Agricultural Institute of Slovenia

PARENTAGE VERIFICATION USING IMPUTED MICROSATELLITE AND SNP DATA IN SLOVENIAN BROWN SWISS POPULATION

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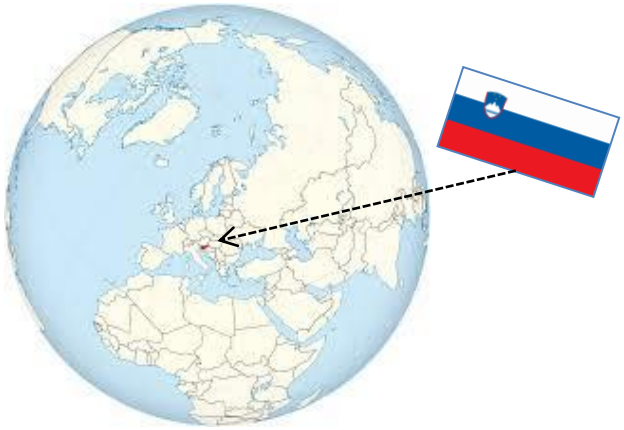
Outline - Slovenian case



- parentage verification
- recording scheme
- genomic selection
- imputation of MS from SNP in BSW
- parentage testing with imputed MS
- parentage testing with SNP markers

Parentage verification in Slovenia

- **base** - zootecnical data (documentation) and exterier of animals
  - all new born animals in recording scheme
- **supplementary** - using 12 ISAG microsatellite markers (MS)
  - all 'candidate' male calves
  - animals in progeny test stations (beef)
  - breeding material (i.e. semen, embryos and ovary cells)
  - random supervision of base parentage recording
    - No ♀ ≅ 1% of newborn calves in recorded herds

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Dairy recording scheme in Slovenia

82,000 cows
in recording scheme

11% Brown Swiss

36% Holstein

39% Simmental

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Genomic selection in Slovenia

- in Brown Swiss (BSW) started with participation in project interGenomics
- SNP data for some BSW breeding animals
  - breeding bulls
  - candidate male calves
  - some other breeding animals
    - app. 200 animals/year

82,000 cows
in recording sheme

11% Brown Swiss

36% Holstein

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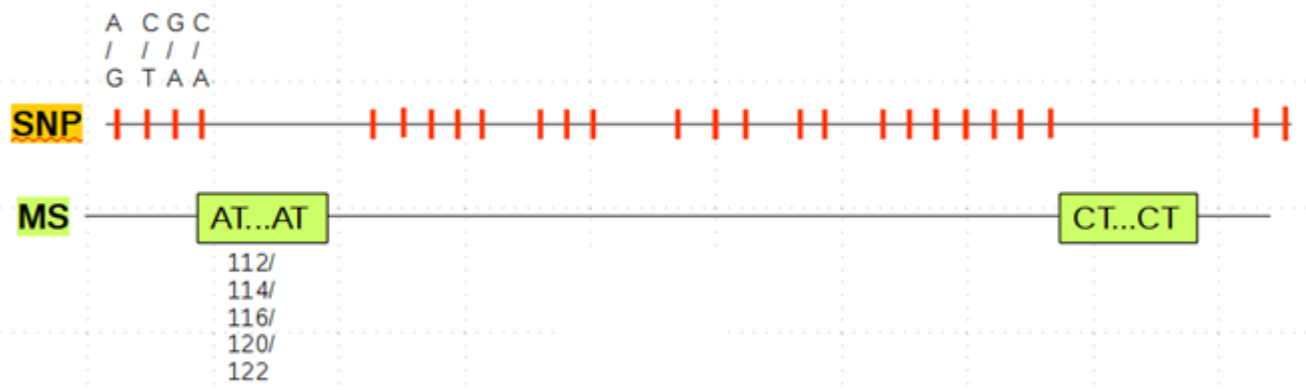
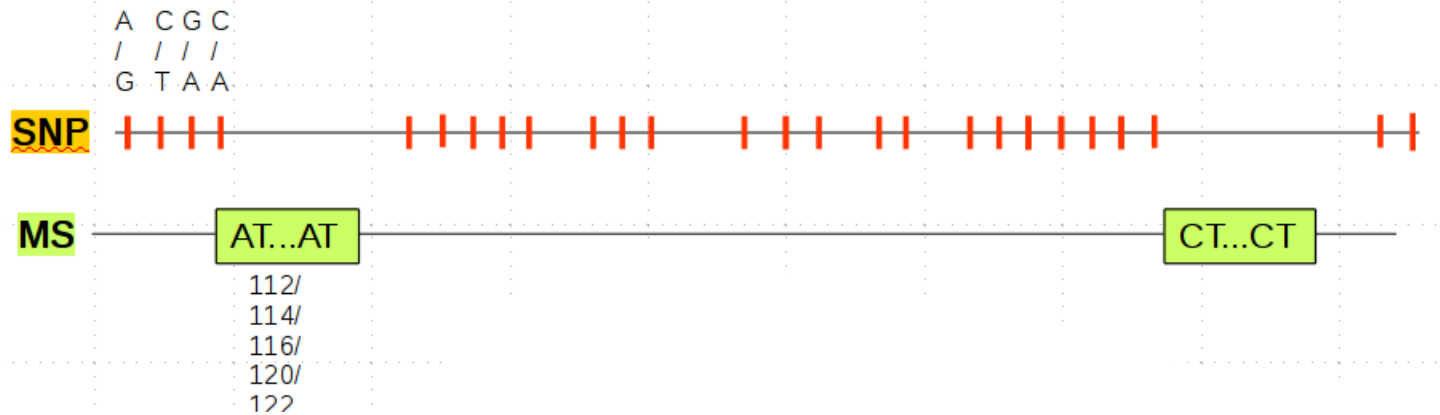
MS/SNP data

- discordance between genotypic data for different animals (MS/SNP)
- not suitable for parentage verification



MS/SNP data

- avoid re-genotyping SNP-genotyped animals for MS-genotypes
- imputation of MS from SNP data implemented



Imputation of MS from SNP

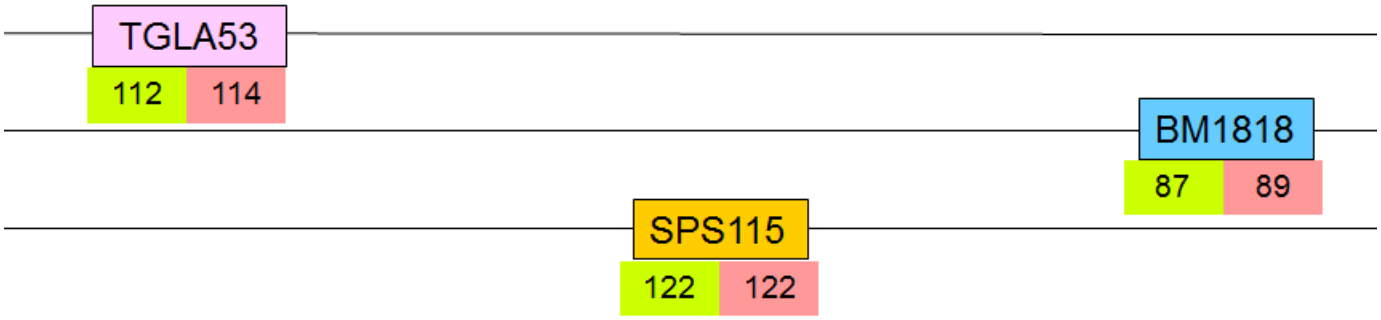
- animals SNP-genotyped on different chips
  - not all containing minimum set of 880 SNPs required
- SNP-genotypes first imputed onto the chip with max no. required SNPs (*FIMPUTE)*
- subsequently MS imputed (*BEAGLE 3.3.2*)

CHIP	#SNPs
GGPv02	607
GGPv03	682
GGPv04	**878**
HD	751
HDv02	840
Ill 50Kv01	57
Ill50Kv02	56

Imputation of MS from SNP results

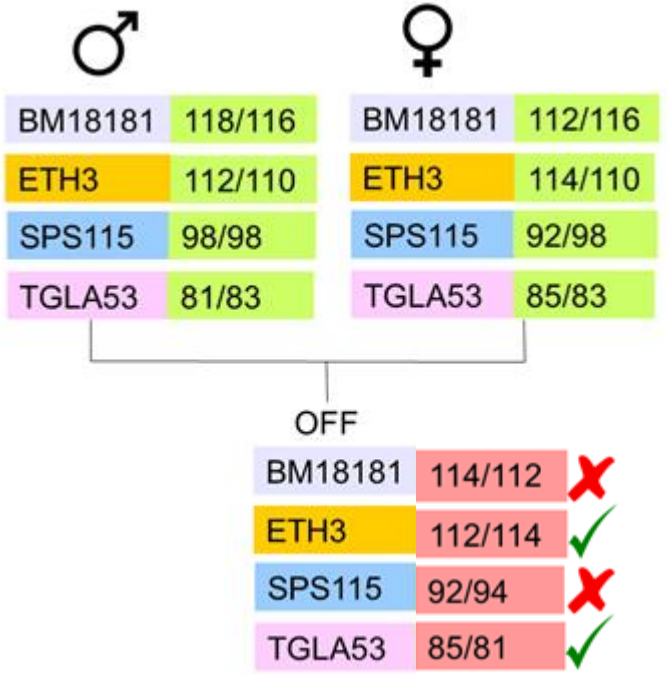
- 91.7% overall MS imputation accuracy
- 4 MS accuracy < 90%

  (ETH10, ETH3, TGL53, BM1818)



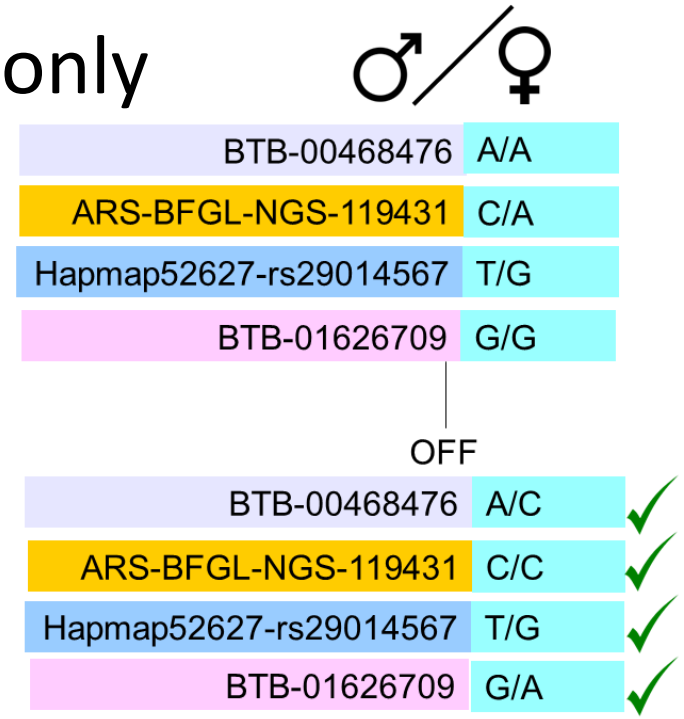
Parentage testing with imputed MS

- offspring‘s (OFF) parentage already confirmed based on genotyped MS
- 65 cases
  - 15.4% (10) 0 mismatches
    → confirmed
  - 44.6% (29) 1 mismatch
    → confirmed
  - 40.0% (26) ≥ 2 mismatches
    → rejected



Parentage testing using SNP markers

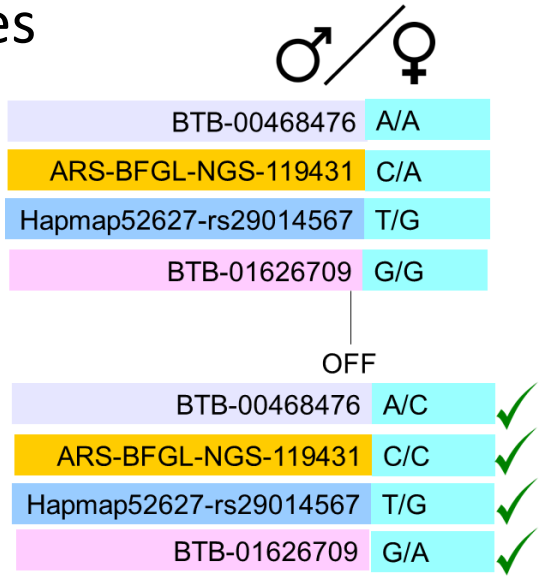
- verification as proposed by McClure (2015)
- 800 SNPs used
- verification of one parent only
  - 1% genotype mismatches allowed



Parentage testing using SNP markers

- 43 cases of one parent testing
  - 90,7% (39) 0 genotype mismatches → confirmed
  - 9.3% (4) 1 genotype mismatch → confirmed
    - verification of all tested parentages
- replacing the parent with a half-sibling or grand-parent
  - >25 genotype mismatches

    → rejected



Conclusion

- MS imputation needs additional optimization to reach required accuracies
  - possibly by using a haplotype reference
    consisting of animals
    that are genetically more similar
    to the studied BSW population
- verification using SNPs has proven as a reliable tool for routine use

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Thank you for your attention!

♂	♀
BTB-00468476	A/A
ARS-BFGL-NGS-119431	C/A
Hapmap52627-rs29014567	T/G
BTB-01626709	G/G

OFF

BTB-00468476	A/C	✓
ARS-BFGL-NGS-119431	C/C	✓
Hapmap52627-rs29014567	T/G	✓
BTB-01626709	G/A	✓