Early Detection of Chromosomal Abnormalities in Cattle using SNP beadchip intensity data

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INTRODUCTION

Objective: Identify chromosomal abnormalities in *in vitro* embryos (IVP) and calves for herd renewal

How: Develop a detection process using genotyping array intensity data from animals routinely genotyped for genomic selection

Interest: Prevent genetic defects, improve fertility, and minimize economic losses and unproductive periods

Provides early diagnosis for improved herd management

MATERIAL

Analysis on B Allele Frequency and Log R Ratio from genotyping array intensity signals

Two datasets :

- 505 embryos genotyped with CR > 0.8
- 238 individuals carrying partial aneuploidy *(Jourdain et al. 2023)*

Translocation	Regions of interest	Dataset
t(24;29)	24:58,418,701-end	87 monosomy, 78 control
t(24;29)	29:start-3,257,559	87 monosomy, 78 control
inv ins (8;4)	4:65,642,811-76,557,774	1 monosomy, 16 trisomy

METHODS, RESULTS AND DISCUSSION

Identification of aneuploidy on IVP embryo

Filters :

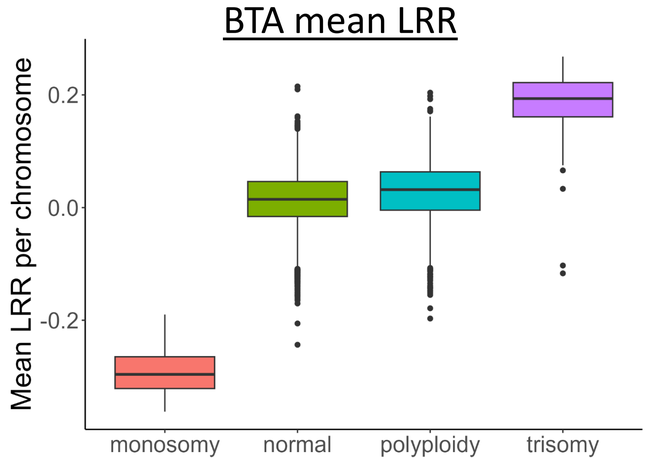
Able to compare with a visual characterization

Embryo with CR > 0.8 and sdLRR < 0.40

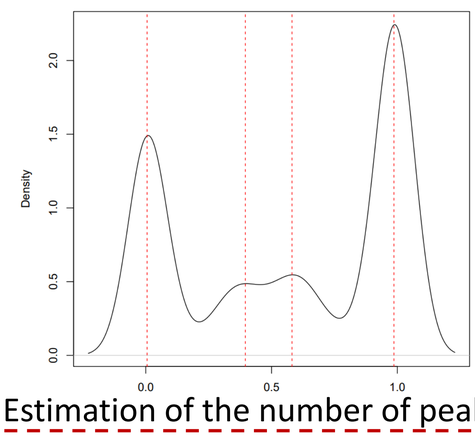
n = 14627 (embryo x BTA)

Percentage of heterozygosity → Haploids n=3

BTA mean LRR



BAF distribution



→ Estimation of the number of peaks

		Prediction			
		normal	haploidy	monosomy	polyploidy / trisomy
Reference	normal	13160	0	0	34
	haploidy	0	87	0	0
	monosomy	3	0	78	0
	polyploidy	86	0	0	1179

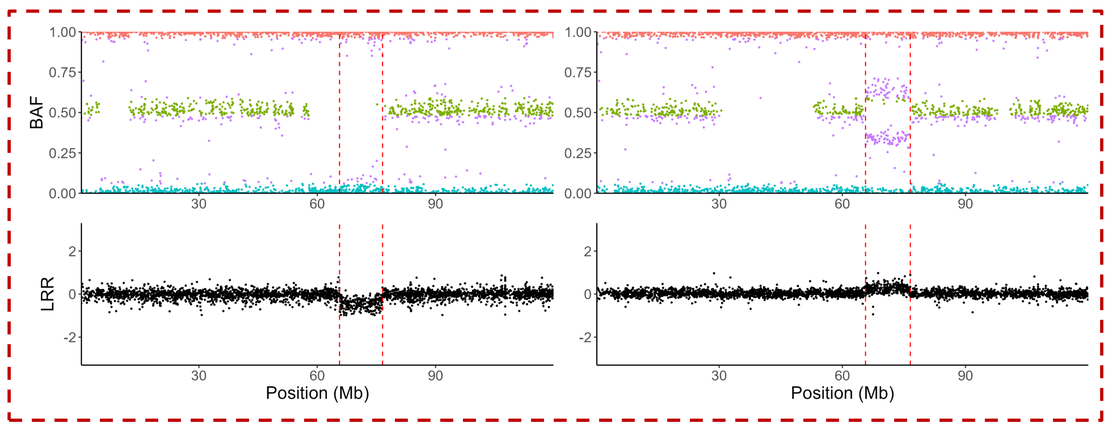
Although the status of each chromosome may be inaccurate for a polyploid embryo, aneuploidy would still be detected at embryo level

99% of embryos correctly assigned

Incoherence between the visual assessment and the prediction principally occurred in cases of an unclear LRR-BAF profile

What's next ? **Morphological analyses** to clarify these profiles

Identification of partial aneuploidy on known cases



Example: BTA4 of two individuals with monosomy and trisomy for translocation inv ins (8;4)

Calculation of a local mean of LRR and comparison with a control region & Distribution of BAF

Transloc.	Bta	Number of markers	
		Region	Control
t(24;29)	24	155	1909
t(24;29)	29	104	1886
inv ins (8;4)	4	498	3498

100 % concordance

Detection of already known partial aneuploidy.

AND

Detection of **new deletions** that have yet to be characterized

What's next ?

Implementation of a **weekly status calculations** for carriers in all animals genotyped for genomic selection

CONCLUSION

- Log R Ratio and B Allele Frequency can easily be used to calculate status for deletion (>1Mb)
- LRR and BAF can efficiently be used to discriminate embryo with genomic abnormalities even with low CR (0.8 – 0.95)
- A pipeline is currently being developed to calculate the status of known deletions for animals that are genotyped for French genomic evaluation

ELIANCE Des éleveurs. Une ambition. UMT eBIS INRAE la science pour la vie, l'humain, la terre

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