LIÈGE université
Gembloux
Agro-Bio Tech

**Using milk MIR spectra
to identify candidate genes associated
with climate-smart traits in cattle**

**H. HAMMAMI, R.R. MOTA,S. VANDERICK, S. NADERI,
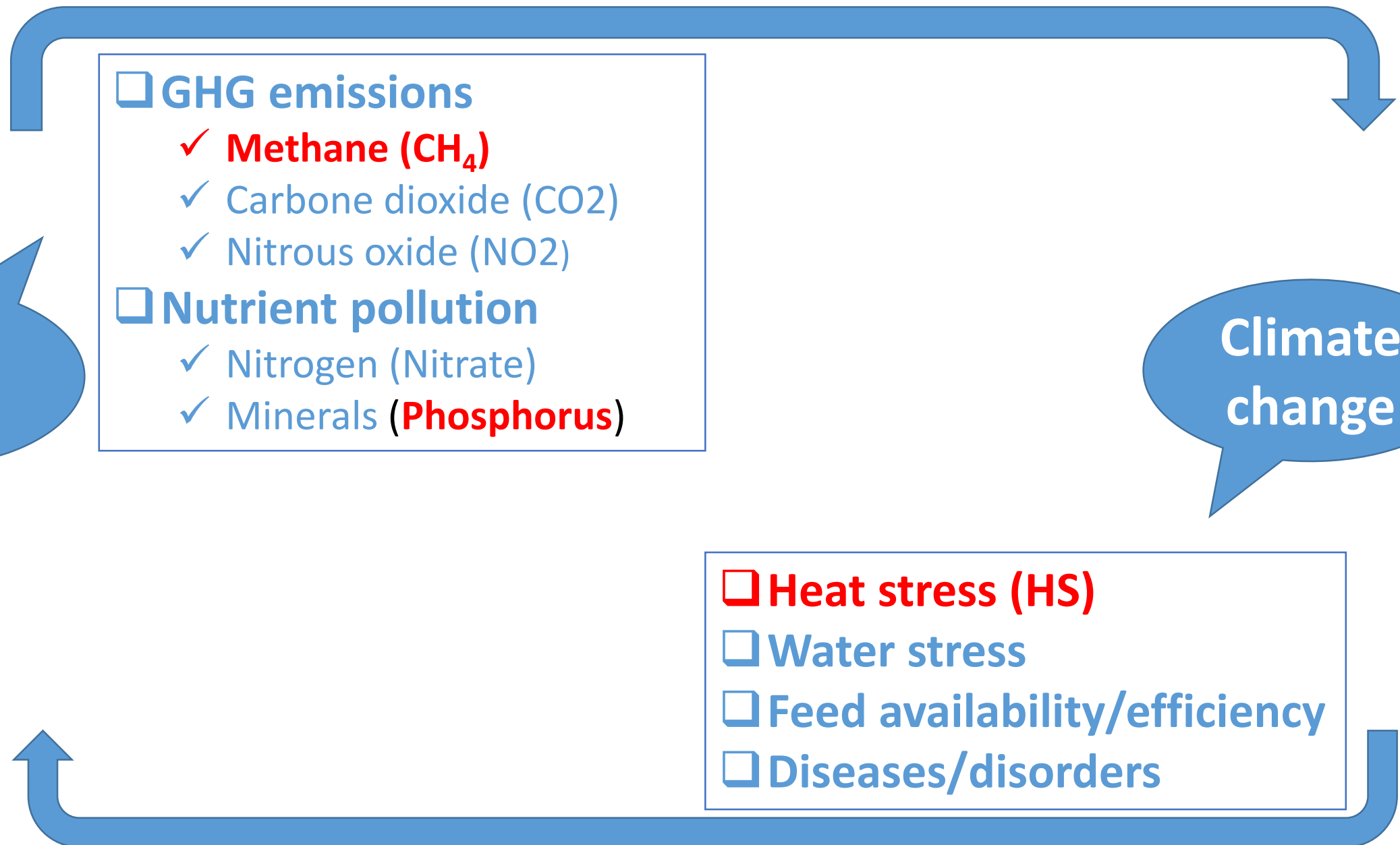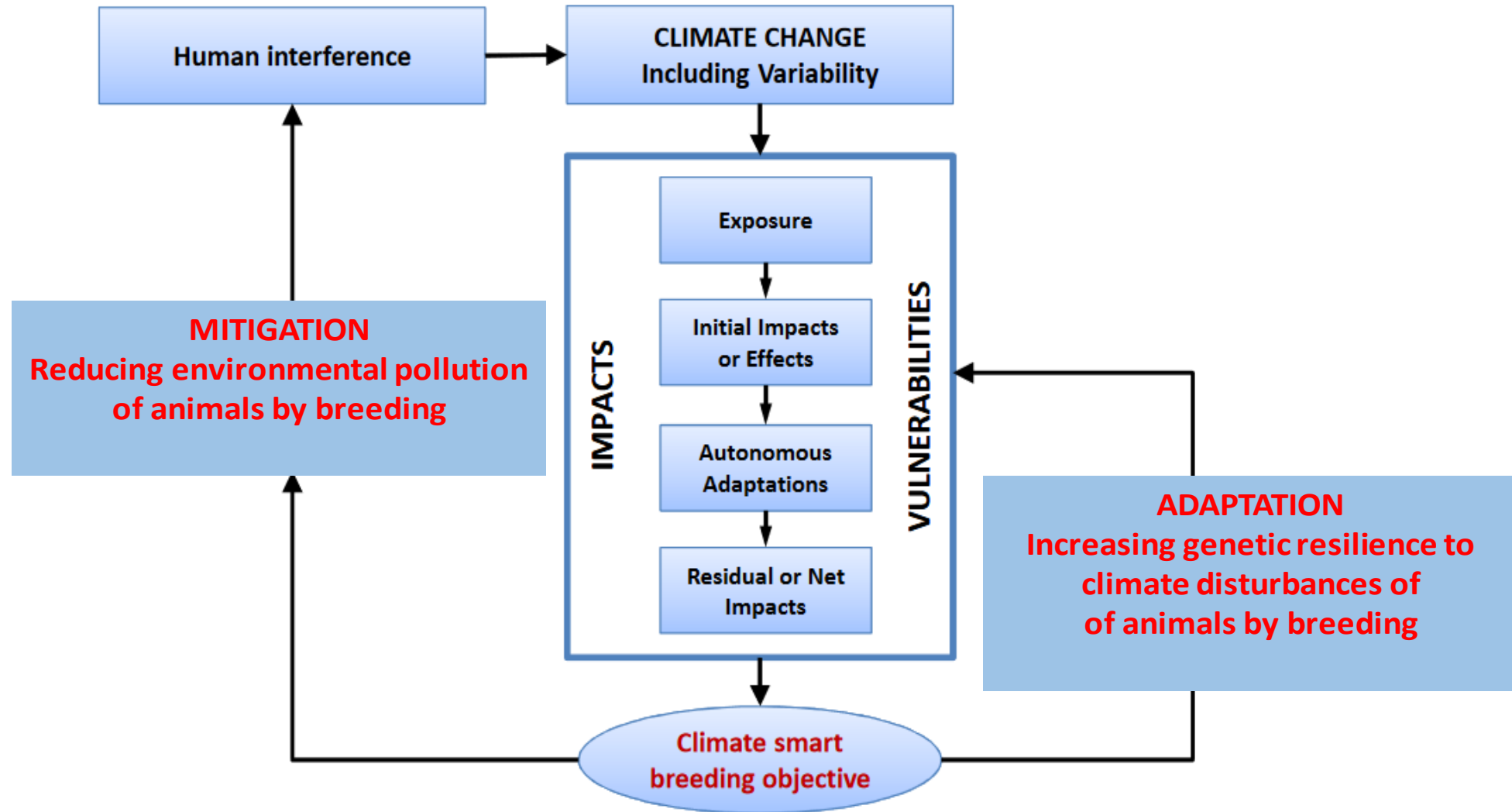C. BASTIN, N. GENGLER & GPLUSE CONSORTIUM**

CONTEXTE

Dairy cows

☐ **GHG emissions**
- ✓ **Methane (CH_4)**
- ✓ Carbone dioxide (CO2)
- ✓ Nitrous oxide (NO2)

☐ **Nutrient pollution**
- ✓ Nitrogen (Nitrate)
- ✓ Minerals (**Phosphorus**)

Climate change

☐ **Heat stress (HS)**
☐ **Water stress**
☐ **Feed availability/efficiency**
☐ **Diseases/disorders**

CLIMATE-SMART BREEDING

Human interference → CLIMATE CHANGE Including Variability

MITIGATION
Reducing environmental pollution of animals by breeding

IMPACTS — VULNERABILITIES

Exposure → Initial Impacts or Effects → Autonomous Adaptations → Residual or Net Impacts

ADAPTATION
Increasing genetic resilience to climate disturbances of of animals by breeding

Climate smart breeding objective

Modified from IPCC TAR 2001 WG2 after Smit *et al.*, 1999 (Mitigation and Adaptation Strategies for Global Change 4: 199-213)

N. Gengler , ASGN Workshop @ WCGALP 2014

MITIGATION & RESILIENCE TRAITS

❑ Gaps to record individual, direct and large-scale phenotyping

❑ Limited knowledge about the biological basis

❑ Milk Mid-Infrared (MIR) spectroscopy promising tool for such difficult-to expensive- traits

  ✓ Individual and large scale measurements

  ✓ Cost effective, rapid, robust and reliable

❑ Linking the milk phenome with the genome can help to underpin and elucidate the biological basis of such traits

MILK MIR-BASED PHENOTYPES

☐ **MITIGATION**

 ✓ **CH4**

 ✓ **Phosphorus**

Milk mid-infrared spectra enable prediction of lactation-stage-dependent methane emissions of dairy cattle within routine population-scale milk recording schemes

Amélie Vanlierde[A,*], Marie-Laure Vanrobays[B,G,*], Nicolas Gengler[B], Pierre Dardenne[A], Eric Froidmont[C], Hélène Soyeurt[B], Sinead McParland[D], Eva Lewis[D], Matthew H. Deighton[D,E], Michaël Mathot[F] and Frédéric Dehareng[A]
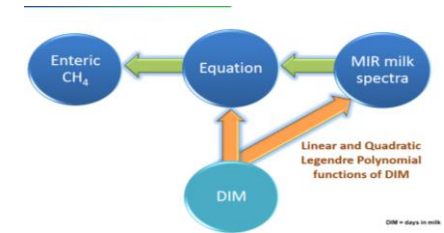
Potential estimation of major mineral contents in cow milk using mid-infrared spectrometry

H. Soyeurt,[*1] D. Bruwier,[*] J.-M. Romnee,[†] N. Gengler,[*‡] C. Bertozzi,[§] D. Veselko,[#] and P. Dardenne[†]

☐ **RESILIENCE TO HS**

 ✓ Key Milk MIR-based biomarkers changes as reacting to THI
 (Milk, C18:1cis9, LCFA, Acetone, BHB, and Citrates)

Genetic analysis of heat stress effects on yield traits, udder health, and fatty acids of Walloon Holstein cows

H. Hammami,[*†1] J. Vandenplas,[*†] M.-L. Vanrobays,[*] B. Rekik,[‡] C. Bastin,[*] and N. Gengler[*]

GE Genotype plus Environment
Integration for a more sustainable dairy production system

Gembloux Agro-Bio Tech
Université de Liège

Assessing fertility and welfare of dairy cows through novel mid-infrared milk-based biomarkers

H. Hammami, A. Lainé, F.G. Colinet, N. Gengler

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40th Biannual Session of ICAR, Puerto Varas Chile, 24 - 28 Oct 2016

SCIENTIFIC REPORTS

OPEN **Integrated Metabolomics Study of the Milk of Heat-stressed Lactating Dairy Cows**

He Tian[1,*], Nan Zheng[1,*], Weiyu Wang[2,*], Jianbo Cheng[3], Songli Li[1], Yangdong Zhang[1] & Jiaqi Wang[1]

Materials & Methods: Mitigation

Data

First lactation test-day records (**awé data**)   *61,174* *TD*
- MIR predicted CH4 and Phosphorus   *7,830*   Cows
- Pedigree   *24,489* Animals
- Genotypes (**50 k, cows & sires**)   4,221   Animals
                                                                              32,687 SNP's

Models

- ssGBlup Random Regression Test day models
  - GEBV's for early, middle, and late lactation stage
- Estimation of SNP effects & proportion of variation explained by 20 adjacent SNP windows

PostGWAS

- Significant SNPs related to each trait at early, middle, and late stage
- Annotated list of genes related to each trait / lactation stage (from NCBI & Mesh)

Resilience to HS

Data

- Third lactation test-day records Milk yield
  - Milk, C181cis9 , LCFA, Acetone, BHB, and Citrates
  - Temperature-Humidity Index (THI) associated to TD
  - Pedigree
  - Genotypes (**50 k, cows & sires**)

53,981 *TD*
5,893 Cows

16,627 Animals
3,443 Animals
32,687 SNP's

Models

- ssGBlup reaction norm models (**_Intercept_**: Level of the trait independent of THI; **_Slope_**: individual reaction to THI trajectory)
- Estimation of SNP effects & proportion of variation explained by 20 adjacent SNP windows
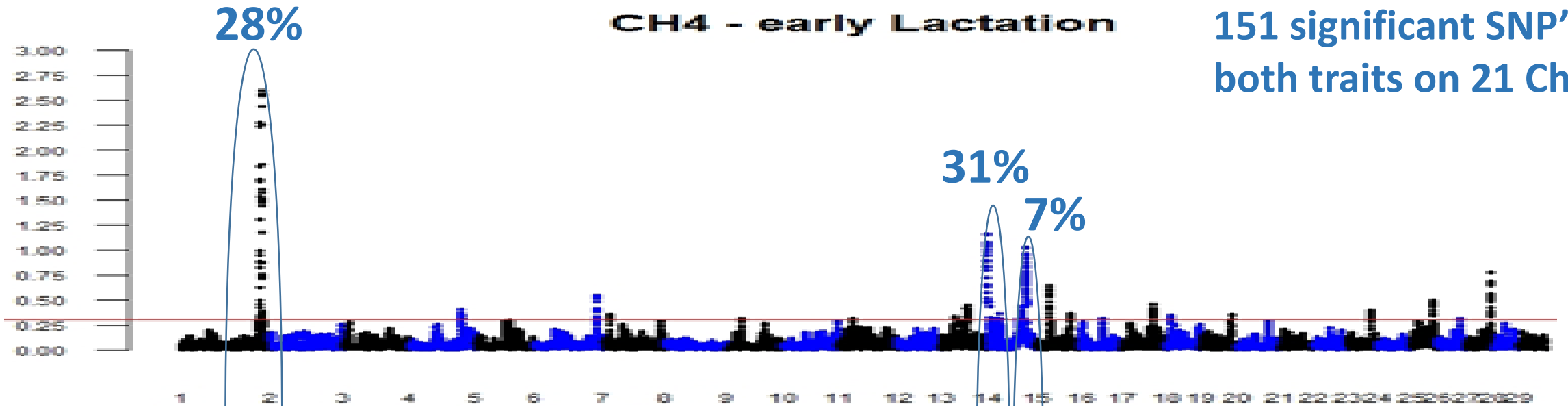
PostGWAS

- Significant SNPs related to each trait at early, middle, and late stage
- Annotated list of genes related to each trait / slope & intercept (from NCBI & Mesh)
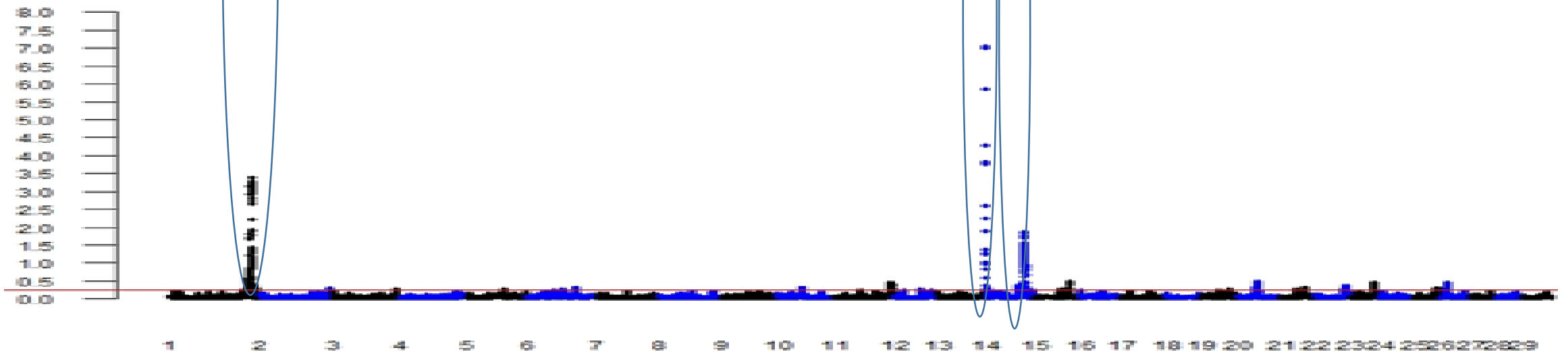
SNP WINDOWS: Mitigation

151 significant SNP's for both traits on 21 Chromo.

GENE MAPPING: Mitigation

❏ Top 20 regions explaining the highest proportion of the additive variance of CH4 and P traits

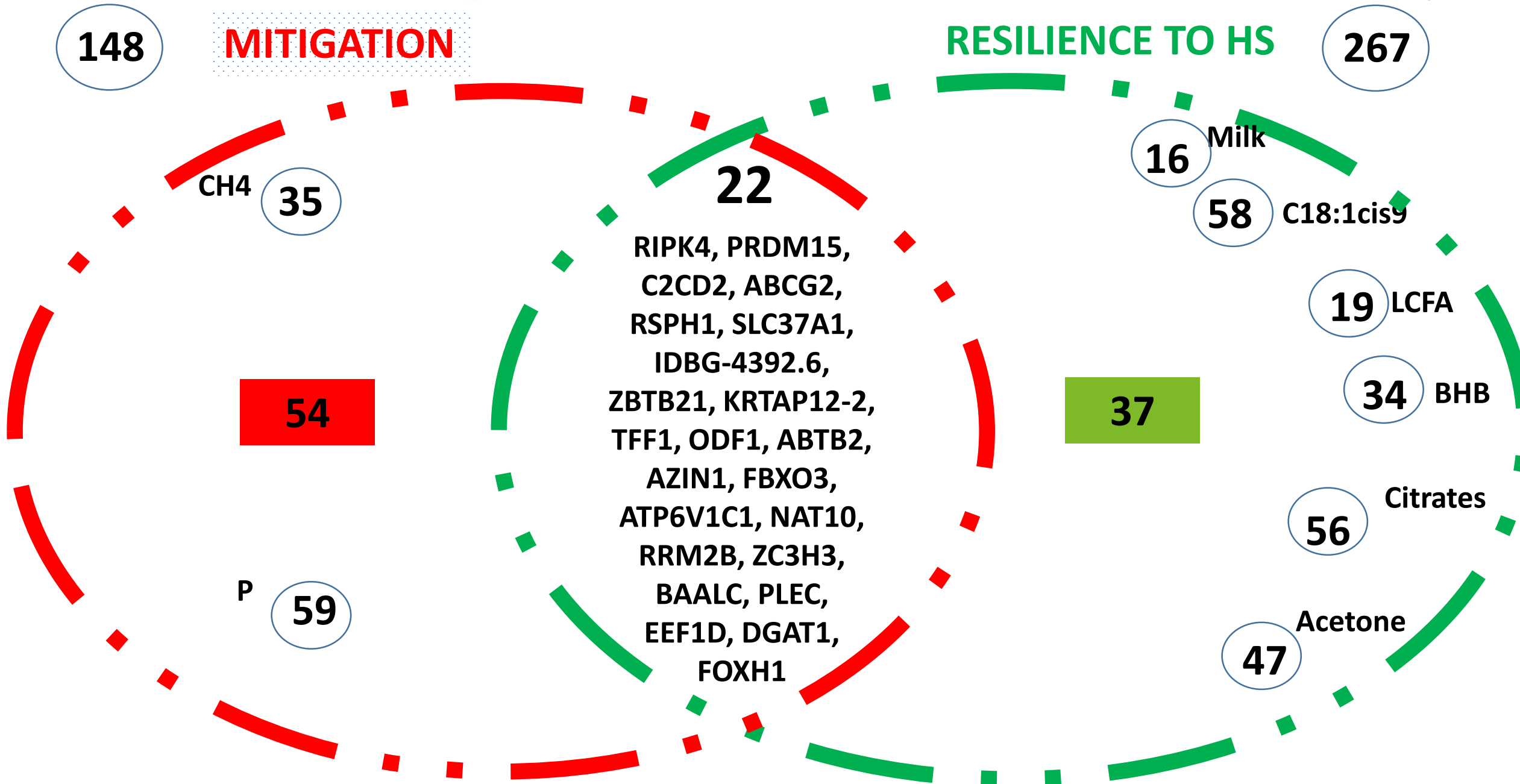| TRAIT(S)	Nbr of SNP's	CHROMOSOME	GENES
Common to CH4 & P	13	1	*RIPK4*, *ZBTB21*, *PRDM15*, *C2CD2*, *KRTAP12-2*, *ABCG1*, *SLC37A1*, *UBASH3A*, *RSPH1*, *TFF1*, *FAM3B*
Common to CH4 & P	2	14	*DGAT1*, *CYHR1*, *PLEC*

✓ **RIPK4**: Associated with the lipid/oxo-acid metabolism in the rumen

✓ **ABCG1**: Cholesterol metabolism & hepatic regulation in dairy cows during transition and early lactation

✓ **PRDM15**: Overexpressed gene in human lymphomas

✓ **SLC37A1**: Gene involved in the homeostasis of blood glucose

Annotated gene list: Resilience to HS

Chromosome	Gene	Trait	Gene name
BTA14	DGAT1	Level (Milk, C18:1cis9, LCFA, BHB)	diacylglycerol O-acyltransferase 1 [Source:VGNC Symbol;Acc:VGNC:28020]
BTA14		Slope (Acetone, Citrates)	diacylglycerol O-acyltransferase 1 [Source:VGNC Symbol;Acc:VGNC:28020]
BTA14	HSF1	Level (Milk, C18:1cis9, LCFA, BHB)	heat shock transcription factor 1 [Source:VGNC Symbol;Acc:VGNC:29981]
BTA14		Level (Acetone, Citrates)	heat shock transcription factor 1 [Source:VGNC Symbol;Acc:VGNC:29981]
BTA14	MAPK15	Slope (Acetone) Level (BHB)	mitogen-activated protein kinase 15 [Source:VGNC Symbol;Acc:VGNC:31217]
BTA13	TOMM34	Slope (LCFA)	translocase of outer mitochondrial membrane 34 [Source:VGNC Symbol;Acc:VGNC:49135]
BTA20	DNAJC21	Slope (Acetone)	DnaJ heat shock protein family (Hsp40) member C21 [Source:NCBI gene;Acc:509302]
BTA13	DNAJC5	Slope (LCFA)	DnaJ heat shock protein family (Hsp40) member C5 [Source:NCBI gene;Acc:282216]
BTA26	HSPA12A	Slope (C18:1cis9)	heat shock protein family A (Hsp70) member 12A [Source:VGNC Symbol;Acc:VGNC:55956]
BTA12	HSPH1	Slope (Acetone)	heat shock protein family H (Hsp110) member 1 [Source:VGNC Symbol;Acc:VGNC:53817]
BTA13	OSER1	Slope (LCFA)	oxidative stress responsive serine rich 1 [Source:VGNC Symbol;Acc:VGNC:32469]
BTA19	ACOX1	Slope(C18:1cis9, LCFA, BHB)	acyl-CoA oxidase 1 [Source:VGNC Symbol;Acc:VGNC:25552]
BTA19	ACADVL	Slope (Citrates)	acyl-CoA dehydrogenase very long chain [Source:VGNC Symbol;Acc:VGNC:50246]

✓ Slope: Associated with the mechanism of heat tolerance and oxidative stress
✓ Level: genes affecting milk yield and composition

Annotated gene list: Climate-smart

148   MITIGATION   RESILIENCE TO HS   267

CH4   35   16 Milk

22   58 C18:1cis9

54   RIPK4, PRDM15, C2CD2, ABCG2, RSPH1, SLC37A1, IDBG-4392.6, ZBTB21, KRTAP12-2, TFF1, ODF1, ABTB2, AZIN1, FBXO3, ATP6V1C1, NAT10, RRM2B, ZC3H3, BAALC, PLEC, EEF1D, DGAT1, FOXH1   37   19 LCFA

34 BHB

Citrates

P   59   56

Acetone

47

TAKE HOME MESSAGES

❑ Integration of MIR and genomics can provide a powerful tool for climate-smart breeding programs

❑ Further investigation with high density SNP panel while considering the trade-off between mitigation and resilience is required

❑ Study of gene ontology and network analyses is needed

ACKNOWLEDGEMENTS
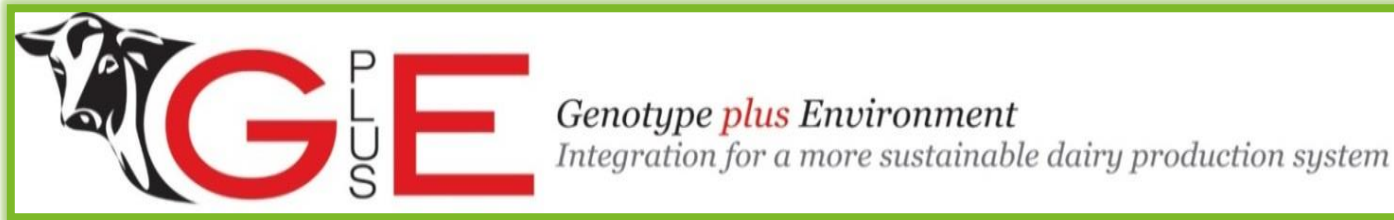
MIRHeatStress project

AGROMET project

THANK YOU!

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