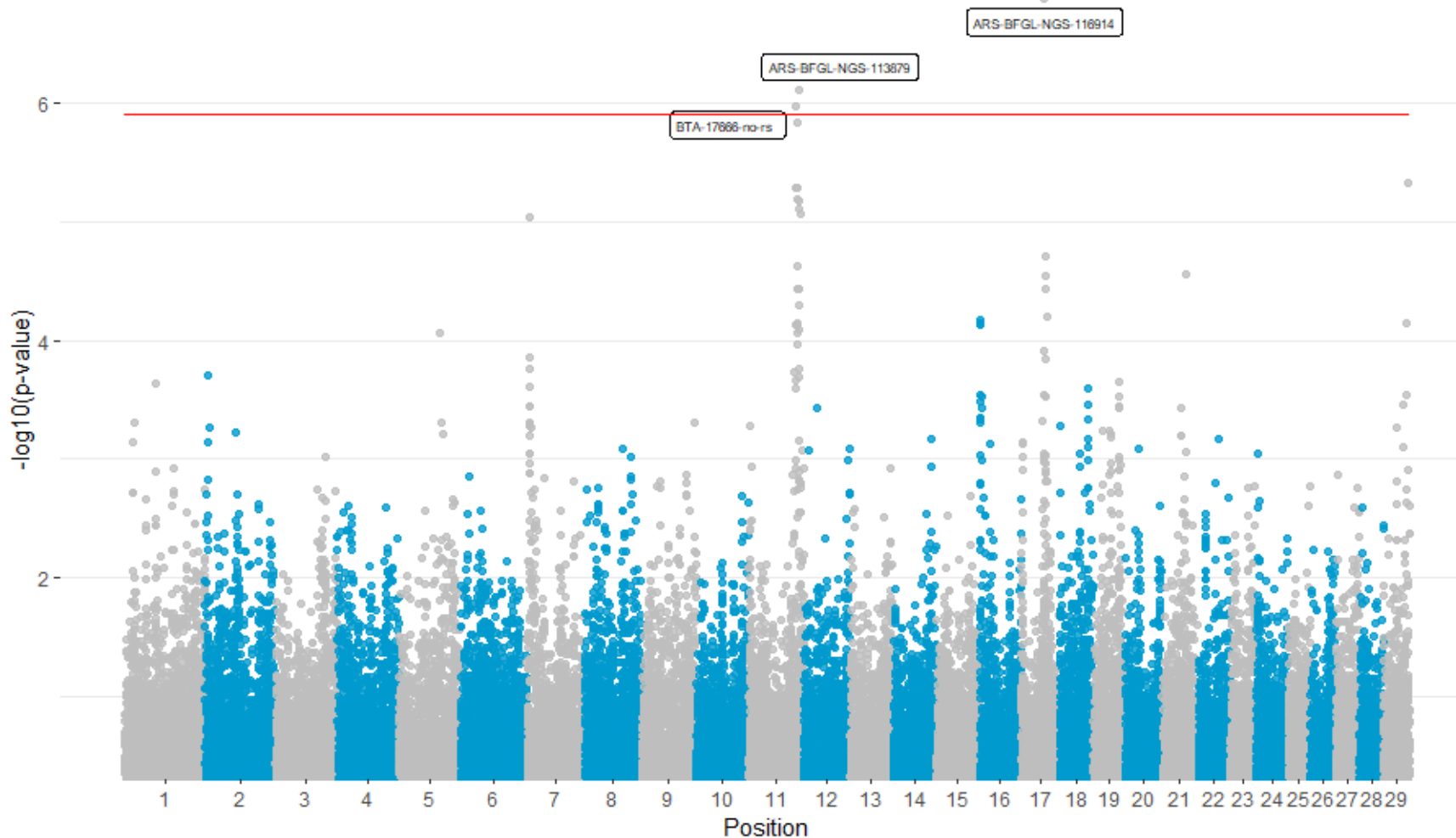
- Highest estimates of genetic parameters :

	Number of oocytes	Viable embryos	Development rate
Data transformation	Anscombe	None	None
heritability	0.24	0.13	0.09
repeatability	0.36	0.20	0.13

- ➔ Simpler traits lead to more satisfactory results
- ➔ Additionnal data may be needed to handle more complex traits (or transformed one)
- ➔ Heritability remain promising owing to the control environment of donors barn
- ➔ Despite these caveats gEBV can be obtained for candidate to donors station (predictive ability ranging from 0,27-0,14)

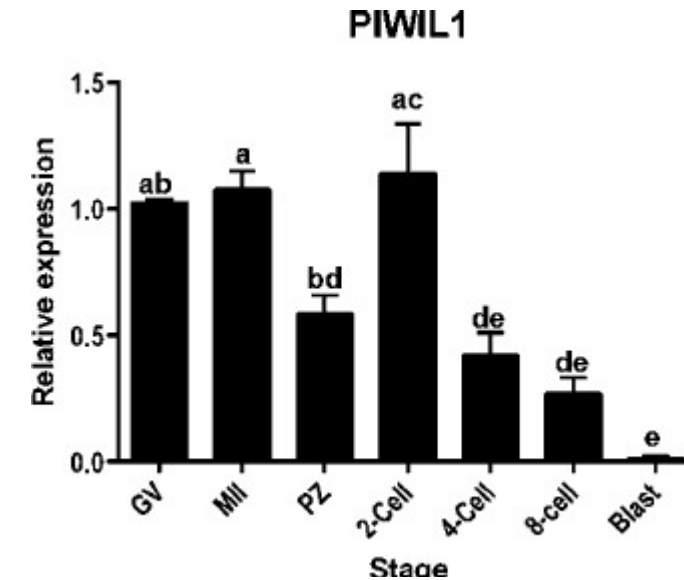
Results 3: First insight from GWAS

Manhattan plot of Number of Oocytes



Results 4: First insight from GWAS

- PPP6C (BTA11): Protein Phosphatase 6 Protects Prophase I-Arrested Oocytes by Safeguarding Genomic Integrity (Hu et al., 2016)
 - ANGPTL2 (BTA11): Aberrant expression of angiopoietin-like proteins 1 and 2 in cumulus cells is potentially associated with impaired oocyte developmental competence in polycystic ovary syndrome (Liu et al., 2016)
 - ADGRD1 (BTA17): Control of oviductal fluid flow by the G-protein coupled receptor *Adgrd1* is essential for murine embryo transit (Bianchi et al., 2021)
 - PIWIL1 (BTA17): Production of functional oocytes requires maternally expressed PIWI genes and piRNAs in golden hamsters (Hasuwa et al., 2021)
- ➔ Additional data, models adaptation and sequence data will help to refine genetic architecture behind these QTL



PIWIL1 expression during oocyte maturation and embryogenesis. (Russel et al., 2016)

Conclusion and perspectives

- **A First promising work on OPU/IVF**
 - Simpler traits (Number of oocyte) already offer interesting results
 - Continuous data collection will improve our understanding of key gene in the OPU/IVF production by use of finer model
 - In house gEBV are already available for some first test
- **2 QTL found on BTA17 and BTA11**
 - Literature review identify candidate gene
 - Additional investigations will allow to refine the list of candidate gene



The Perfect Fit

SYNETICS

