French experience with recognition of laboratories providing genotypes to the official genomic evaluation of dairy cattle

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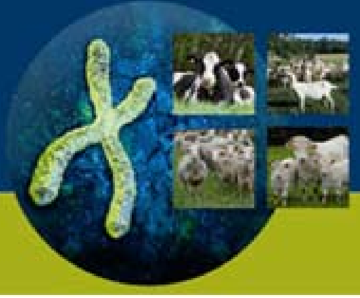
Introduction: context (1/2)

- ISAG
- ICAR
- Interbull
- ….

Guidelines to improve the quality of data and methods used for genetic evaluations



Introduction: context (2/2)

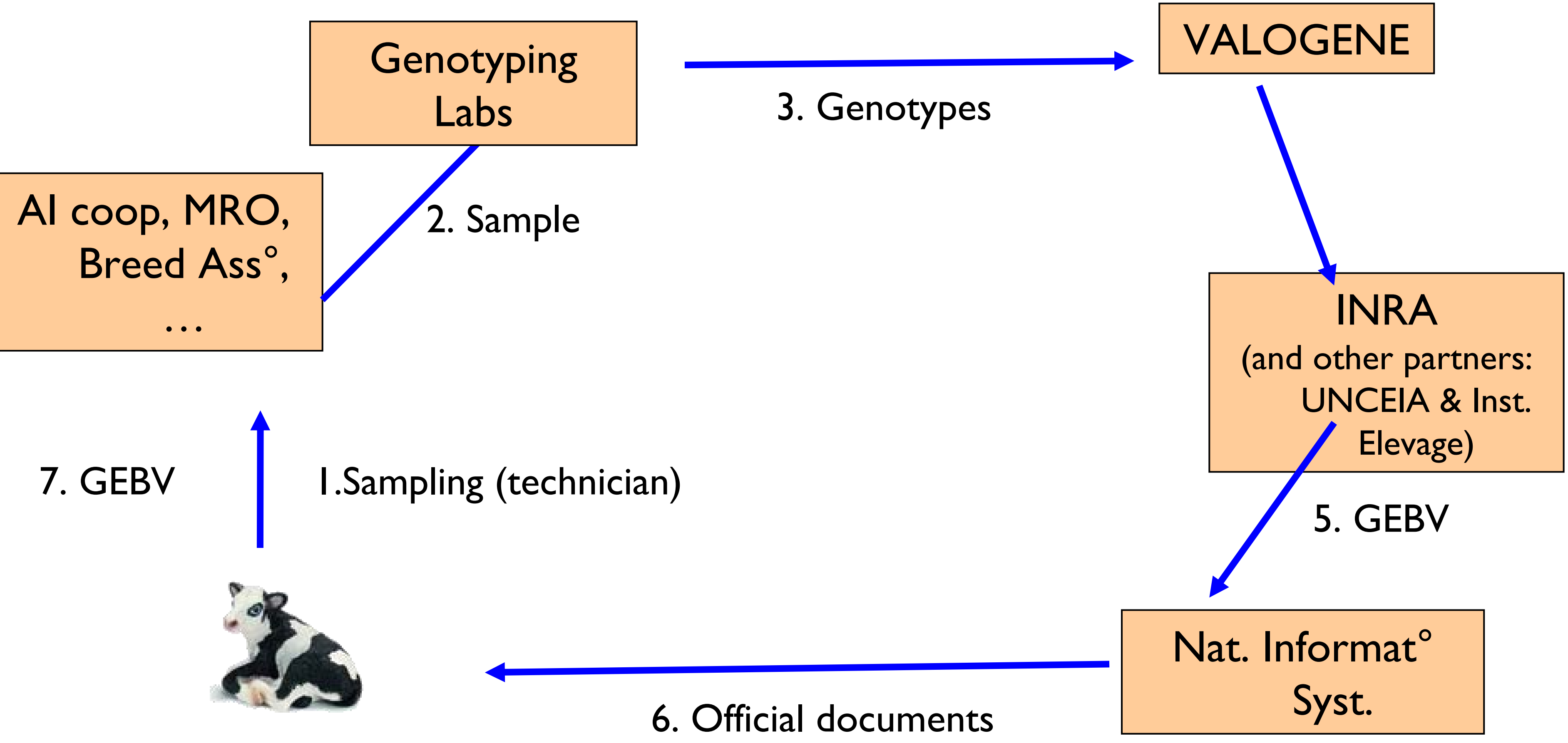
- Now: genetic evaluations enhanced with genomic data
- => raises the same questions!
- Data must be:
  - of high quality level,
  - obtained with standardized procedures,
  - normalized nomenclature.
- Genotypes have often a higher weight than own performances…
- BUT: no international recommendation developed!

⇨ *France has developed its own quality system (procedure included in the Quality Management System of France Genetique Elevage)*

French genomic evaluations: historical context

- 2001:
  - MAS research program (INRA, UNCEIA, LABOGENA); microsatellites
- 2008:
  - Illumina 50k beadchip
- 2009:
  - Publication of GEBVs for bulls
  - Eurogenomics
- 2010:
  - VALOGENE (management of genotyping process, from farm to INRA)
  - New genotyping laboratories (6 labs presently) => need for harmonized procedures!
- 2011:
  - Genomic evaluations available for farmers (females)

Main players



Genotyping Labs

3. Genotypes

VALOGENE

AI coop, MRO, Breed Ass°, …

2. Sample

INRA (and other partners: UNCEIA & Inst. Elevage)

7. GEBV

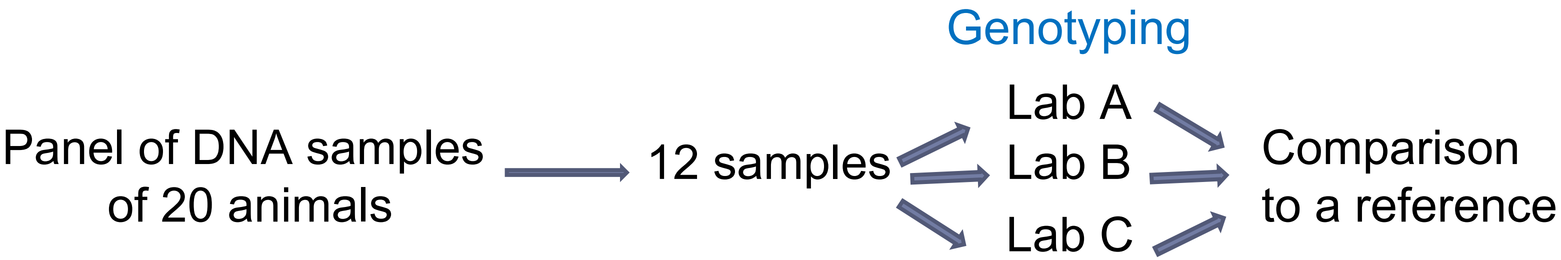
1.Sampling (technician)

5. GEBV

Nat. Informat° Syst.

6. Official documents

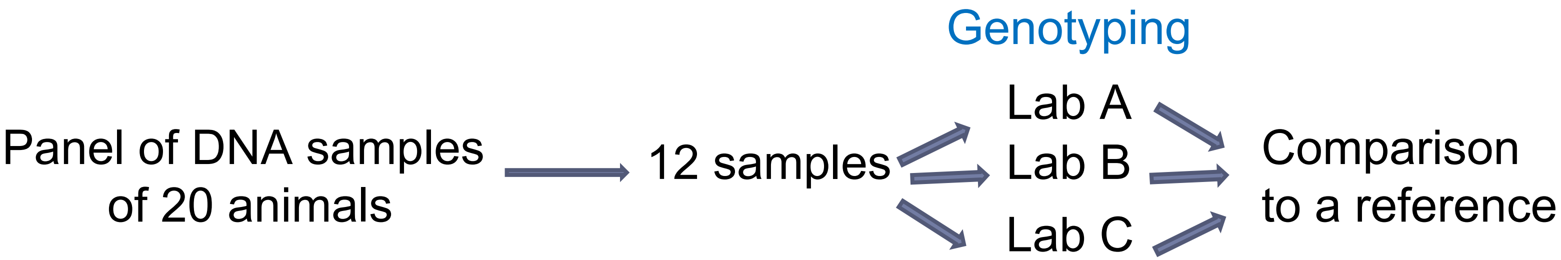
Organization of the ring tests



Genotyping

Panel of DNA samples of 20 animals → 12 samples → Lab A, Lab B, Lab C → Comparison to a reference

Organization of the ring tests



Genotyping

Panel of DNA samples of 20 animals → 12 samples → Lab A, Lab B, Lab C → Comparison to a reference

A new laboratory :
- must sign an agreement with Valogene
- pass the test before sending 1st data for genomic evaluations

3 possible dates each year to participate to a ring test

Organization of the ring tests

Genotyping

Panel of DNA samples
of 20 animals

12 samples

Lab A
Lab B
Lab C

Comparison
to a reference

A new laboratory :
- must sign an agreement with Valogene
- pass the test before sending 1st data for genomic evaluations

3 possible dates each year to participate to a ring test

3 files requested:
- Genotypes (TOP ACGT format)
- Call Rate (% of analyzed SNP)
- Cross reference table sample x animal

Reference genotypes

- Defined by LABOGENA
  - ISAG member, French reference laboratory for parentage analyses & identification
  - Historical partner in the MAS research program
- Criteria
  - Broad range of breeds => maximise the nb of observed alleles:
    - Males, females
    - Dairy, beef, exotic, crossbred animals
  - High DNA quality
  - Genotyped twice for very high confidence in reference genotypes
  - These 20 samples are considered now as control to validate new chips or new SNP technologies

Criteria

1: File name and format ok?

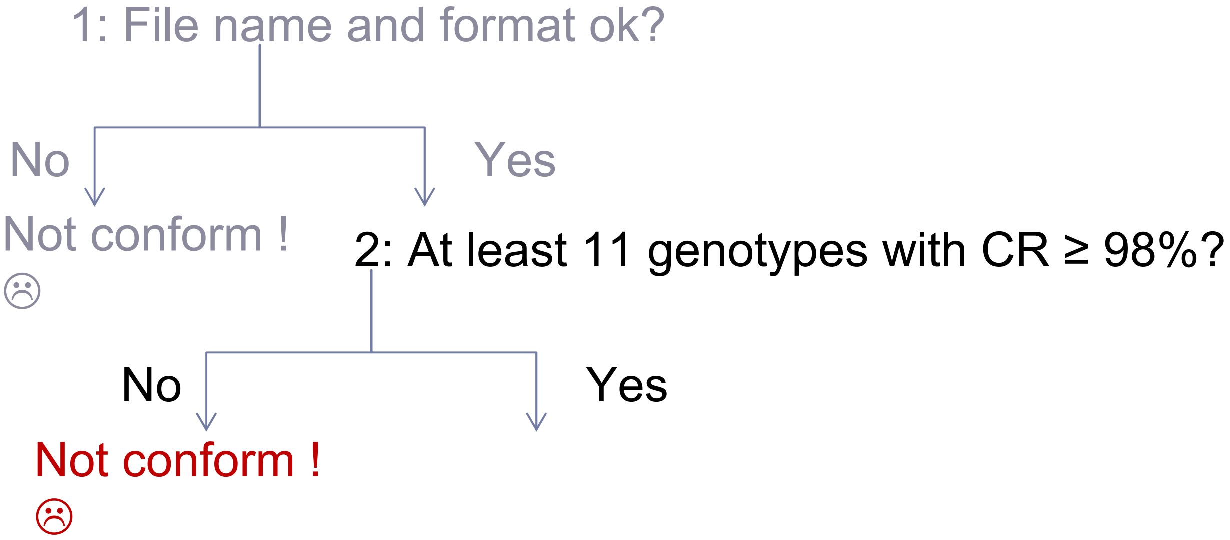
No

Not conform !

☹

Yes

Criteria



1: File name and format ok?

No

Yes

Not conform !

☹

2: At least 11 genotypes with CR ≥ 98%?

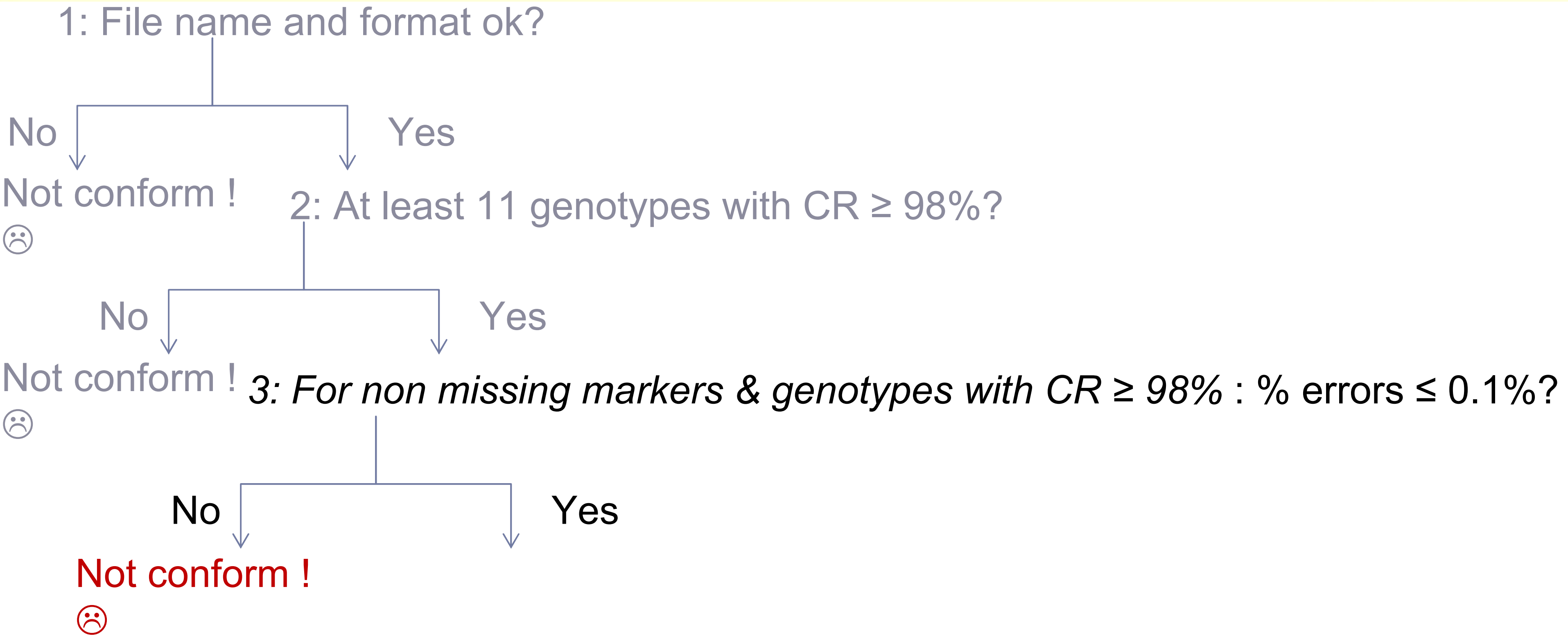
No

Yes

Not conform !

☹

Criteria



1: File name and format ok?

No

Not conform ! ☹

Yes

2: At least 11 genotypes with CR ≥ 98%?

No

Not conform ! ☹

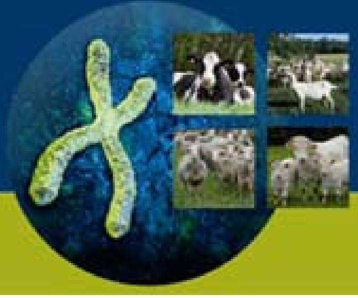
Yes

3: For non missing markers & genotypes with CR ≥ 98% : % errors ≤ 0.1%?

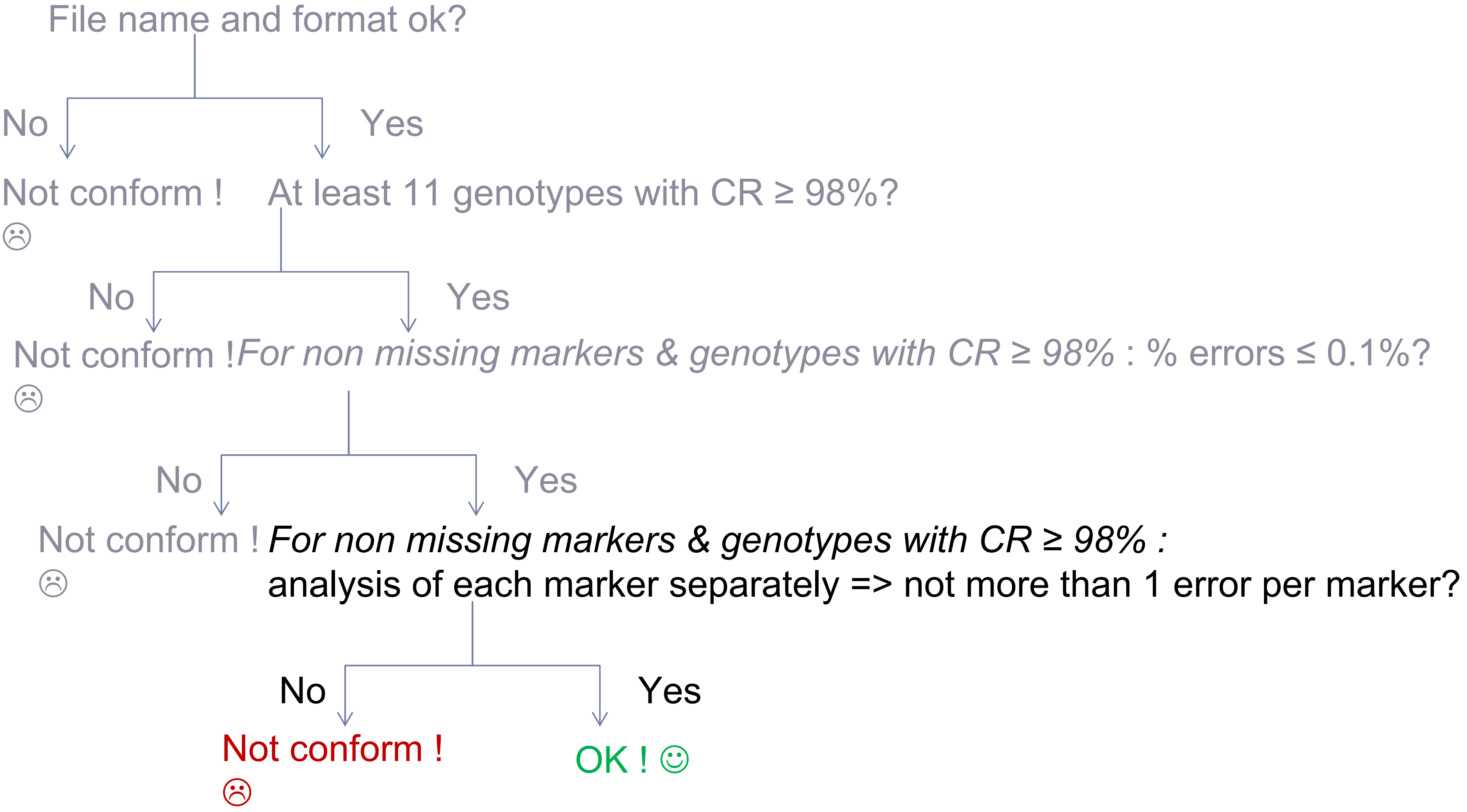
No

Not conform ! ☹

Yes



Criteria



File name and format ok?

No

Not conform ! ☹

Yes

At least 11 genotypes with CR ≥ 98%?

No

Not conform ! ☹

Yes

For non missing markers & genotypes with CR ≥ 98% : % errors ≤ 0.1%?

No

Not conform ! ☹

Yes

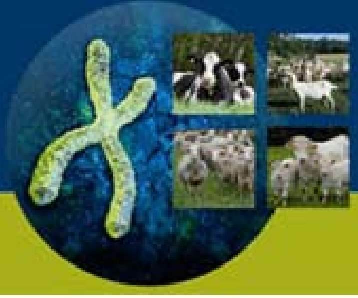
For non missing markers & genotypes with CR ≥ 98% :
analysis of each marker separately => not more than 1 error per marker?

No

Not conform ! ☹

Yes

OK ! ☺

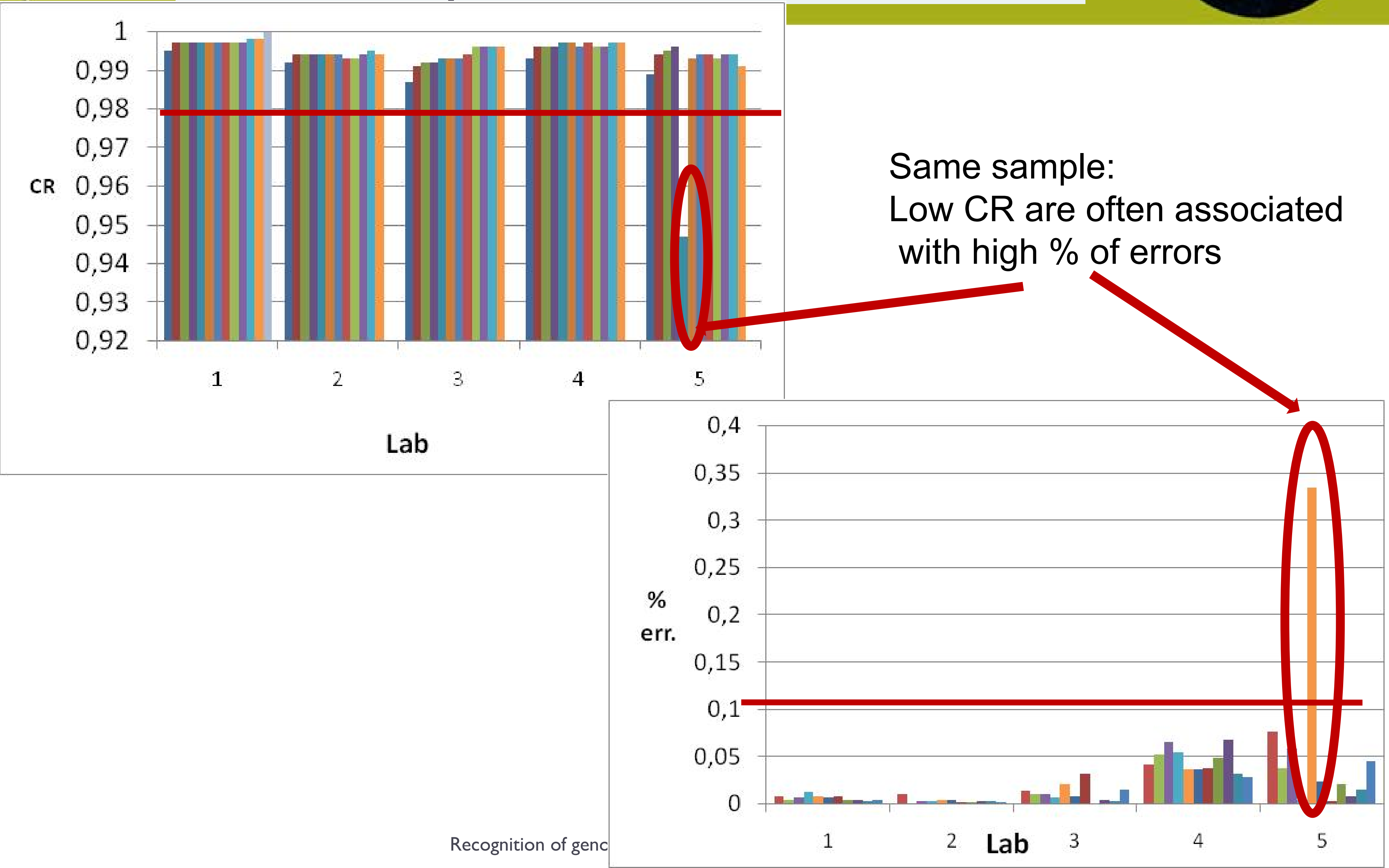


First results

- None of the 5 labs succeeded at the 1st trial !

Lack of respect of the rule	# Laboratories	Comments
Format/Name of files	4	Pb of names, incorrect separator; Top ACGT format always respected
Call Rate of samples	1	3 samples with CR <98%
More than 0.1% discrepancy	1	Incorrect clustering

Results of the successful tests compared to reference



Same sample:
Low CR are often associated
with high % of errors

Since the ring test…

- 12 genomic evaluations, 6 labs, 160 files, more than 100 000 genotypes
  - # times with 1 wrong file format: 4
  - # files with incorrect identifiers: 1
  - Less than 0,2% of genotypes excluded because of low Call Rate (CR≤95%)

Exchanges within Eurogenomics

- **Countries:** Nordic countries (DFS); France; Germany; The Netherlands; (Spain since 2011)
- **Objective:** increase the reference population of each participating country
- **Quality control checks:**
  - % Call Rate
  - Respect of allele definition (Top ACGT format)
  - Rates for all individuals genotyped several times
  - Mendelian consistency for parent-progeny pairs
  - No control of file format (files sent once)

Conclusion

- Quality of procedures used by Genotyping laboratories should (and can) be controlled, for each type of chip separately (ex LD vs 50 k)

- ISAG and ICAR could play a major role :
  - A system of laboratory recognition could be defined, using procedures similar to those implemented for parentage verifications.
  - A laboratory licenced by ICAR could send the genotypes worldwide.

- Exchanges of genotypes ↗, nb of different chips ↗: the nomenclature used to exchange genotypes will be an issue!
  - ICAR and ISAG could provide recommendations, based on objective requirements (size of the transmitted file, easy to use and to check…)

Thank you very much!