Heritability of milk Fourier transform infrared spectra in sheep

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Introduction

The spectroscopic technique is based on the study of the interaction between matter and electromagnetic waves.

Based on the energy supplied and the amount absorbed by the irradiated sample it is possible to determine the chemical composition of the sample and related compounds.

Fourier Transform Mid Infrared (FT-MIR) spectroscopy is a particular technique relatively inexpensive, fast, non destructive and accurate

Introduction

Fourier Transform mid-infrared (FT-MIR) spectroscopy has commonly been used to estimate milk's macro and micro components for economic and selective purposes

- Quantification of fat, protein, and lactose
- Fine milk composition
  - Fatty acids (Soyeurt et al., 2006; De Marchi et al., 2014)
  - Minerals (Malacarne et al., 2018)
  - Milk proteins (Bonfatti et al., 2011; Rutten et al., 2011, Mota et al., 2023)

Introduction

FTIR spectroscopy has been used to develop equations for predicting other components, useful in themselves or as proxies for other traits of interest or to predict complex phenotypes or phenotypes that are not directly related to milk components

- Cheese-making properties (Penasa et al., 2015; Ferragina et al 2017 Stocco et al., 2021)
- Energy balance (McParland et al., 2011; McParland et al., 2015; Ho et al.,2020)
- Health status (Grelet et al.,2016; Walleser et al.,2023)
- Methane emission (Bittante & Cipolat-Gotet 2018; Vanlierde et al.,2018)
- Fertility or pregnancy (Toledo-Alvarado et al., 2018; Tiplady et al.,2022)

IR absorption in milk spectra at each wavenumber has also been considered as a trait in its own right and directly used for genetic parameters' estimation and association studies, especially in dairy cattle (Soyeurt et al., 2010; Bittante & Cecchinato, 2013; Wang et al., 2016, Wang & Bovenhuis 2018; Tiplady et al., 2021; Congiu et al., 2023).

AIM

To estimate heritability of individual spectral wavenumbers of sheep milk to identify those potentially useful for selection purposes

Materials & Methods

PERIOD: 2020-2023

ANIMALS : 1,288 Sarda ewes (1-5 years old) milked twice a day

MILK RECORDING : every 14 days

SAMPLES : 41,722 , collected at a.m. & p.m. milking

INSTRUMENT : MilkoScan FT+(Foss, Hillerød, Denmark)

PHENOTYPES: Absorbance at 1,060 wavenumbers from 5,011.54 to 925.92 cm^{-1}

GENOTYPES: Illumina Inc. OvineSNP50 Beadchip

Materials & Methods

EDITING

Phenotypes:

Standardized Mahalonobis distance >3

(106 records, 101 ewes)

Lactations <3 TD/lactation (188 records, 80 ewes)

1rst parity > 2 years of age (47 records, 2 ewes)

Genotypes:

no genotype (12 animals)

call rate<0.95

MAF<0.01

X chromosome

AFTER EDITING

41,075 samples

1,256 ewes

43,663 SNPs

Materials & Methods

Annata	nSamples	nEwes	nTD	Aver. nSamples/ ewe	Min. nSamples/ ewe	Max nSamples/ ewe
2020	5,031	637	7	8	3	9
2021	12,894	679	12	19	6	23
2022	10,092	735	10	14	4	19
2023	13,058	713	14	18	4	26
Tot	**41,075**	**1,256**	**43**	**15**	**3**	**26**

Materials & Methods

$$y_{ijkl} = \mu + CN_j + LSTD_k + M_l + p_{ij} + w_{ik} + a_i + u_i + e_{ijkl}$$

Fixed effects:

μ is the overall absorbance mean;

CN_J age by parity (6 classes (11,21,22,3x,4x,5x);

$LSTD_k$: lactation stage within test date, 215 levels

- 8 lactation stages in classes of 30 days
- 43 test dates;

M_l: moment of milking (am or pm), 2 levels;

Random effects:

w_{ik} : ewe within LSTD (23,023 levels) ~ $N(0, I*Var(w))$;

p_{ij} : ewe within CN class (2,764 levels) ~$N(0, I*Var(p))$;

a_i : ewe (across lactations), (1,256 levels), ~ $N(0, I*Var(a))$;

u_i : genetic effect of ewe i, ~$N(0, G*Var(u))$, with G = GRM from SNP genotypes using VarRaden method 1;

e_{ijkl} : residual, ~$N(0, I*Var(e))$;

Materials & Methods

$$y_{ijkl} = \mu + CN_j + LSTD_k + M_l + p_{ij} + w_{ik} + a_i + u_i + e_{ijkl}$$

repeatability within date:

$$r = \frac{Var(u) + Var(a) + Var(p) + Var(w)}{Var(u) + Var(a) + Var(p) + Var(w) + Var(e)}$$

repeatability within lactation:

$$rw = \frac{Var(u) + Var(a) + Var(p)}{Var(u) + Var(a) + Var(p) + Var(w) + Var(e)}$$

repeatability across lactations:

$$rb = \frac{Var(u) + Var(a)}{Var(u) + Var(a) + Var(p) + Var(w) + Var(e)}$$

Materials & Methods

$$y_{ijkl} = \mu + CN_j + LSTD_k + M_l + p_{ij} + w_{ik} + a_i + u_i + e_{ijkl}$$

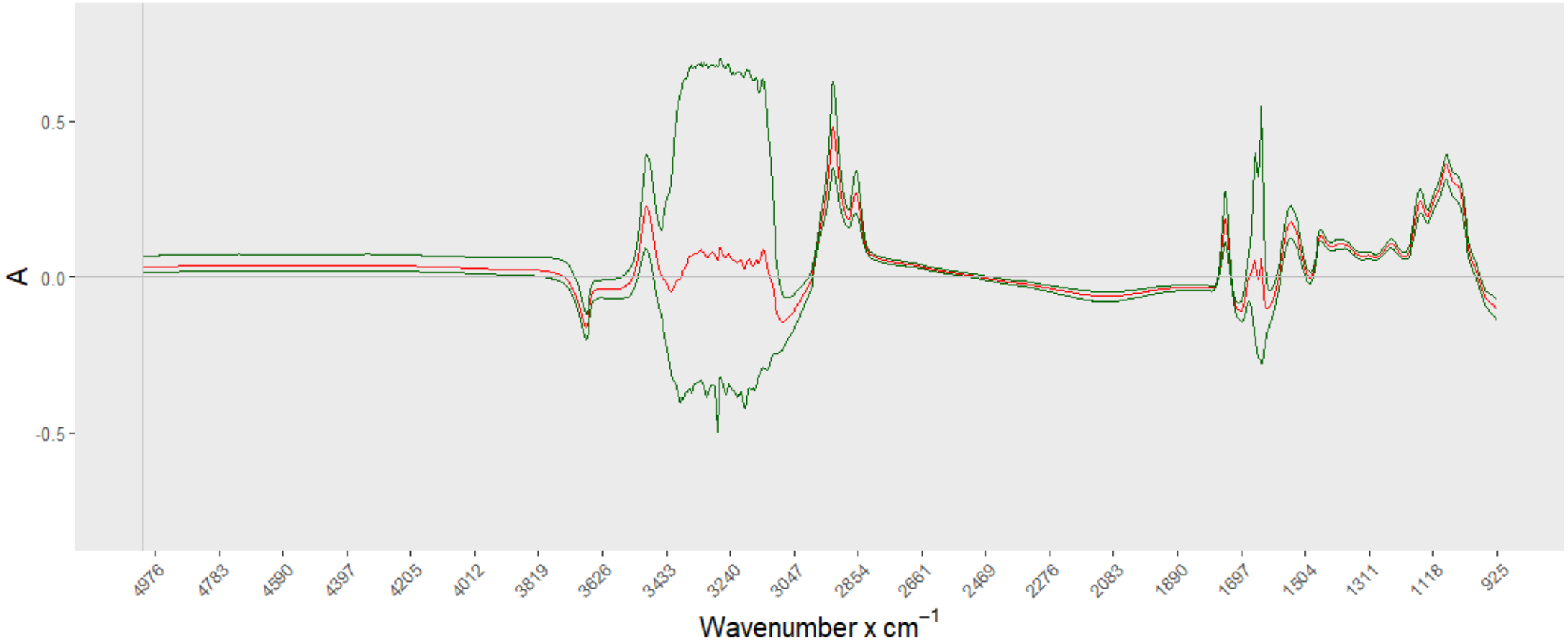
heritability:

$$h^2 = \frac{Var(u)}{Var(u) + Var(a) + Var(p) + Var(w) + Var(e)}$$

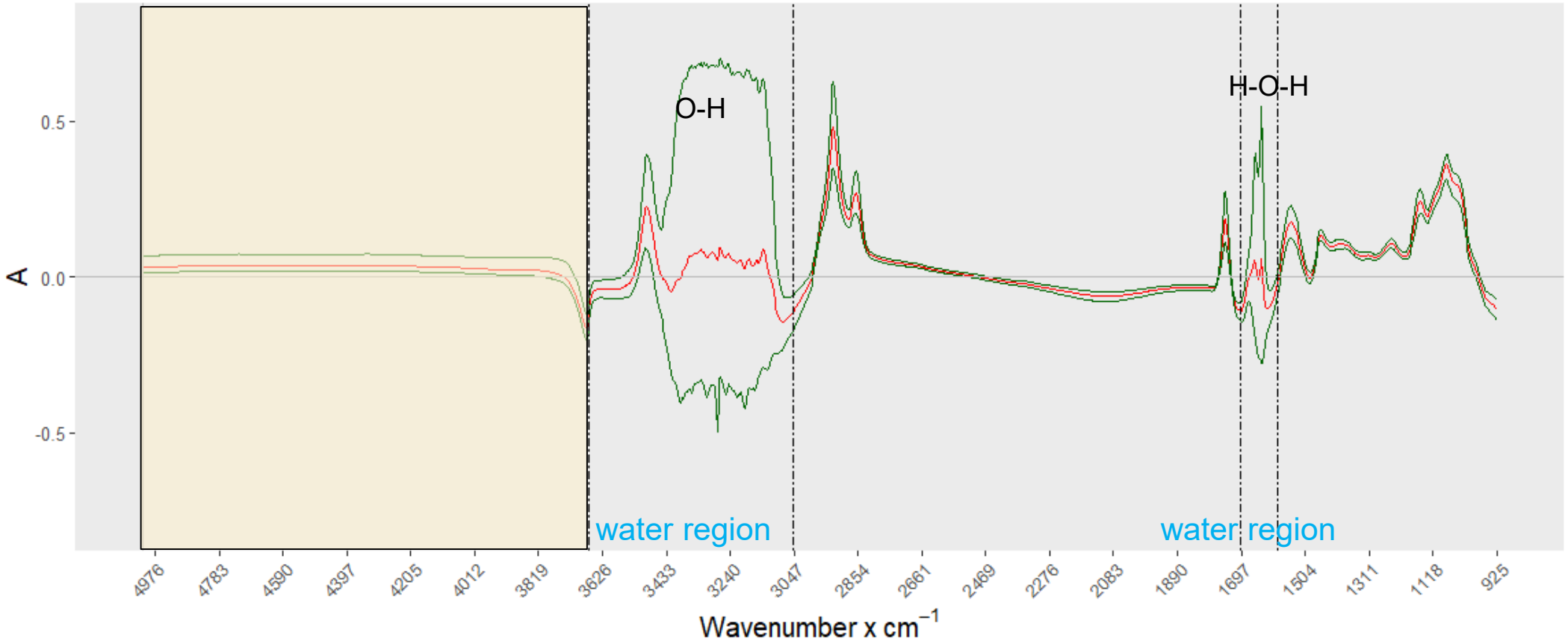
REML procedure implemented in the Asreml-R package version 4.2.

Results

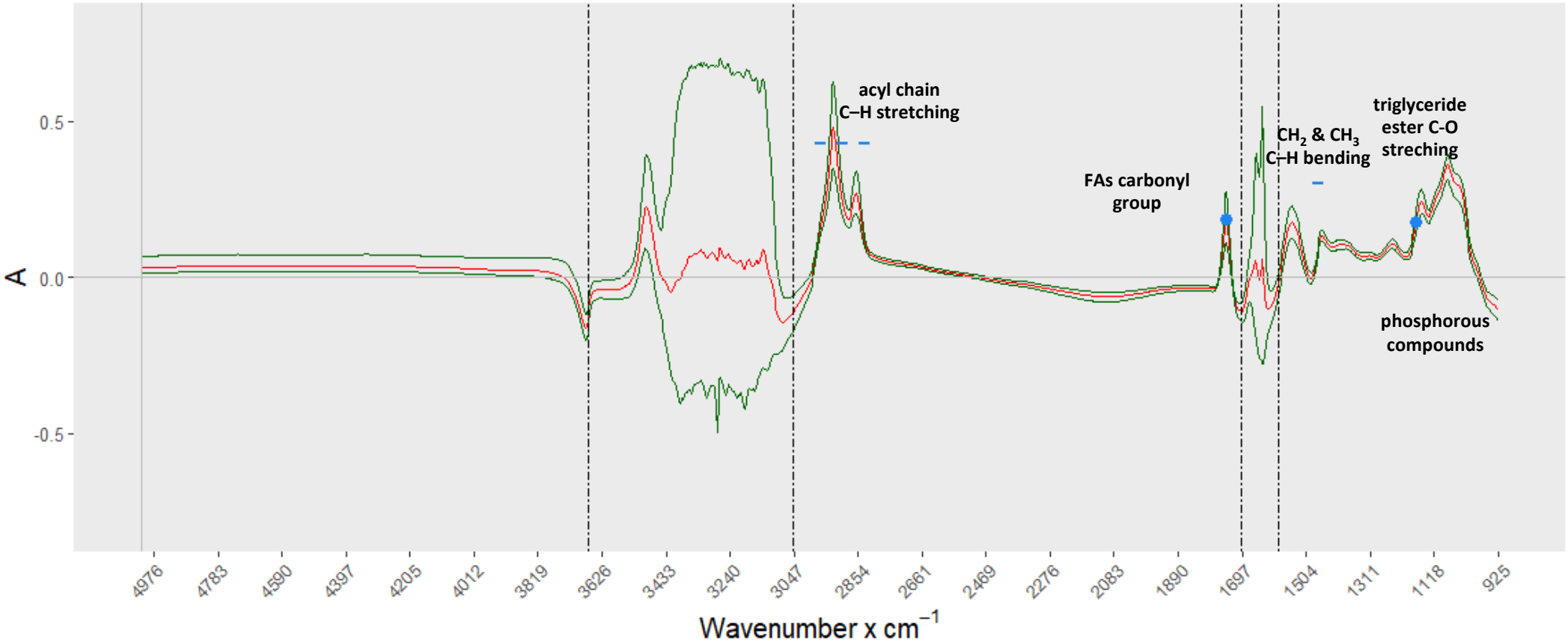
Absorbance


0.5
0.0
-0.5
A
4976
4783
4590
4397
4205
4012
3819
3626
3433
3240
3047
2854
2661
2469
2276
2083
1890
1697
1504
1311
1118
925
Wavenumber x cm^{-1}

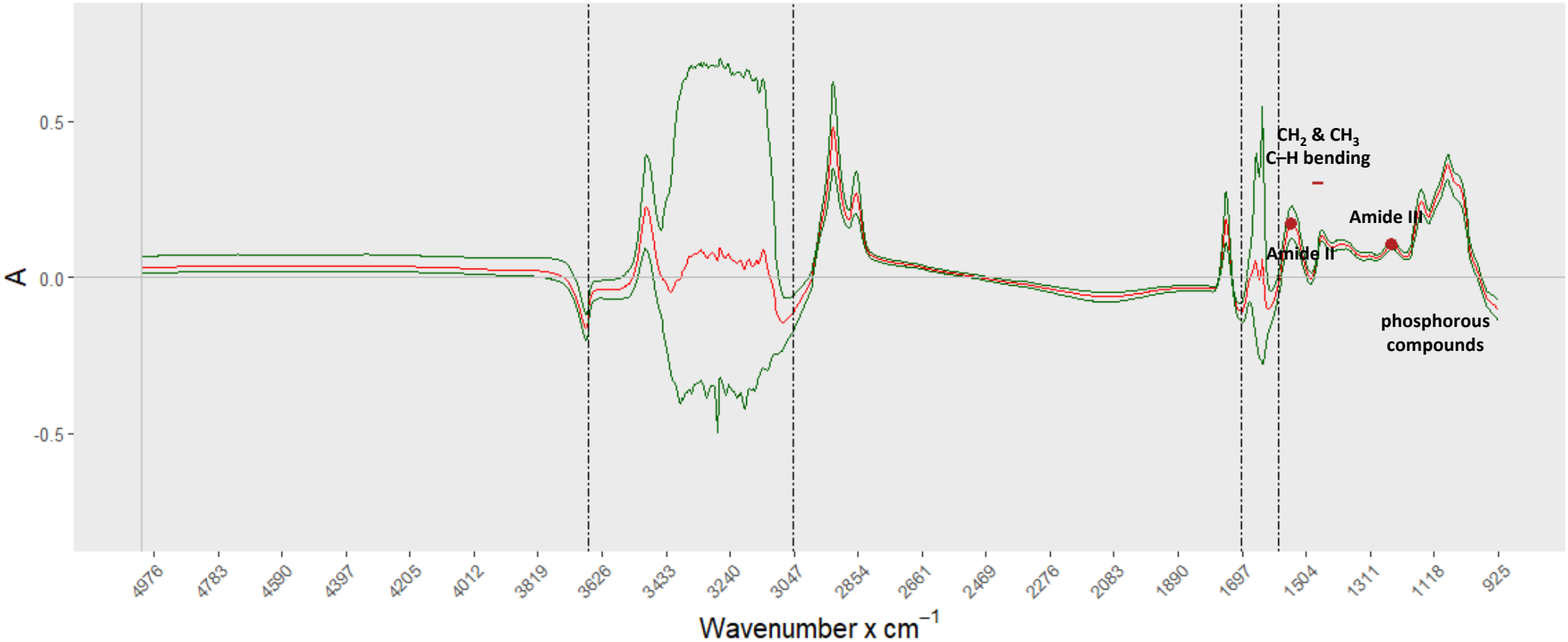
Absorbance


O-H
H-O-H
water region
water region
A
0.5
0.0
-0.5
4976
4783
4590
4397
4205
4012
3819
3626
3433
3240
3047
2854
2661
2469
2276
2083
1890
1697
1504
1311
1118
925
Wavenumber x cm^{-1}

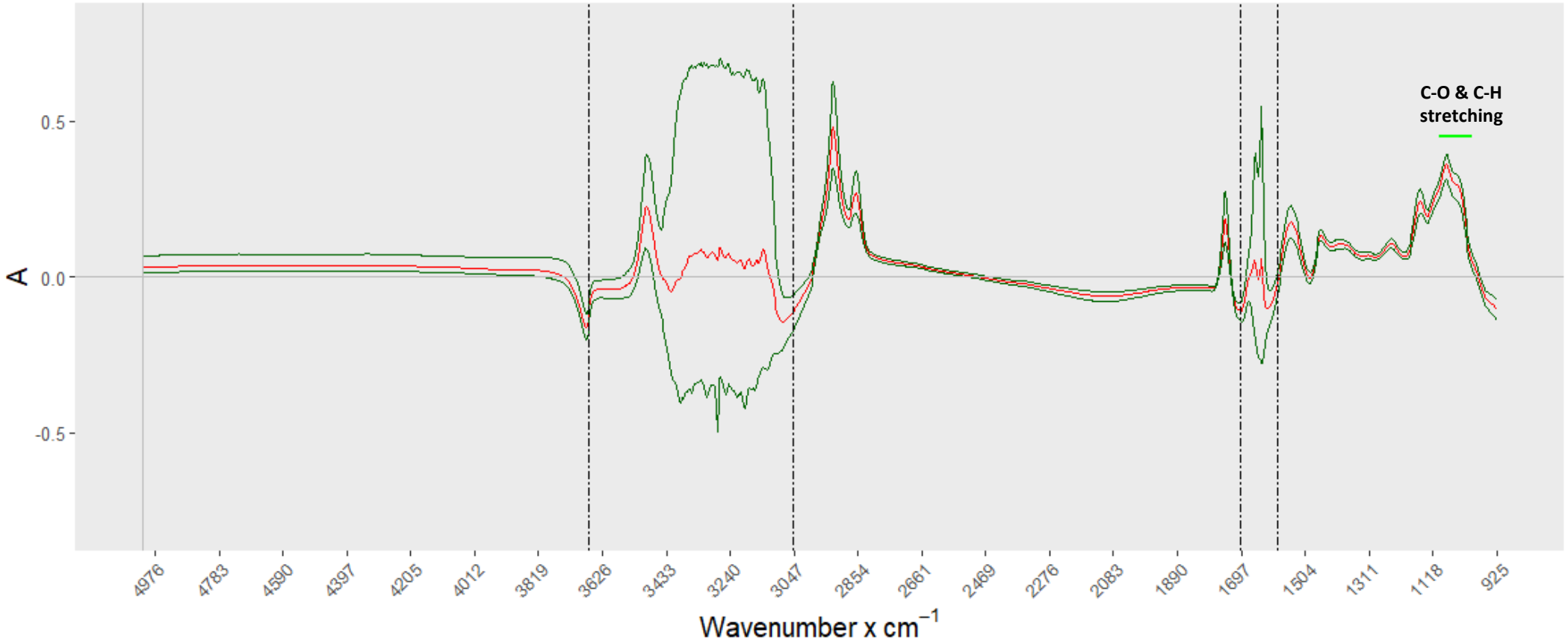
Absorbance


acyl chain
C–H stretching
FAs carbonyl
group
CH2 & CH3
C–H bending
triglyceride
ester C-O
streching
phosphorous
compounds
A
0.5
0.0
-0.5
4976
4783
4590
4397
4205
4012
3819
3626
3433
3240
3047
2854
2661
2469
2276
2083
1890
1697
1504
1311
1118
925
Wavenumber x cm−1

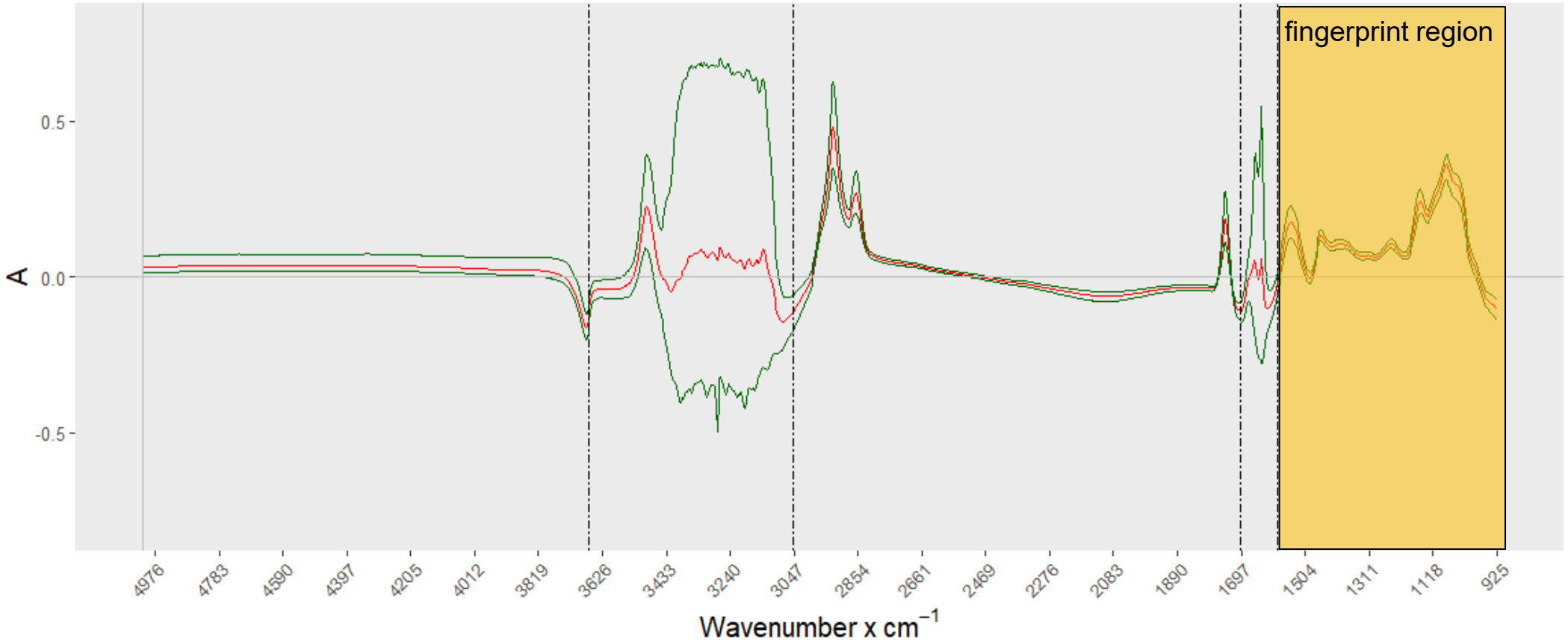
Absorbance


0.5
0.0
-0.5
A
CH_2 & CH_3
C–H bending
Amide III
Amide II
phosphorous
compounds
4976
4783
4590
4397
4205
4012
3819
3626
3433
3240
3047
2854
2661
2469
2276
2083
1890
1697
1504
1311
1118
925
Wavenumber x cm^{-1}

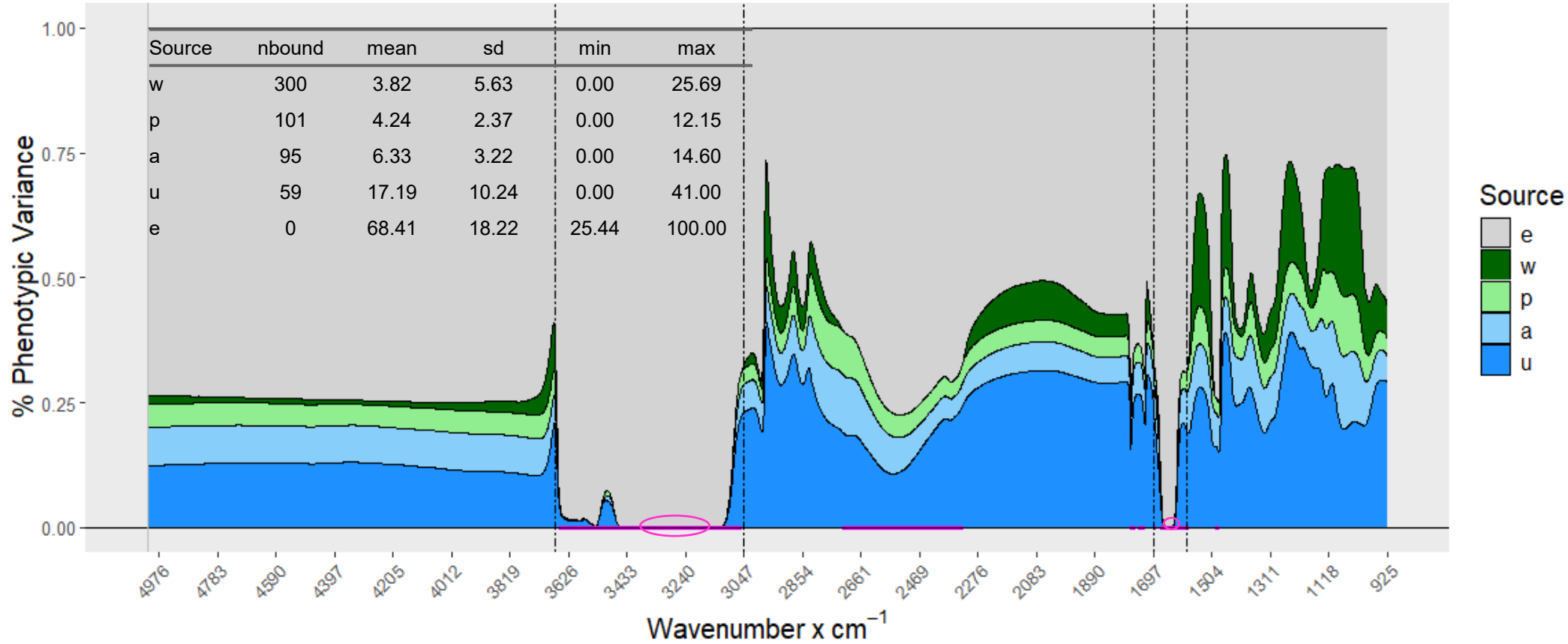
Absorbance


C-O & C-H
stretching
A
0.5
0.0
-0.5
4976
4783
4590
4397
4205
4012
3819
3626
3433
3240
3047
2854
2661
2469
2276
2083
1890
1697
1504
1311
1118
925
Wavenumber x cm^{-1}

Absorbance

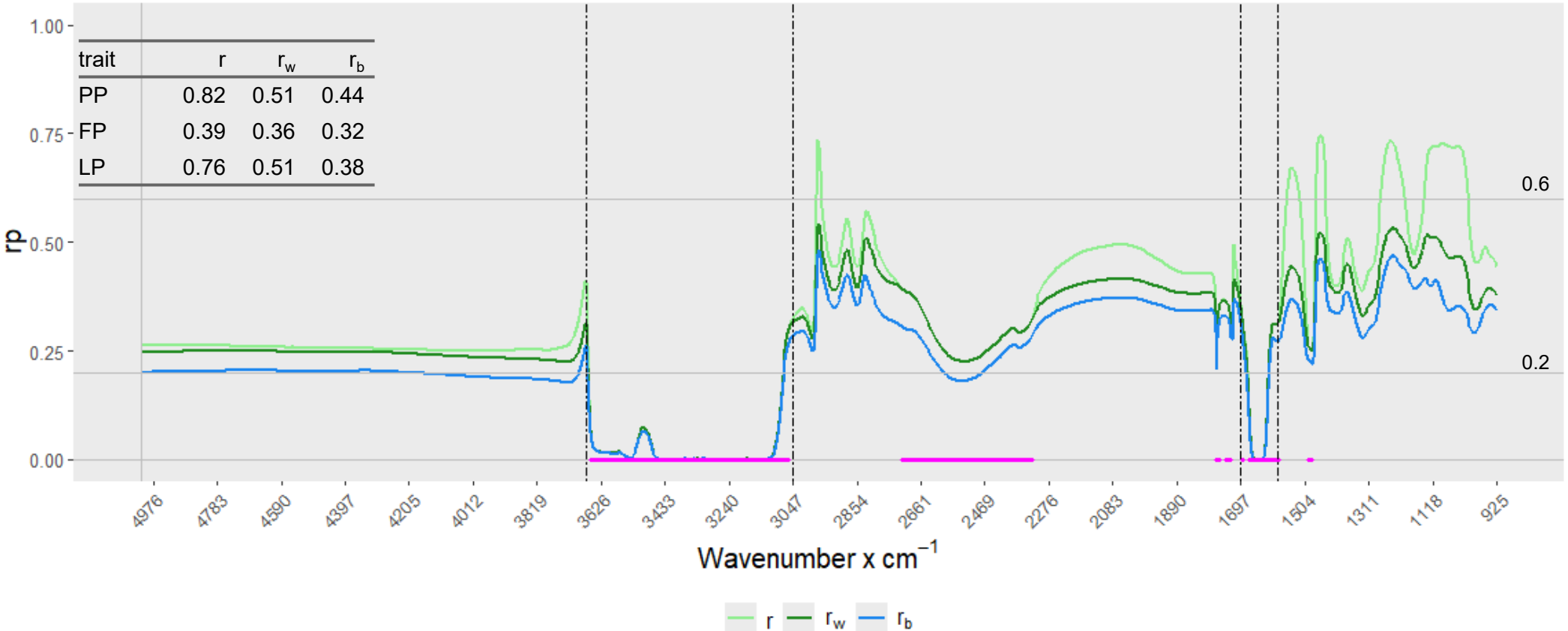

fingerprint region
0.5
0.0
-0.5
A
4976
4783
4590
4397
4205
4012
3819
3626
3433
3240
3047
2854
2661
2469
2276
2083
1890
1697
1504
1311
1118
925
Wavenumber x cm^{-1}

Proportion of variance



Repeatability

trait	r	r_w	r_b
PP	0.82	0.51	0.44
FP	0.39	0.36	0.32
LP	0.76	0.51	0.38



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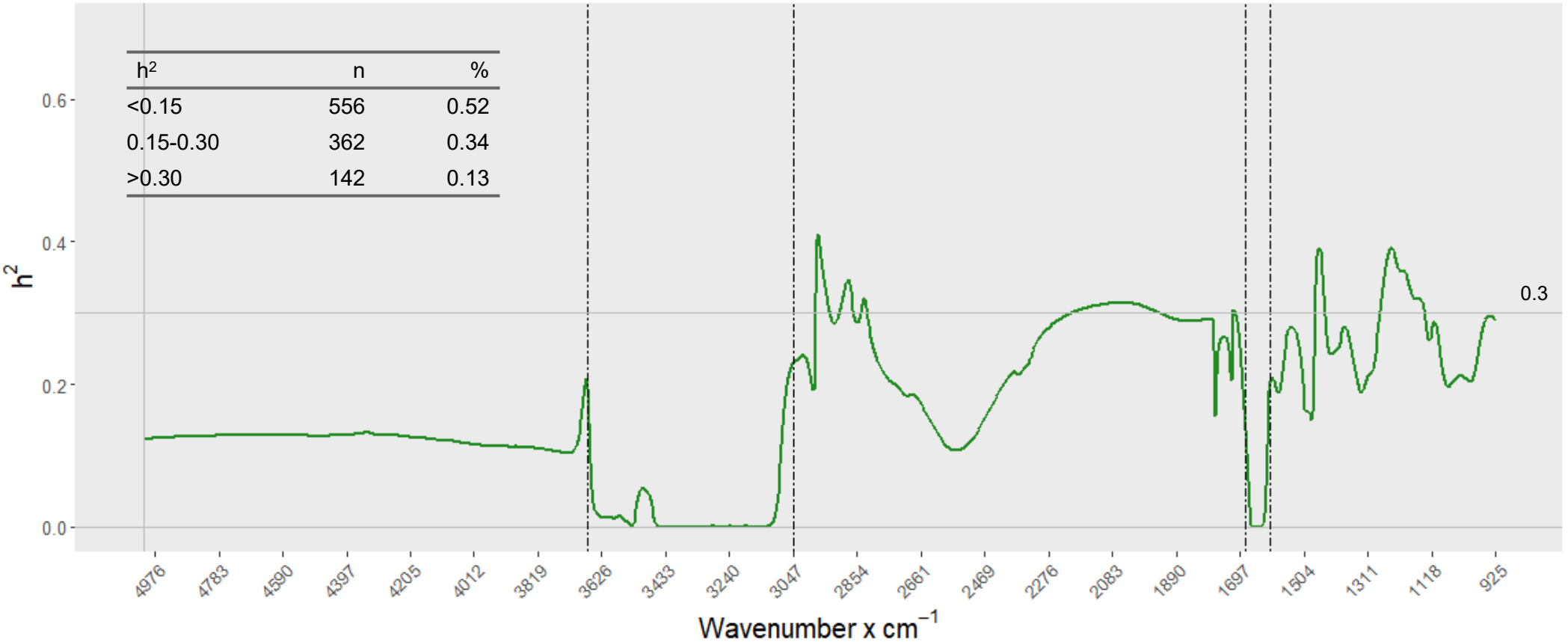
Heritability

h^2	n	%
<0.15	556	0.52
0.15-0.30	362	0.34
>0.30	142	0.13



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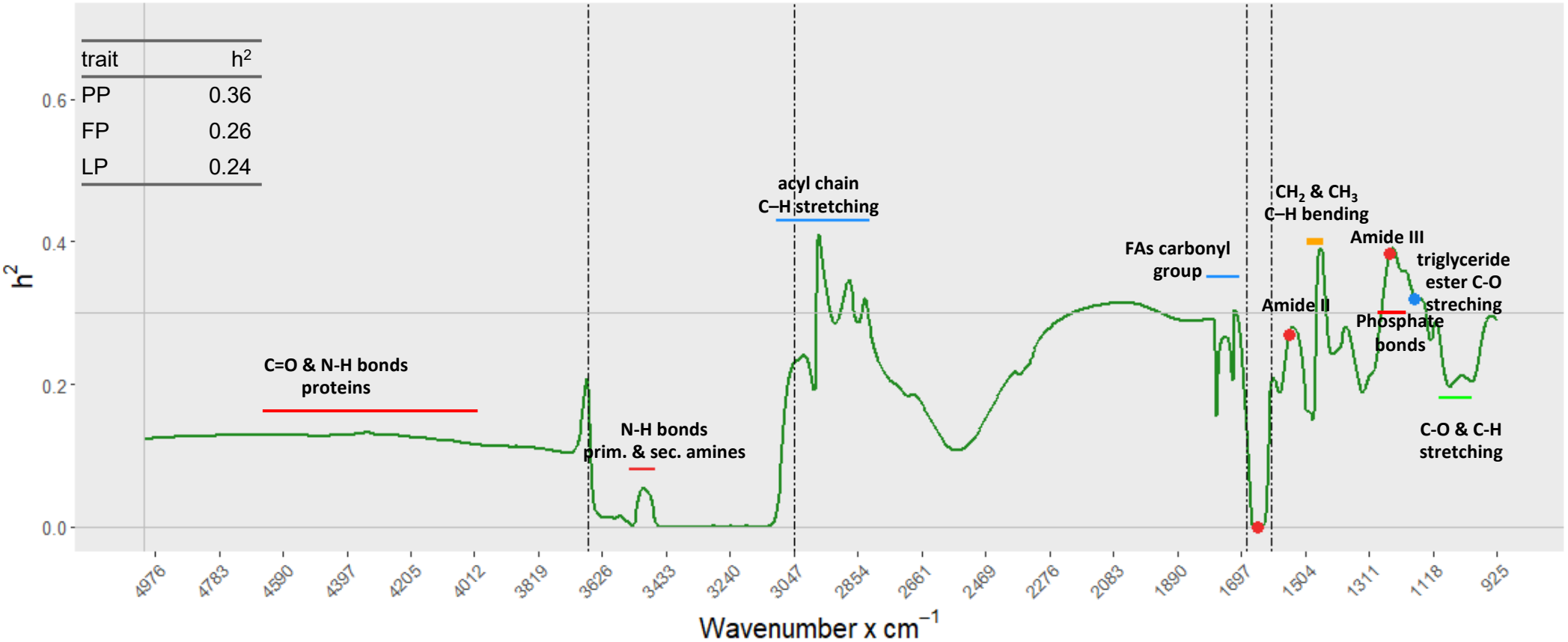
Heritability

trait	h^2
PP	0.36
FP	0.26
LP	0.24



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Conclusions

The absorbance of ovine milk was moderately heritable

Individual wavenumbers exhibit additional genetic signals compared FT-MIR predictions of major milk composition traits

These findings suggest the feasibility of using FTIR spectra for the genetic improvement of dairy sheep:

- indirectly: through phenotypic predictions of traits of interest (milk quality and technological traits for example)
- directly: by selecting on estimated breeding values (EBV) for individual FT-IR wavenumbers or on their linear combination (Tiplady et al., 2020)

A better understanding of the genetic basis of milk absorbance could provide insights into the relationships between specific genes and the underlying chemical structure of milk

Thank you for the attention