UNIVERSITY OF HELSINKI

NaPPI Finnish National Plant Phenotyping Infrastructure

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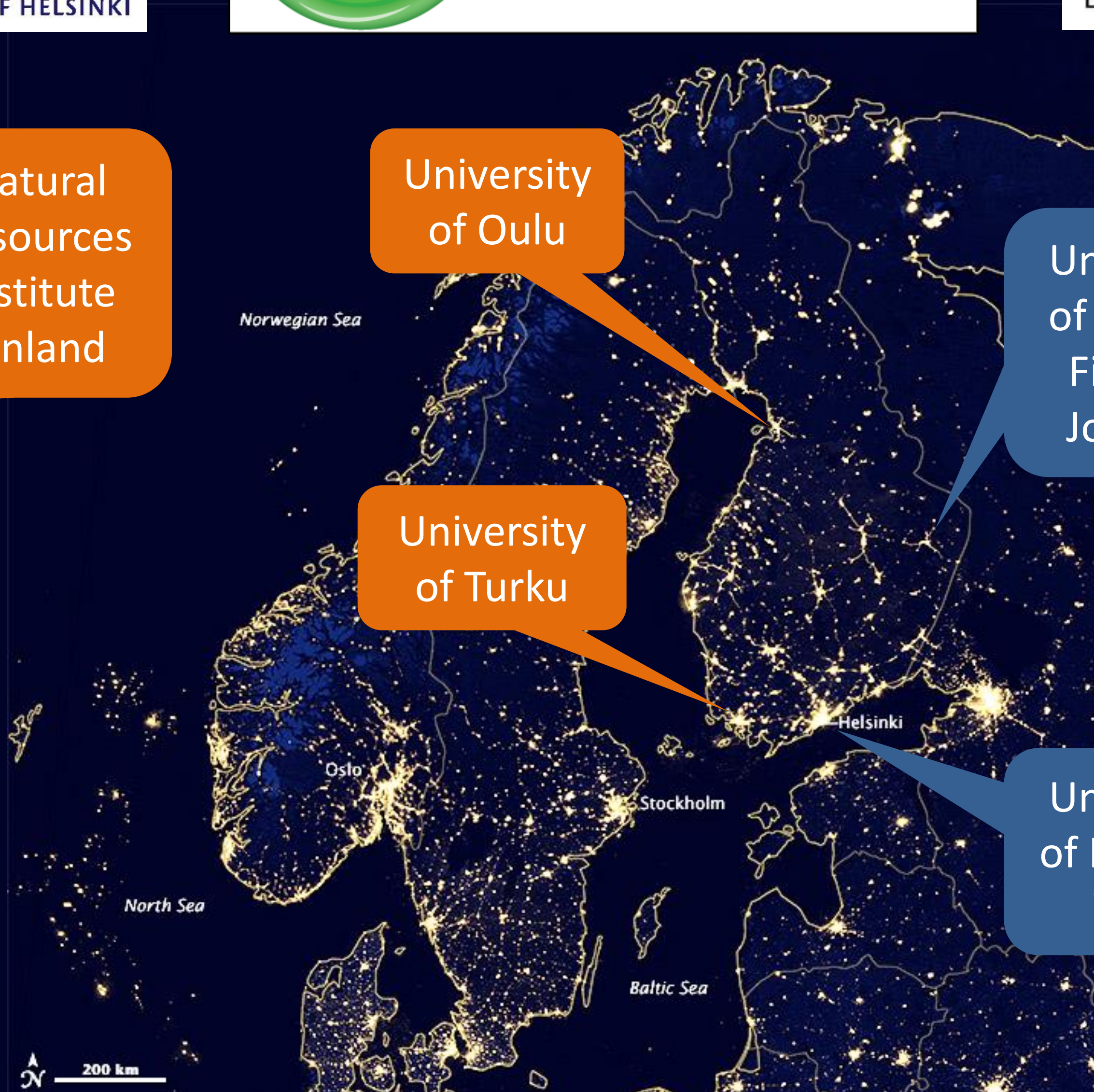

Natural Resources Institute Finland

University of Oulu

University of Eastern Finland, Joensuu

University of Turku

University of Helsinki, Viikki

NaPPI UEF node (Joensuu campus)

Spectromics lab: hyperspectral imaging &c.

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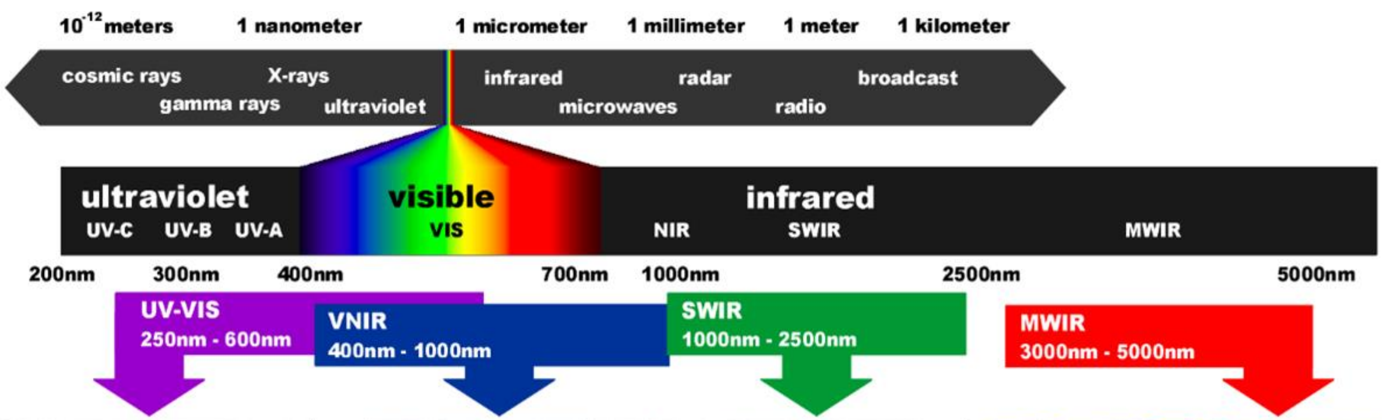
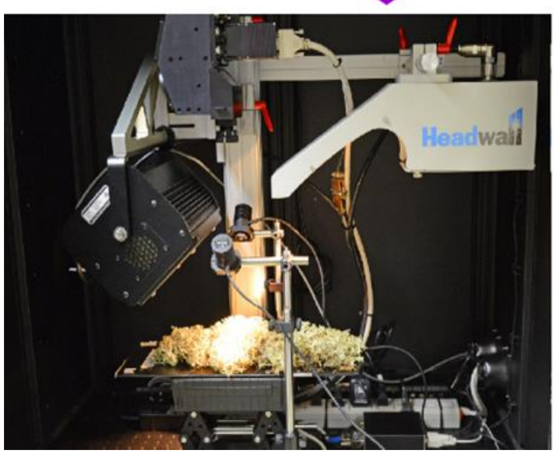
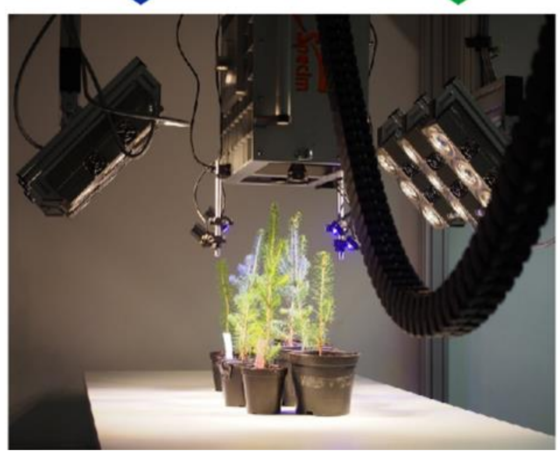
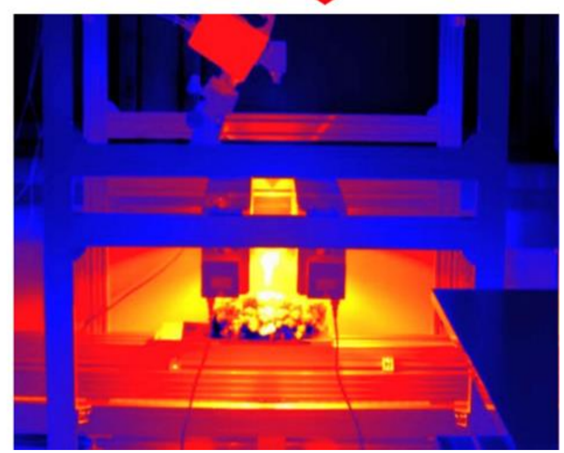
Four hyperspectral cameras covering the range 400 - 5000nm
(+ a battery-operated portable VNIR hyperspectral camera)









Other imaging devices / Spectromics lab

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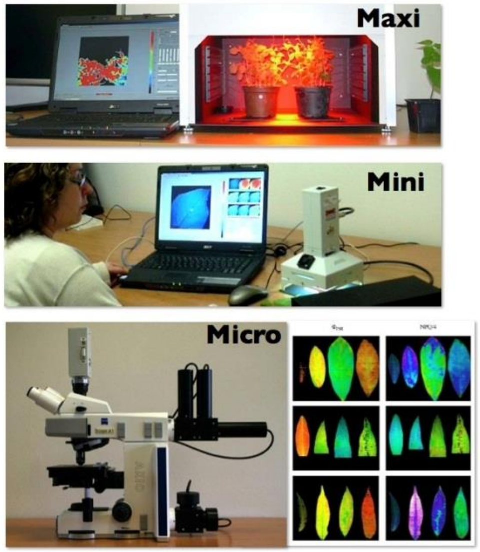
Kinetic chlorophyll fluorescence
'Imaging PAM' technique



UV & IR modified DSLRs

Thermography

Macroscopy & 3D stacking

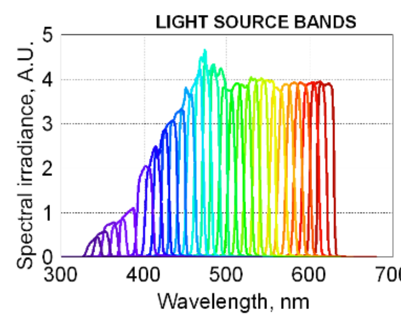
Xenon light source w/ liquid light guides (UV to IR)

Liquid-cooled CCD camera for UV (*200* - 900nm)

Liquid-cooled EMCCD camera

Fast sCMOS camera

Powerful LEDs, also in Deep UV



Angle-tunable filter units

Adjustable
338 – 700 nm
(15 nm BW)

Imaging lichen water content

Seitsemän jäkälälajia

Vesipitoisuus lisääntyy vasemmalta oikealle

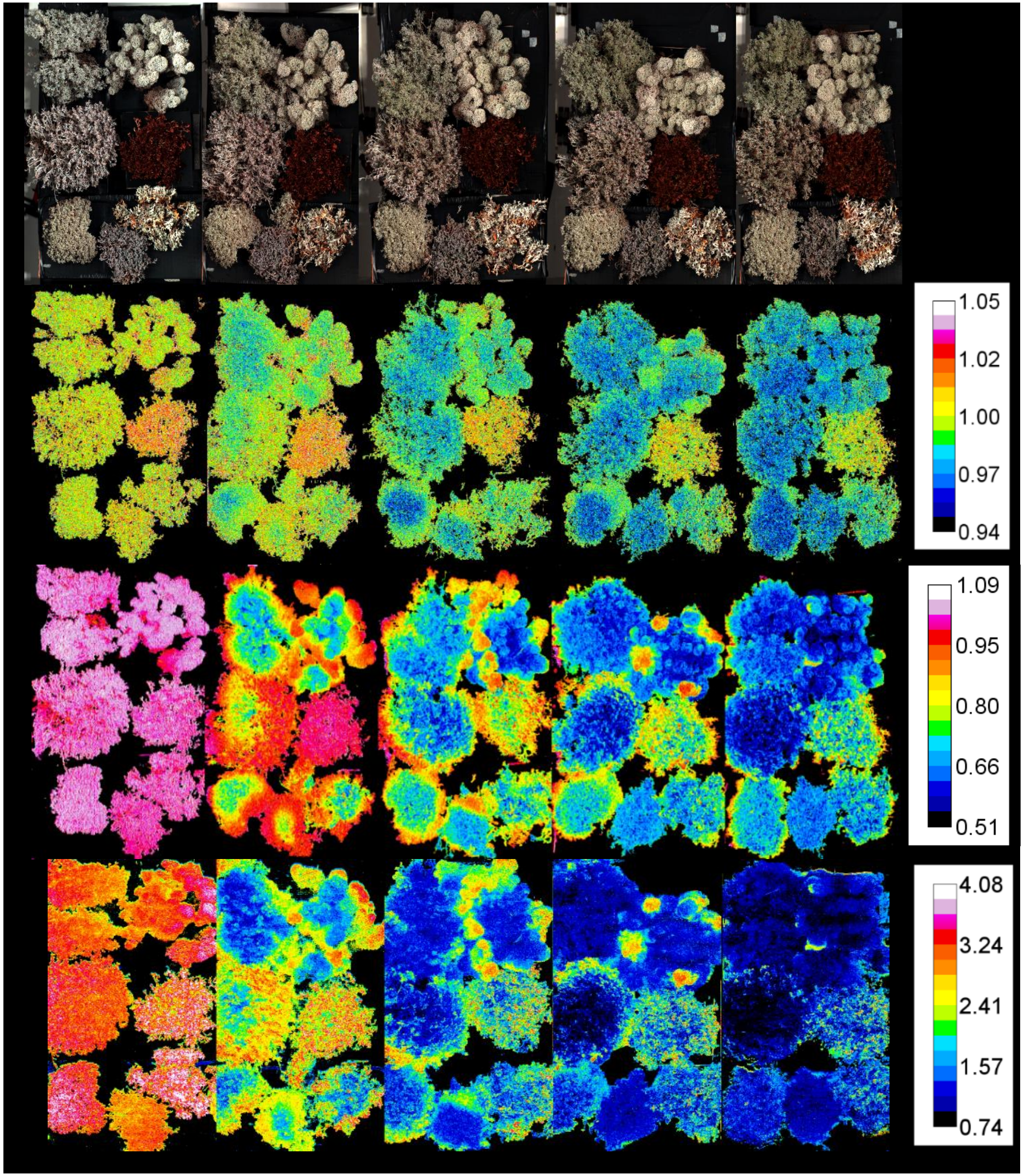
Kamerat ylhäältä lukien

RGB

VNIR

SWIR

MWIR



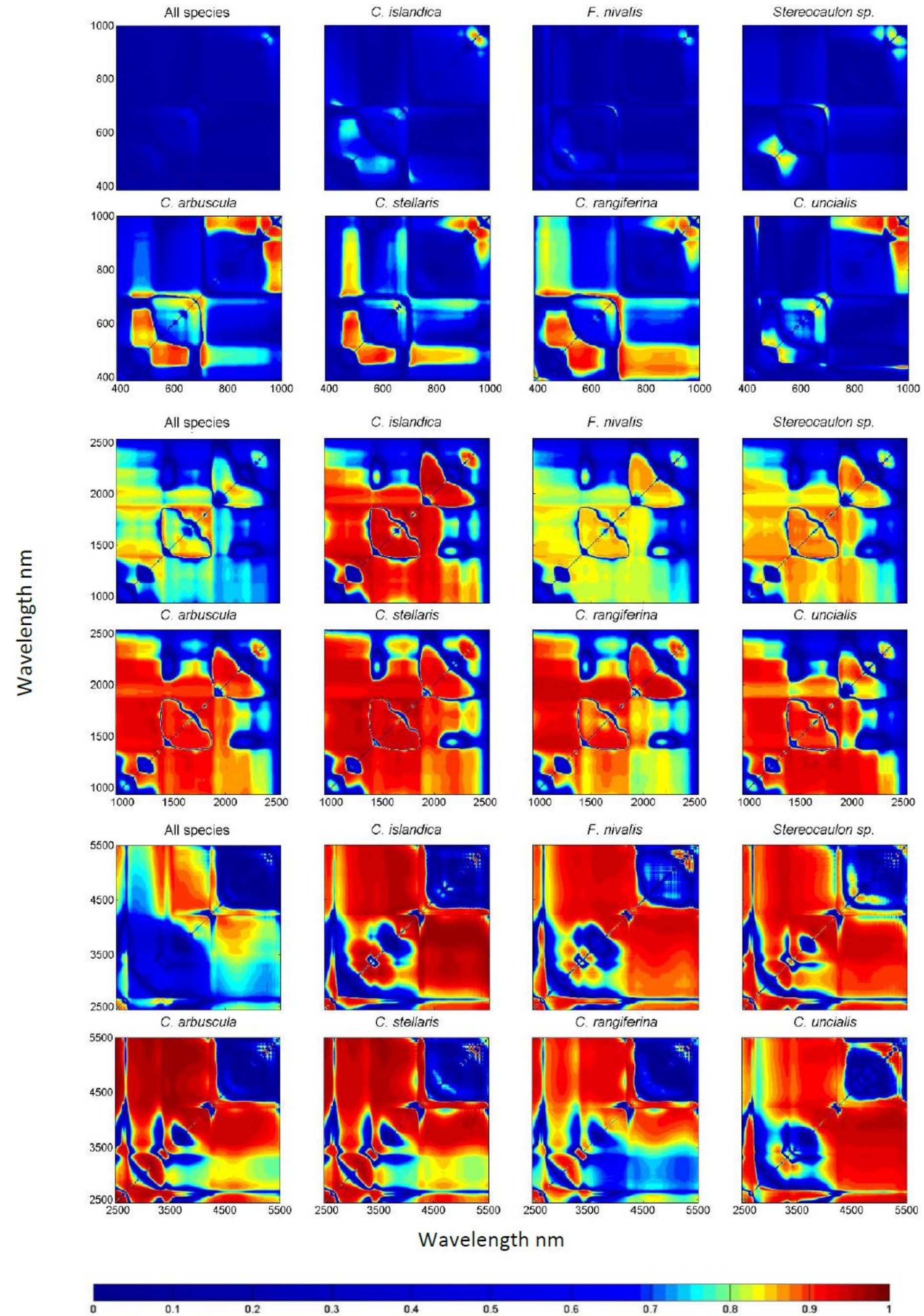
Lars Granlund

Jäkälien heijastusspektrit muuttuvat eri tavoin vesi-pitoisuuden vaihdellessa

Kuvassa kolmen eri kameran tulokset 8 kuvan paneeleina (Lajien keskiarvo + 7 lajia)

Värit ilmentävät aallonpituusparien suhteen korrelaatiota vesipitoisuuteen

Lajit eivät ole samanlaisia: Kaukokartoitus tuottaa luotettavaa tietoa vain jos kunkin lajin ominaisuudet tiedetään



RGB image and hyperspectral false-color images showing the peat type and spatial variability within the peat mesocosms

False-color images combined from 3 main components of PCA of SWIR data

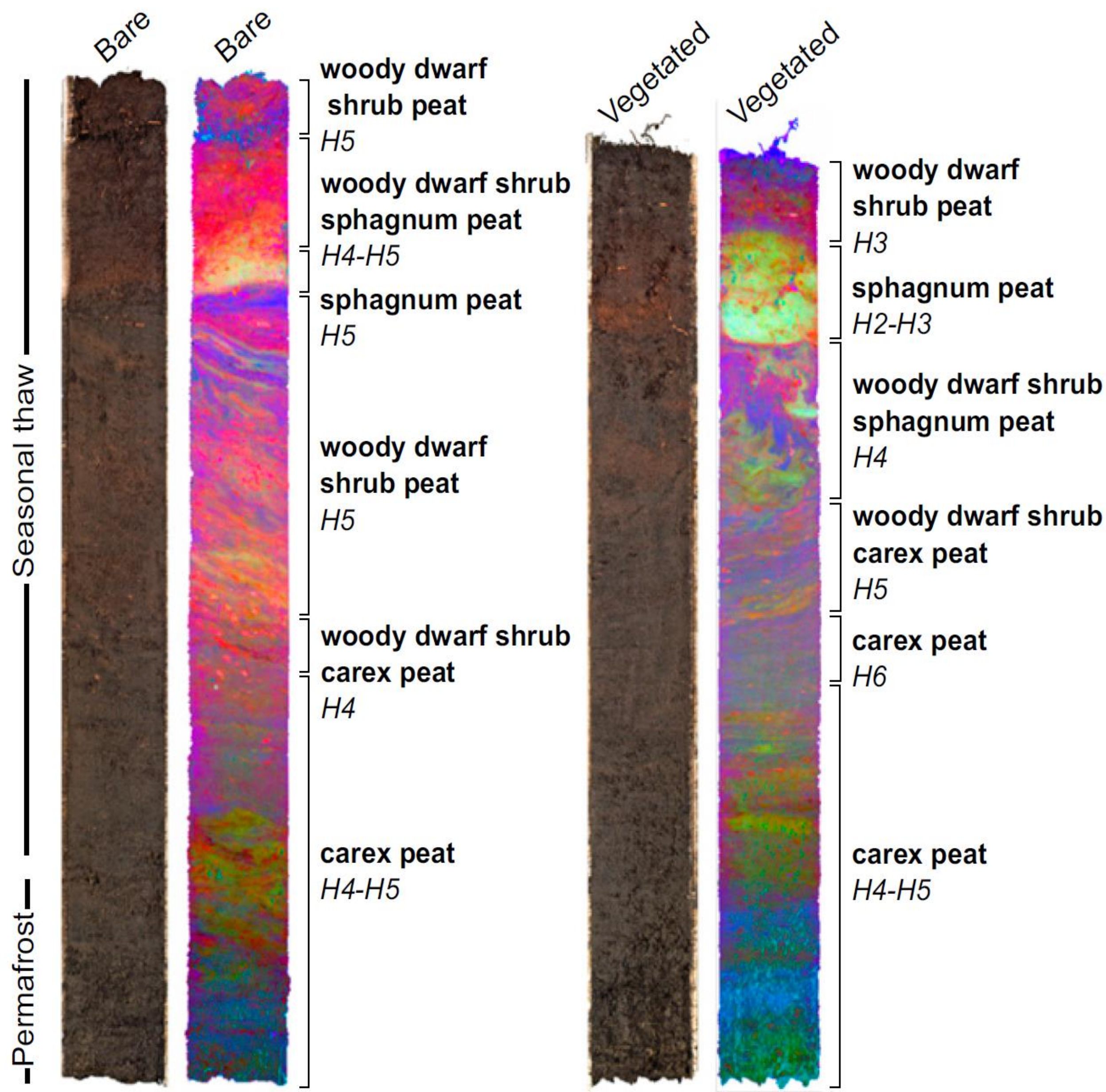
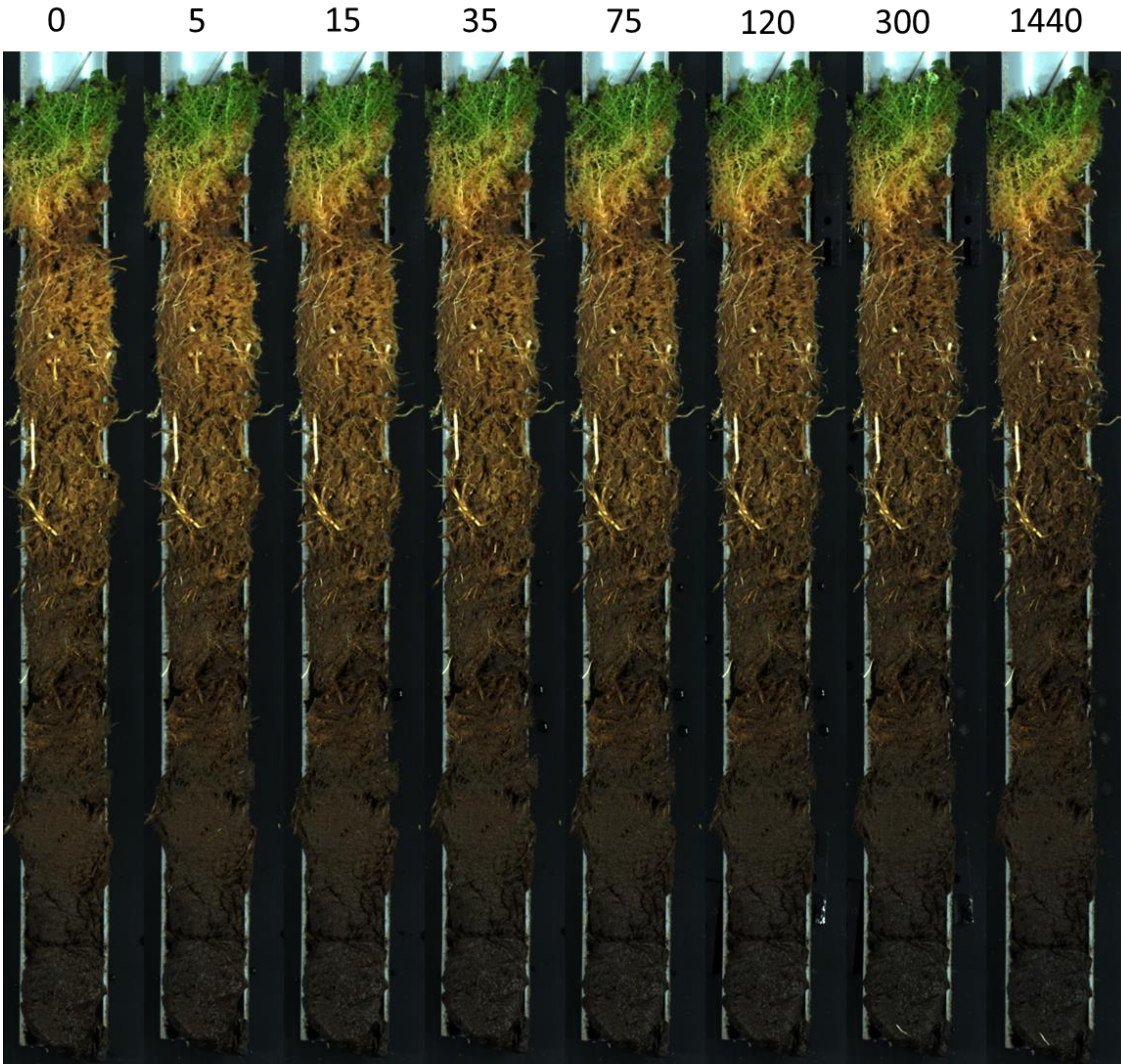


Image: Lars Granlund. Voigt et al 2017. PNAS doi: 10.1073/pnas.1702902114

Menetelmän kehitystä:

Aikasarja turvenäytteen hapettumisen ja muiden muutosten seurantaan (minuutteja)

Kuva ihmissilmän näkemänä

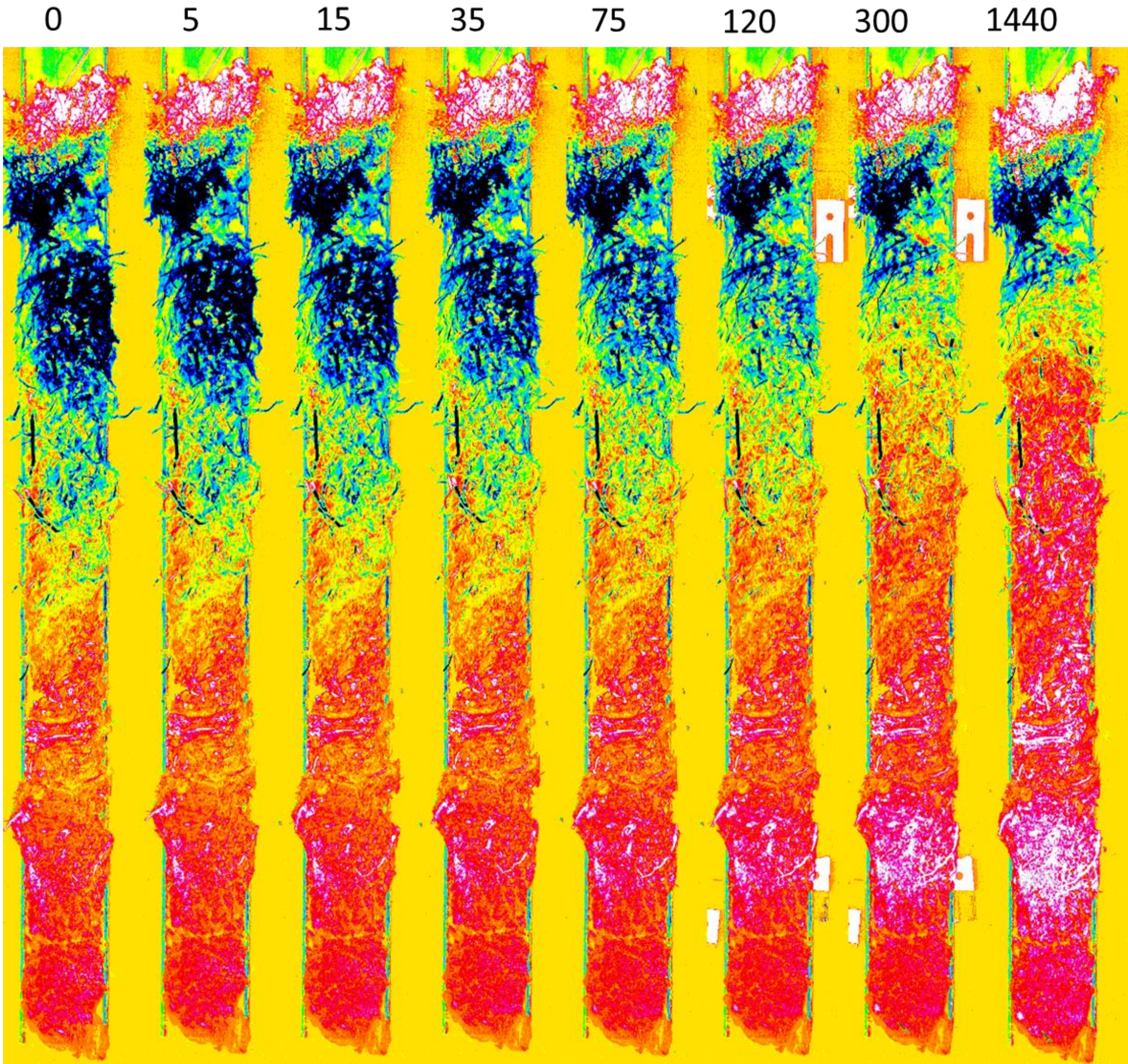


Menetelmän kehitystä:

Aikasarja turvenäytteen hapettumisen ja muiden muutosten seurantaan (minuutteja)

Väärävärikuva spektritiedon pohjalta

Ensimmäinen pääkomponentti: aineiston päävaihtelu

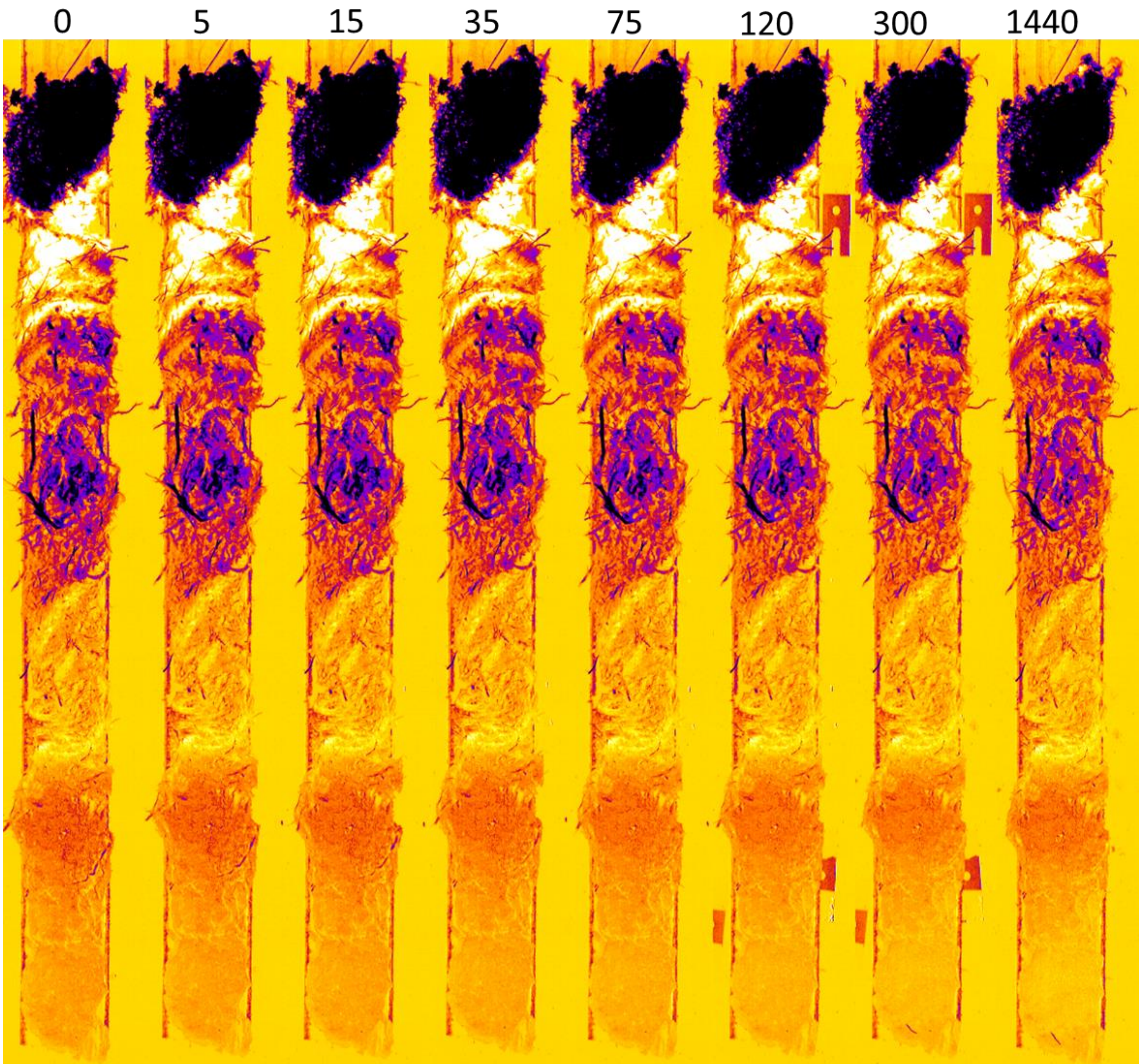


Menetelmän kehitystä:

Aikasarja turvenäytteen hapettumisen ja muiden muutosten seurantaan (minuutteja)

Väärävärikuva spektritiedon pohjalta

Toinen pääkomponentti: toiseksi suurin vaihtelusuunta



Automated phenotyping of berry development

Collaboration with Prof Paula Elomaa (PI), Univ Helsinki

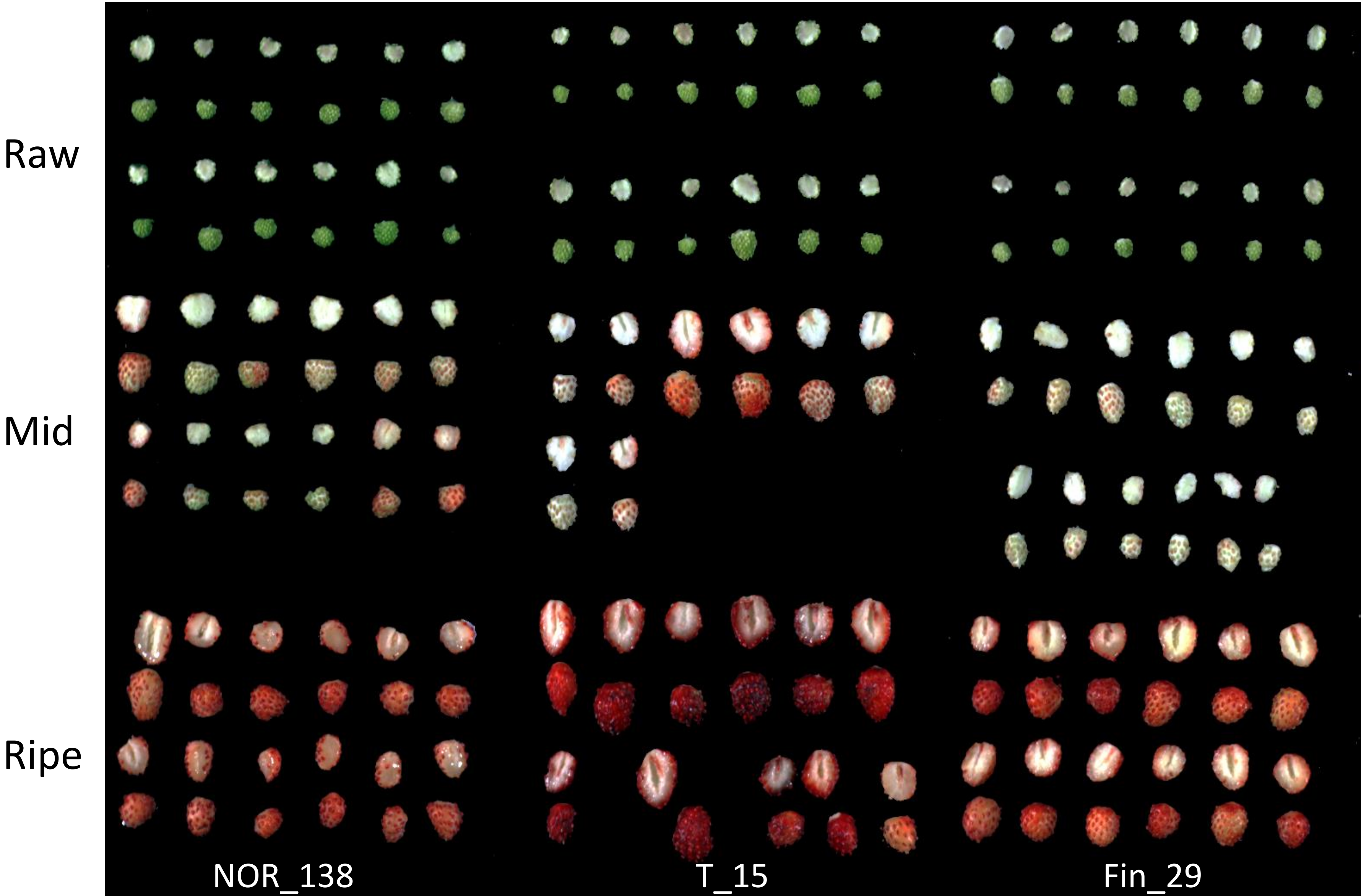
220 woodland strawberry (*Fragaria vesca*) genotypes with fully sequenced genomes

Genome wide association studies to discover genomic regions that explain the observed variability in berry traits

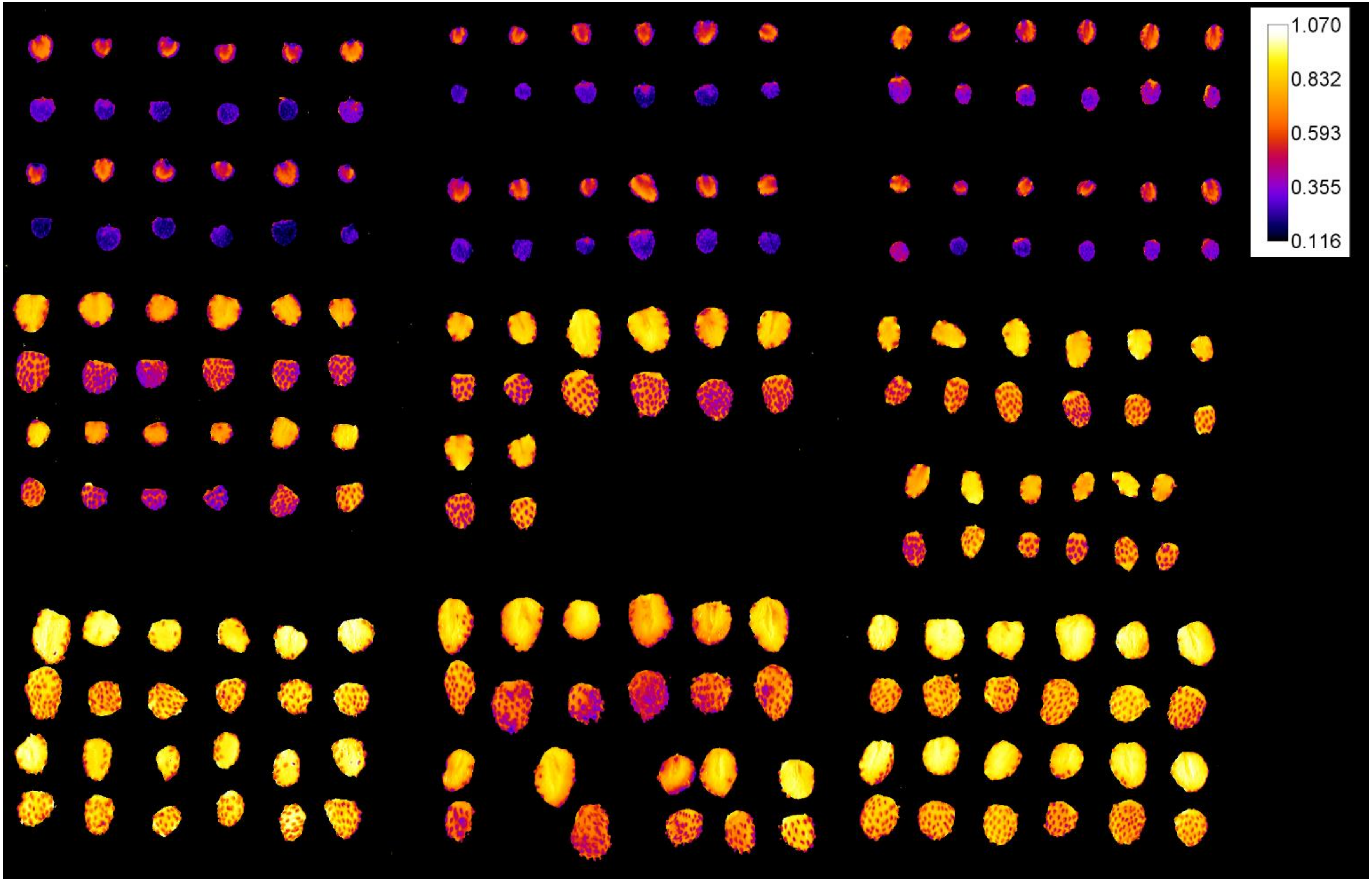
Phenotyping of shape parameters (area, perimeter, eccentricity, &c.) and color attributes by RGB imaging at NaPPI Helsinki facilities

Hyperspectral imaging at the UEF node (Spectromics lab)

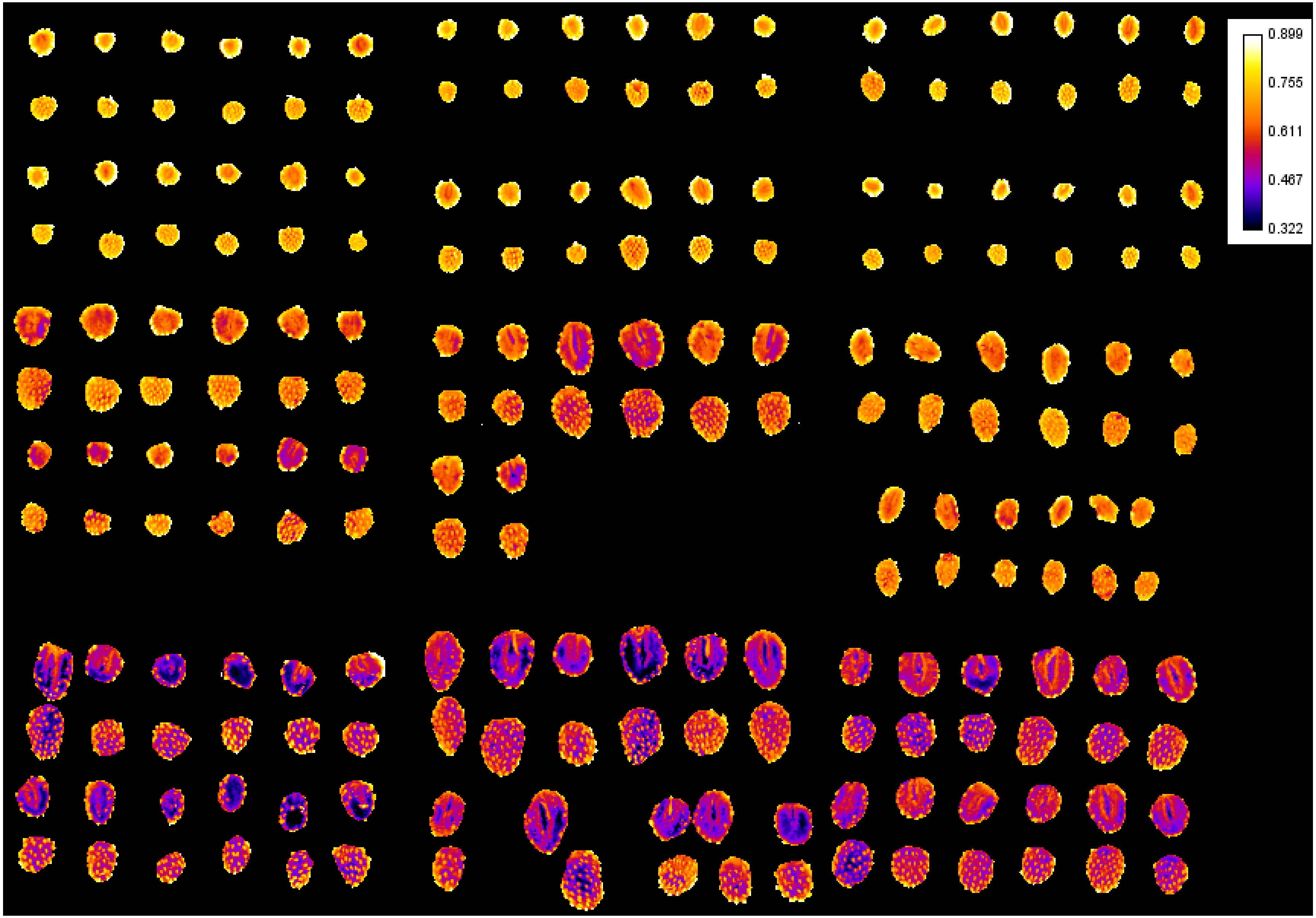
RGB image constructed from VNIR for 3 genotypes



Chlorophyll content (index-based)



Water content (index-based)



Ahomansikan eri genotyypit erottuvat monimuuttuja-analyysissä ryhmiksi

Alustava testaus pienellä aineistolla: 6 genotyyppiä Suomesta, Norjasta, Italiasta, Saksasta ja Espanjasta

Genotyypit erottuvat kaikilla kypsyysasteilla, mutta parhaiten kypsinä (oikealla)

Menetelmä sopii hyvin ahomansikan marjojen laatuominaisuuksien selvittämiseen genomin assosiaatiokartoituksella

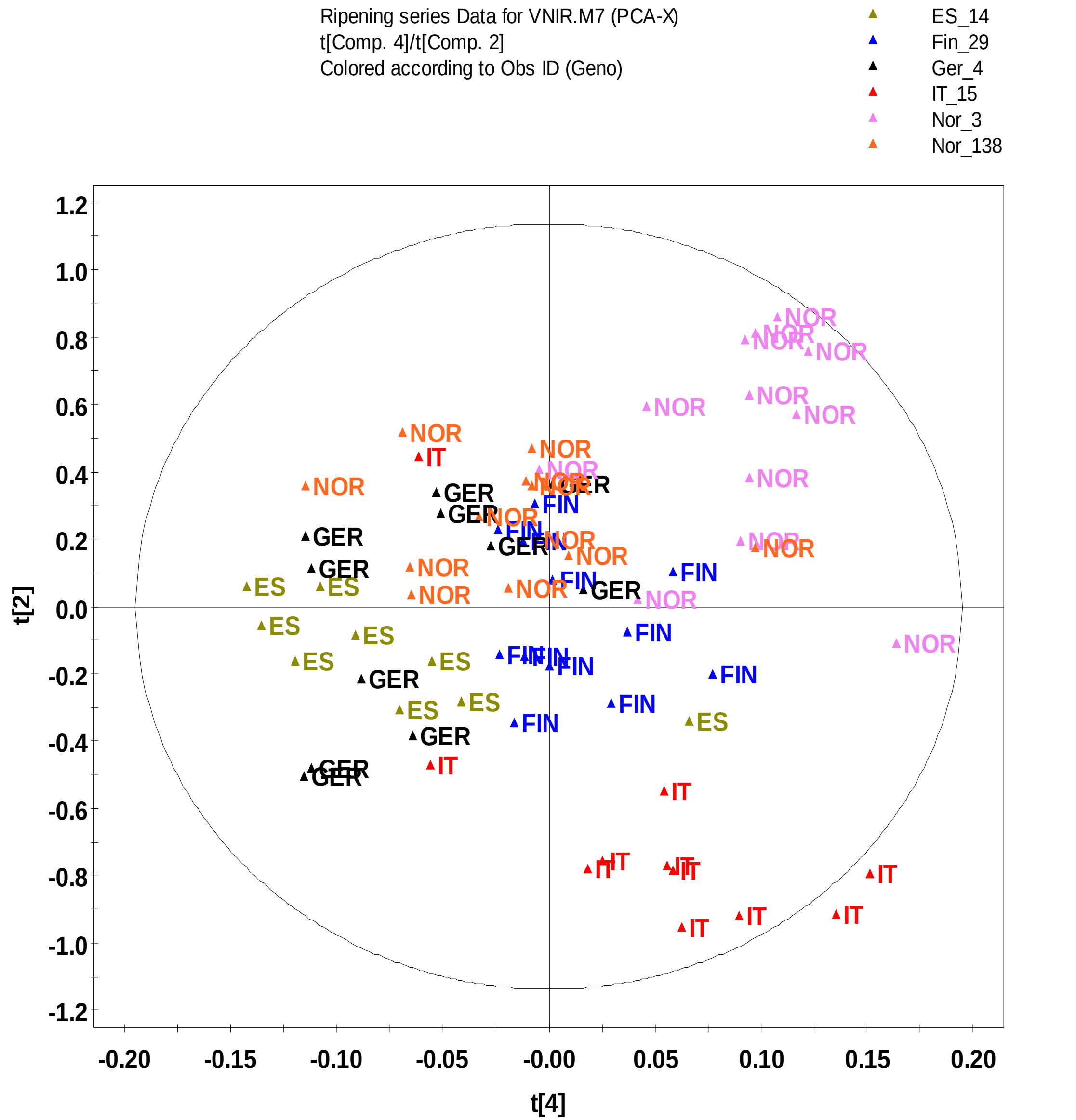
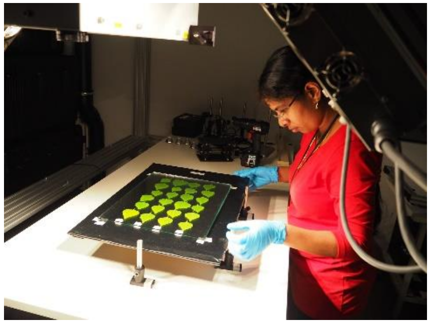


Figure 2. Samples of *Cladonia stellaris* (a), *Cetraria islandica* (b), *Flavocetraria nivalis* (c), *Stereocaulon sp.* (d), *Cladonia arbuscula* (f), *Cladonia rangiferina* (f) and *Cladonia uncialis* (g)

Maastokuvausta kannettavalla spektrikameralla (Specim IQ)

Eri jäkälälajit visualisoitu eri väärävärein oikealla

Silver birch hyperspectral imaging



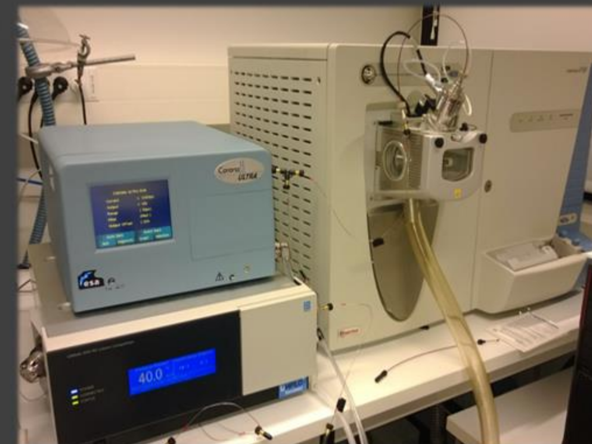
How similar are the leaves of an individual tree?

Can we distinguish between different genotypes and provenances of silver birch grown at the same site?

Leaf surface chemical composition was also analyzed

Common garden, Joensuu

Extraction of leaf secondary metabolites



Mass spectrometry

Hyperspectral reflectance measurement

VNIR and SWIR imaging

Photos: Maya Deepak

One plate from imaging experiment (12 genotypes, 2 leafs each)

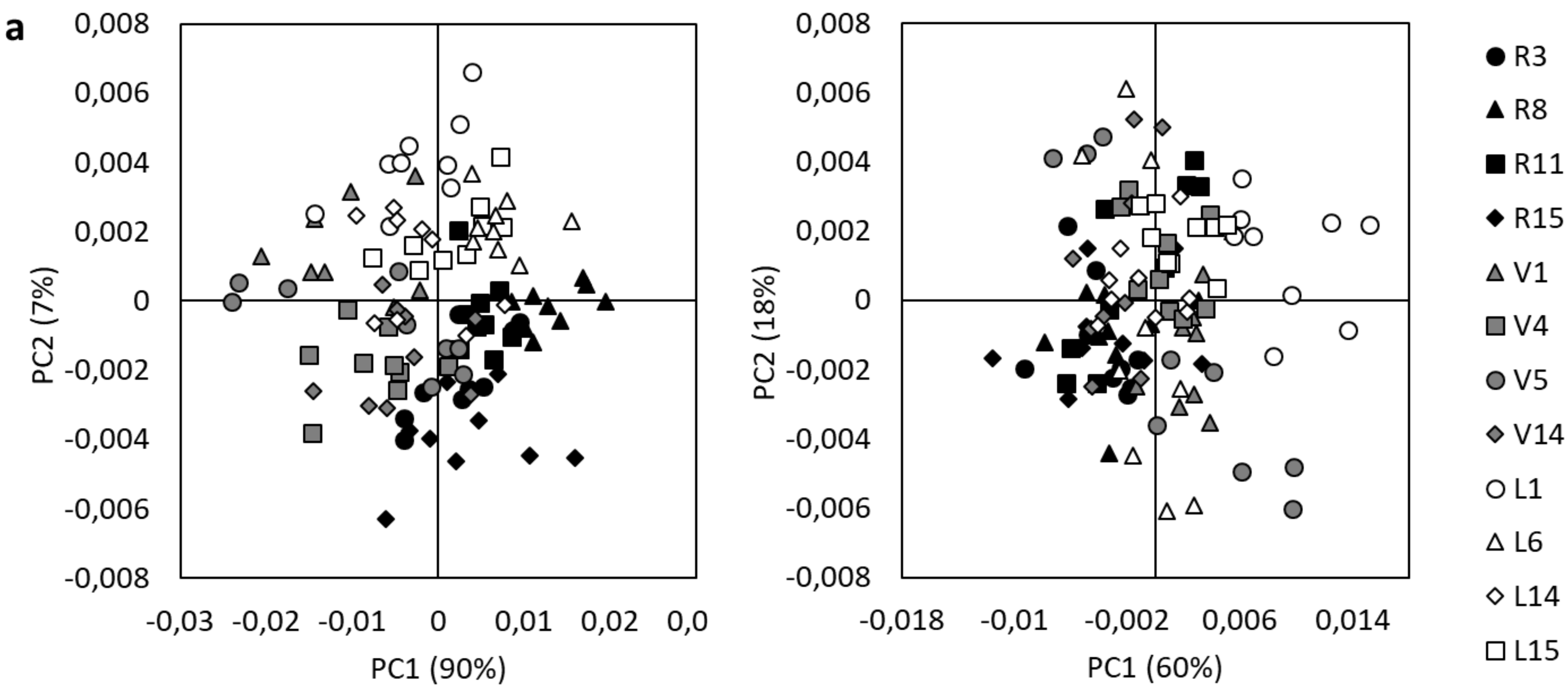


Fig. 1. Principal component analysis (PCA) (*a*) VNIR and (*b*)SWIR scatterplot of the genotypes, based on leaf reflectance (*n* = 9 replicates for genotype). Genotypes are indicated by symbols and provenances are indicated by colors.

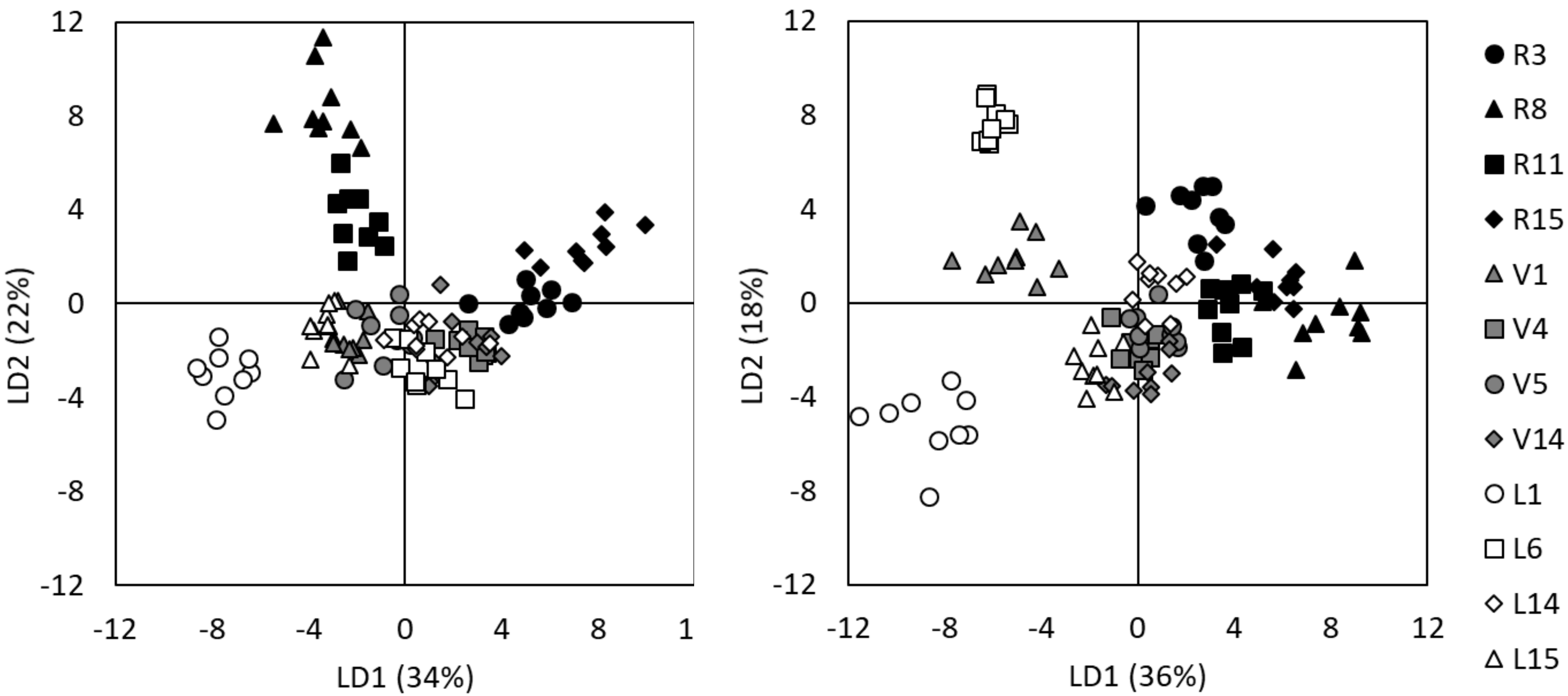


Fig. 2. Discriminant analysis of principal components(DAPC) (*a*) VNIR and (*b*) SWIR scatterplot of the genotypes, based on leaf reflectance (*n* = 9 replicates for genotype). Genotypes are indicated by symbols and provenances are indicated by colors.

2015 and 2016 imaging results compared

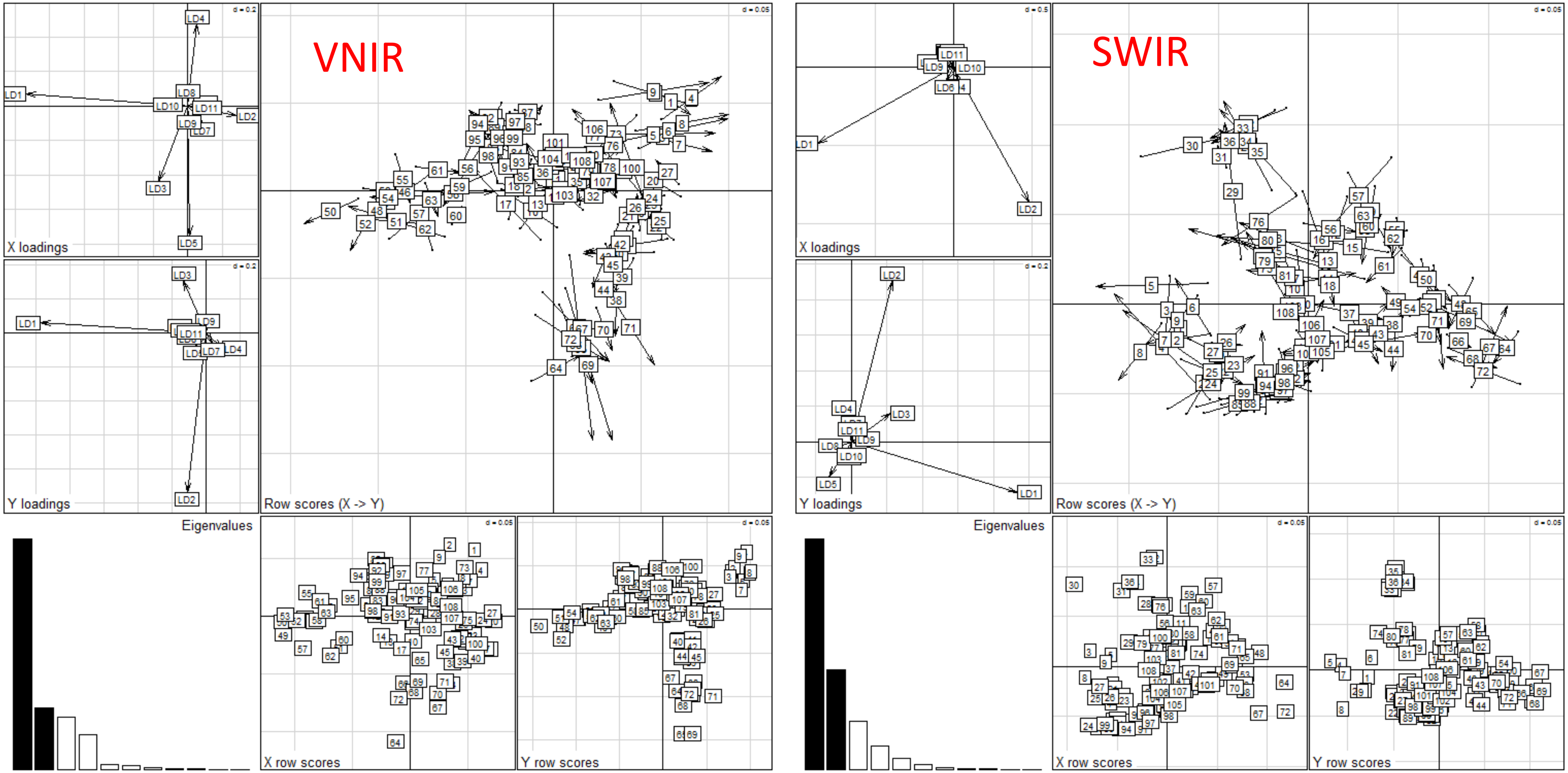
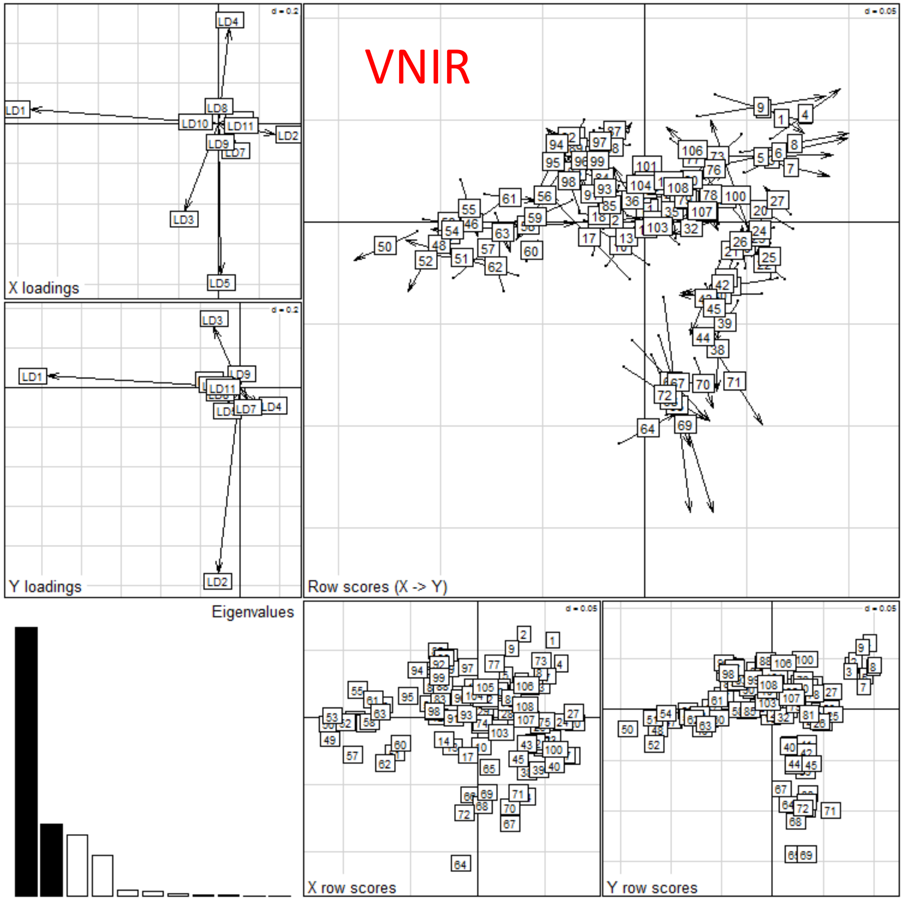
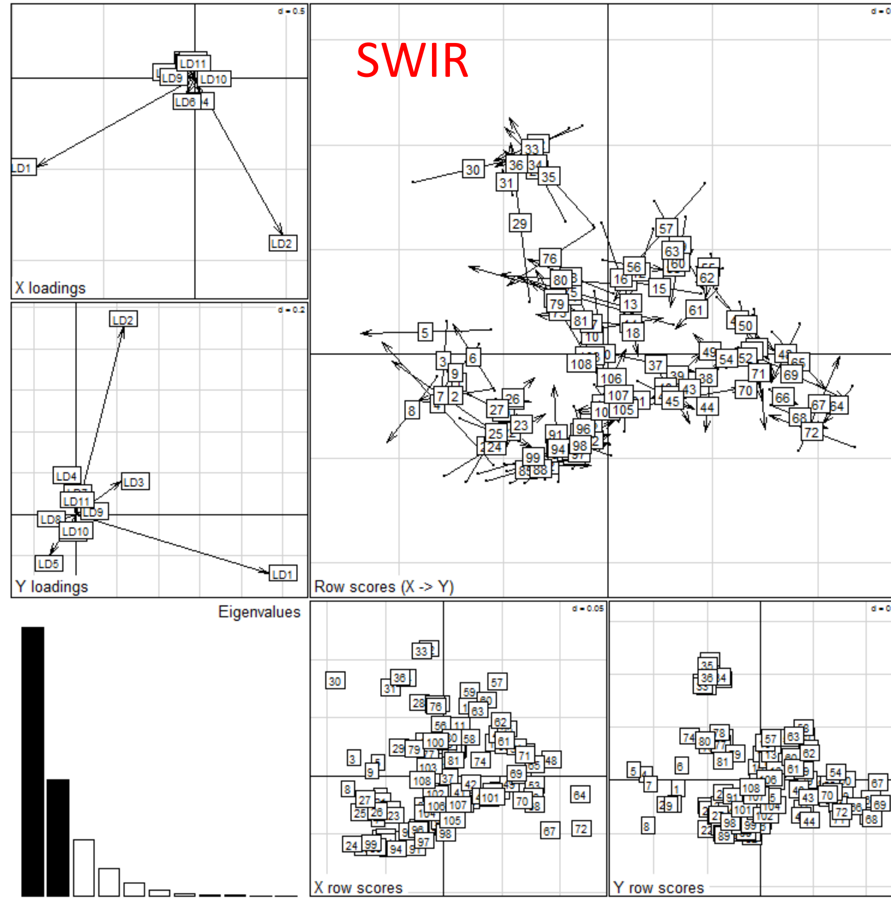
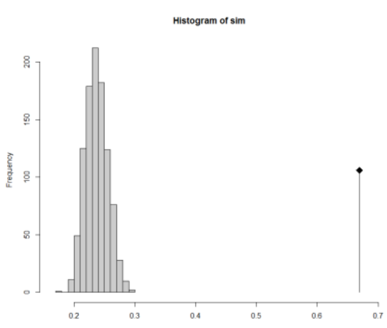


Fig. 5. Procrustes analysis of (a) 2015 and 2016 VNIR variables and (b) 2015 and 2016 SWIR variables. Plots include the loadings (X & Y), eigenvalues screeplot, scores (X and Y row) of the datasets and the projection of the two datasets after rotation. The arrows link the 2015 variable scores to the 2016 variable scores.

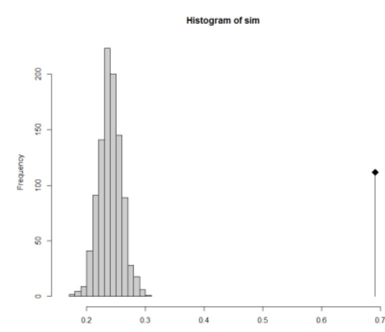
2015 and 2016 imaging results compared







M2: 0.29
T0: 0.551
P-value: 0.001



M2: 0.32
T0: 0.522
P-value: 0.001

Leaf surface chemical composition

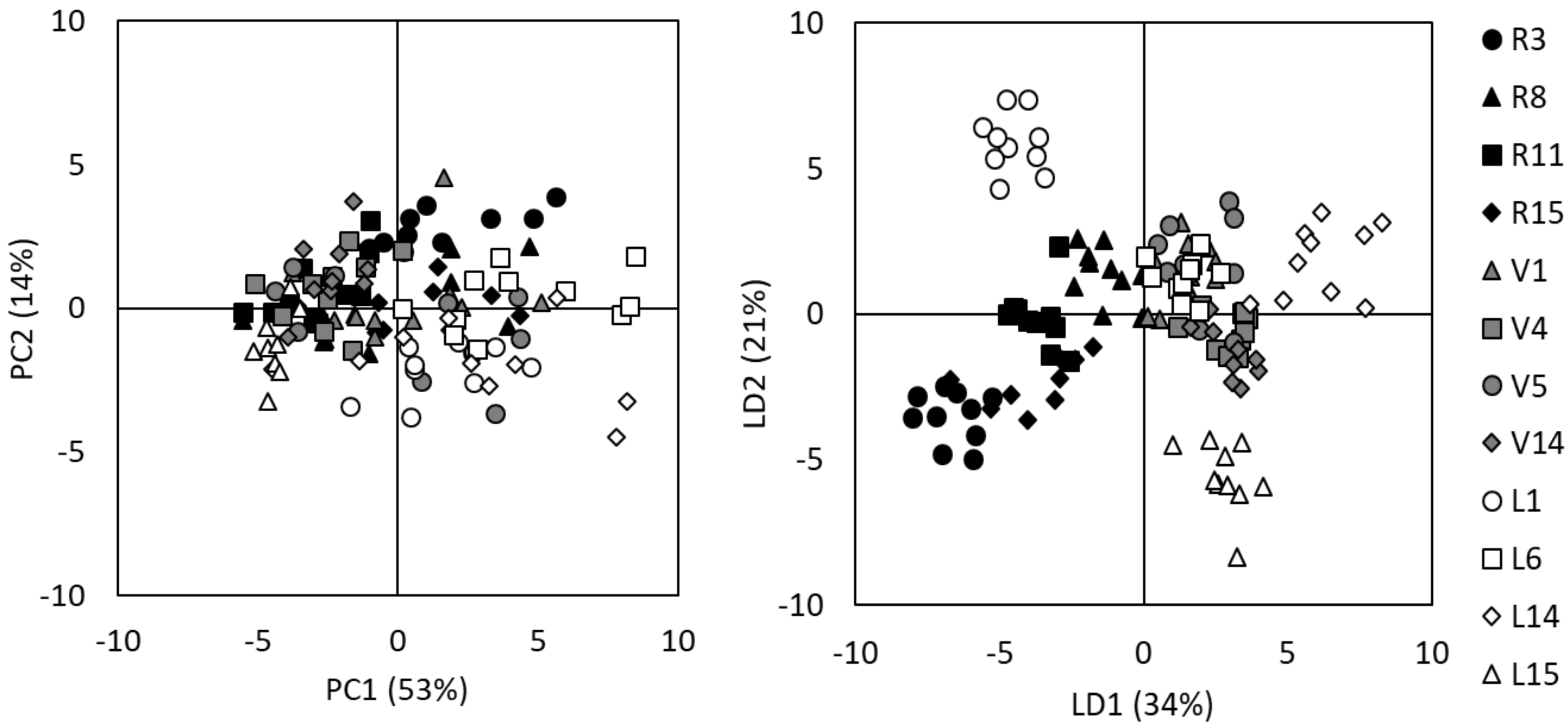
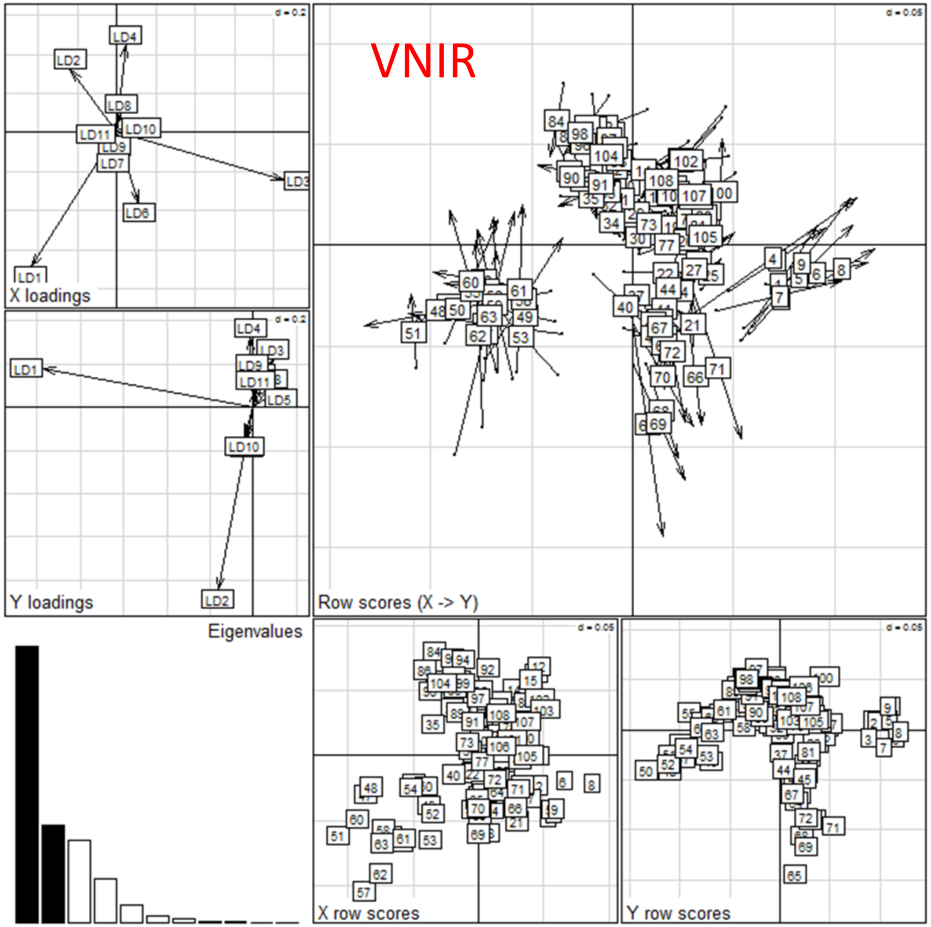
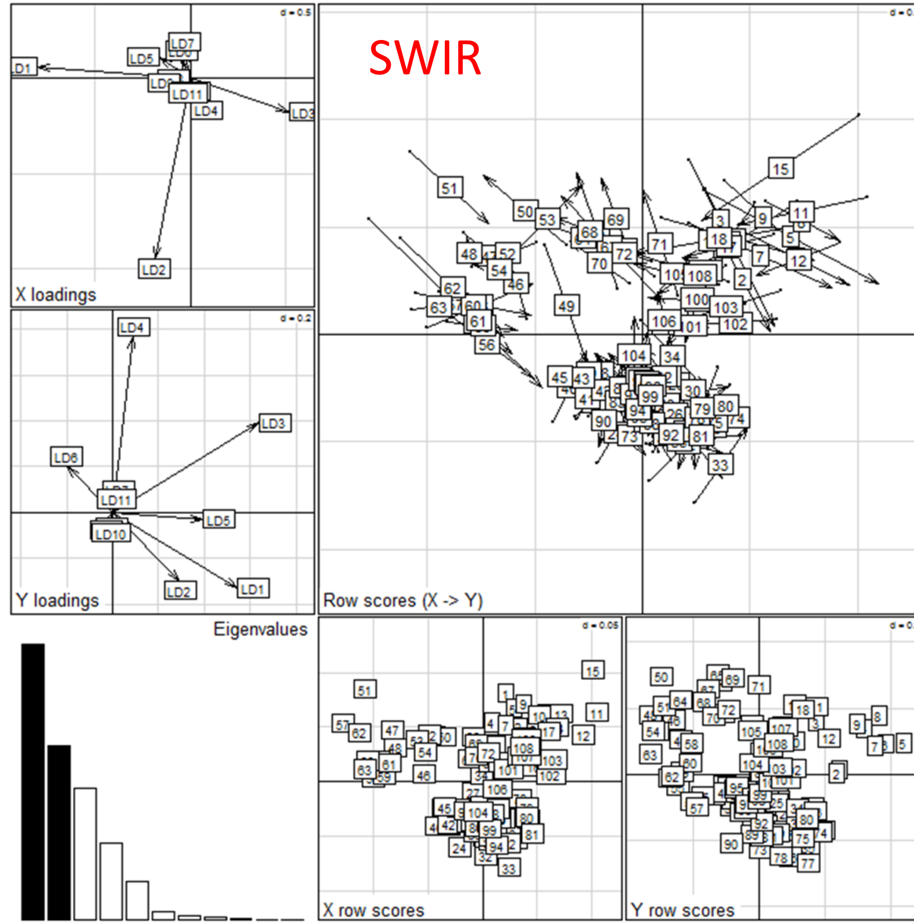
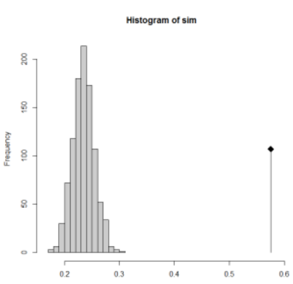


Fig. xx. Principal component analysis (PCA) and linear discriminant analysis (LDA) scatterplots of the Silver birch genotypes, based on leaf surface metabolites (*n* = 9–10 for genotype). Provenances are indicated by colors and genotypes within provenances by different symbols.

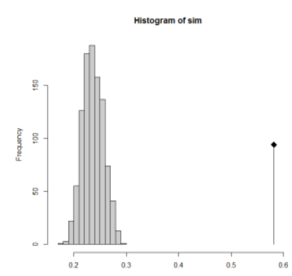
Leaf surface chemistry (2013) and hyperspectral data (2016) compared





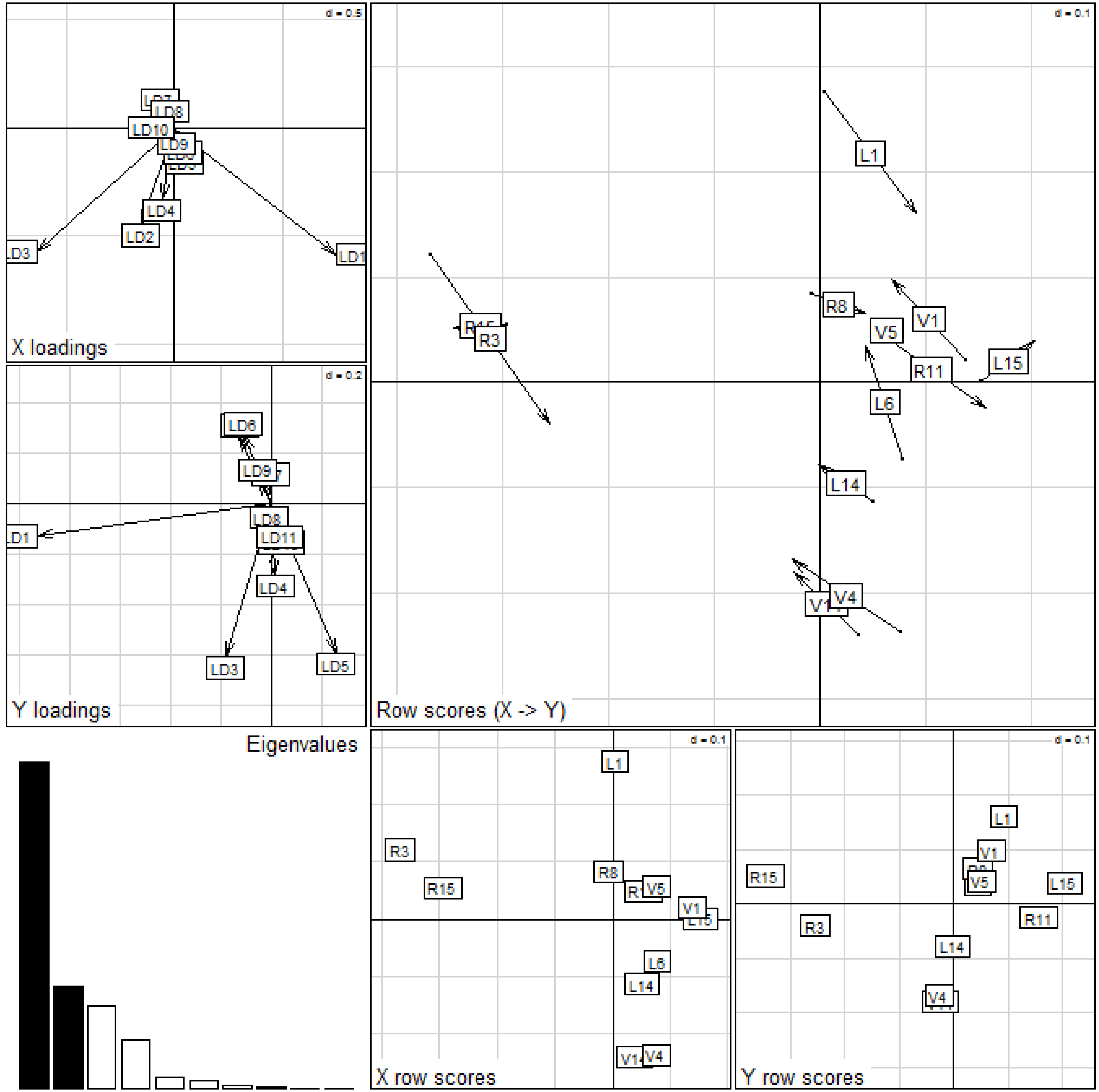


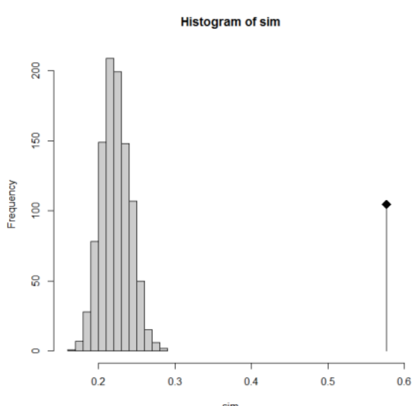
M2: 0.32
T0: 0.67
P-value: 0.001



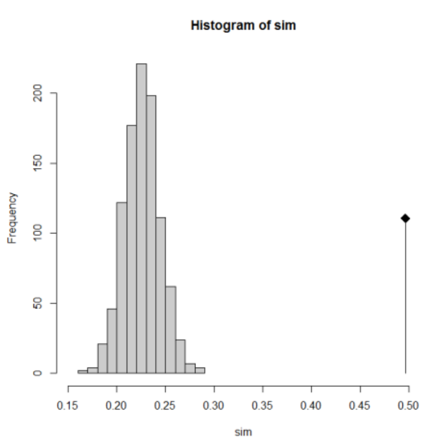
M2: 0.29
T0: 0.66
P-value: 0.001

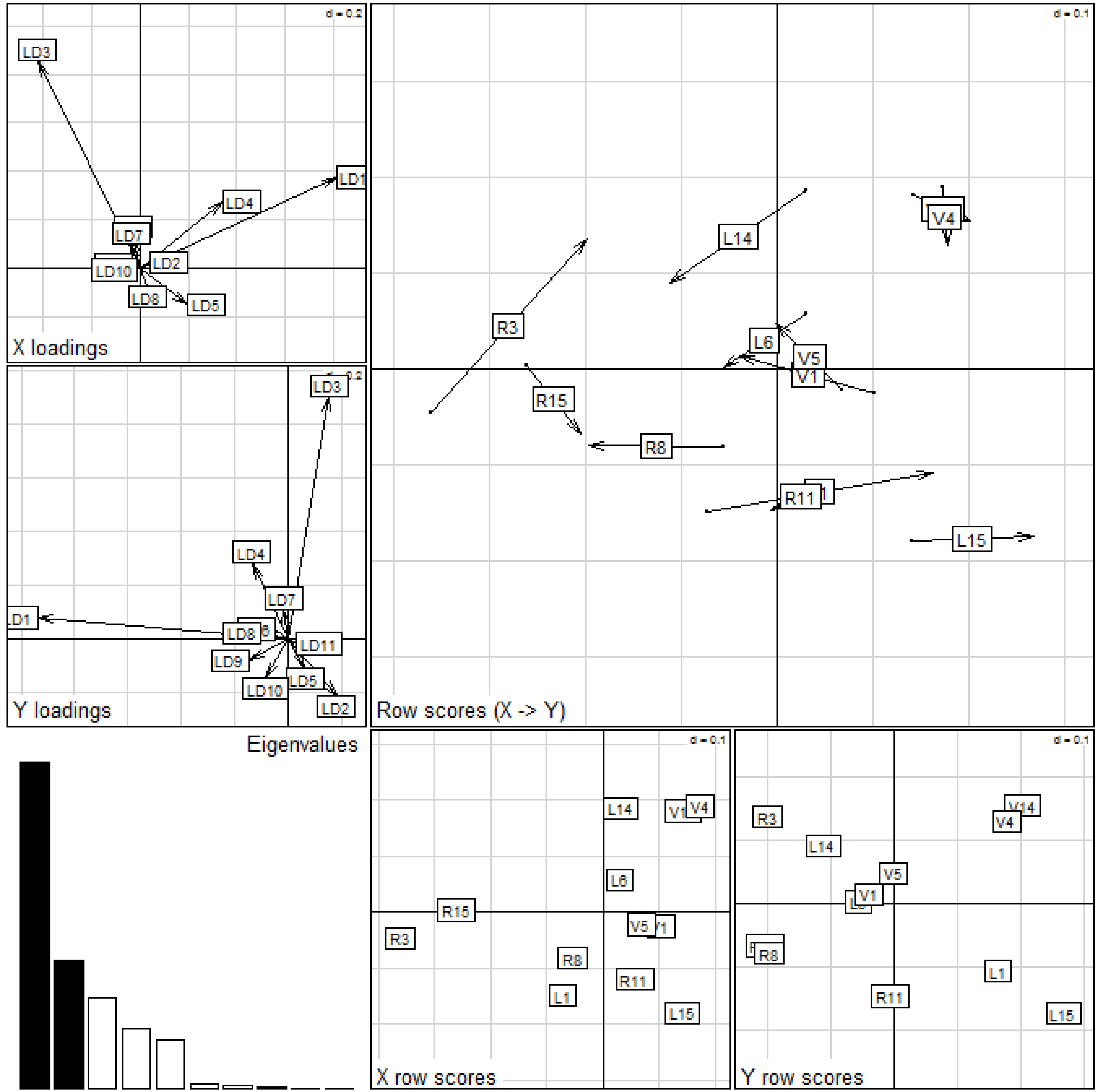
Leaf surface chemistry (2013) and VNIR hyperspectral data (2015) compared





Leaf surface chemistry (2013) and SWIR hyperspectral data (2015) compared

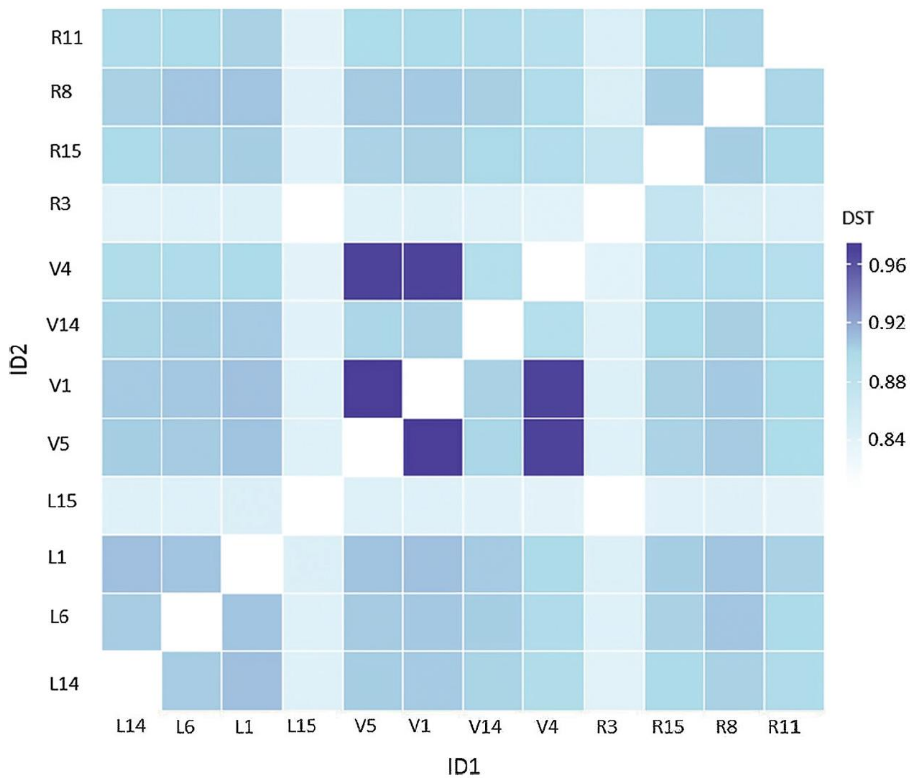




Next step: relationships of chemical and hyperspectral results with genetic data: single-nucleotide polymorphisms

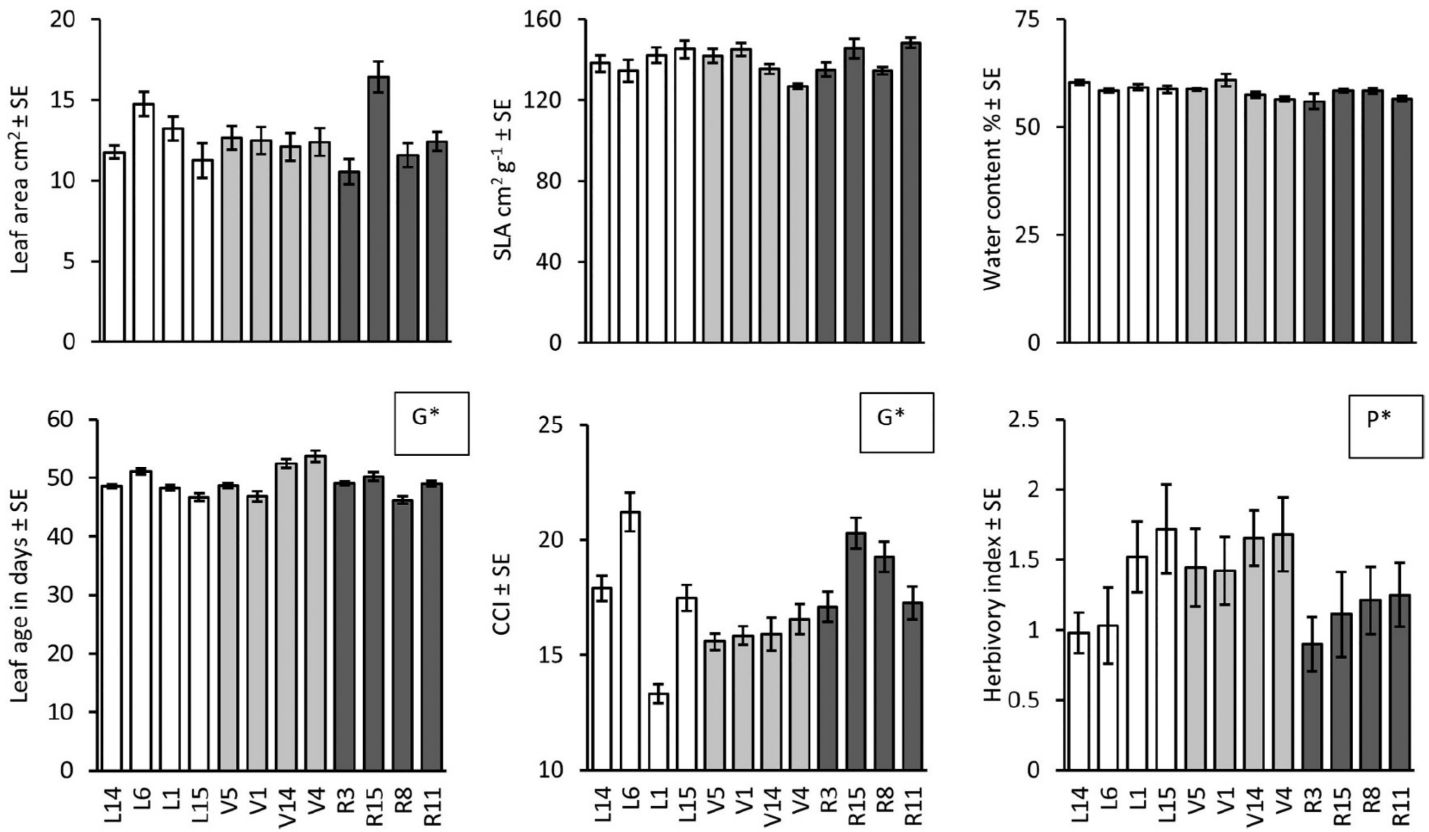
A heatmap of pairwise identity by descent (IBD) values for the genotypes, illustrating the genetic relatedness

High value means high similarity



Single nucleotide polymorphism (SNP) data for the 12 individuals were extracted from the SNP dataset estimated from low coverage Illumina whole genome sequencing of 86 silver birch individuals and the GATK pipeline, as described in (Salojärvi et al. 2017).

Work in progress: how to relate the hyperspectral data with leaf area, SLA, water content, chlorophyll content, herbivory data etc.



Work in progress: how to relate the hyperspectral data with leaf area, SLA, water content, chlorophyll content, herbivory data etc.

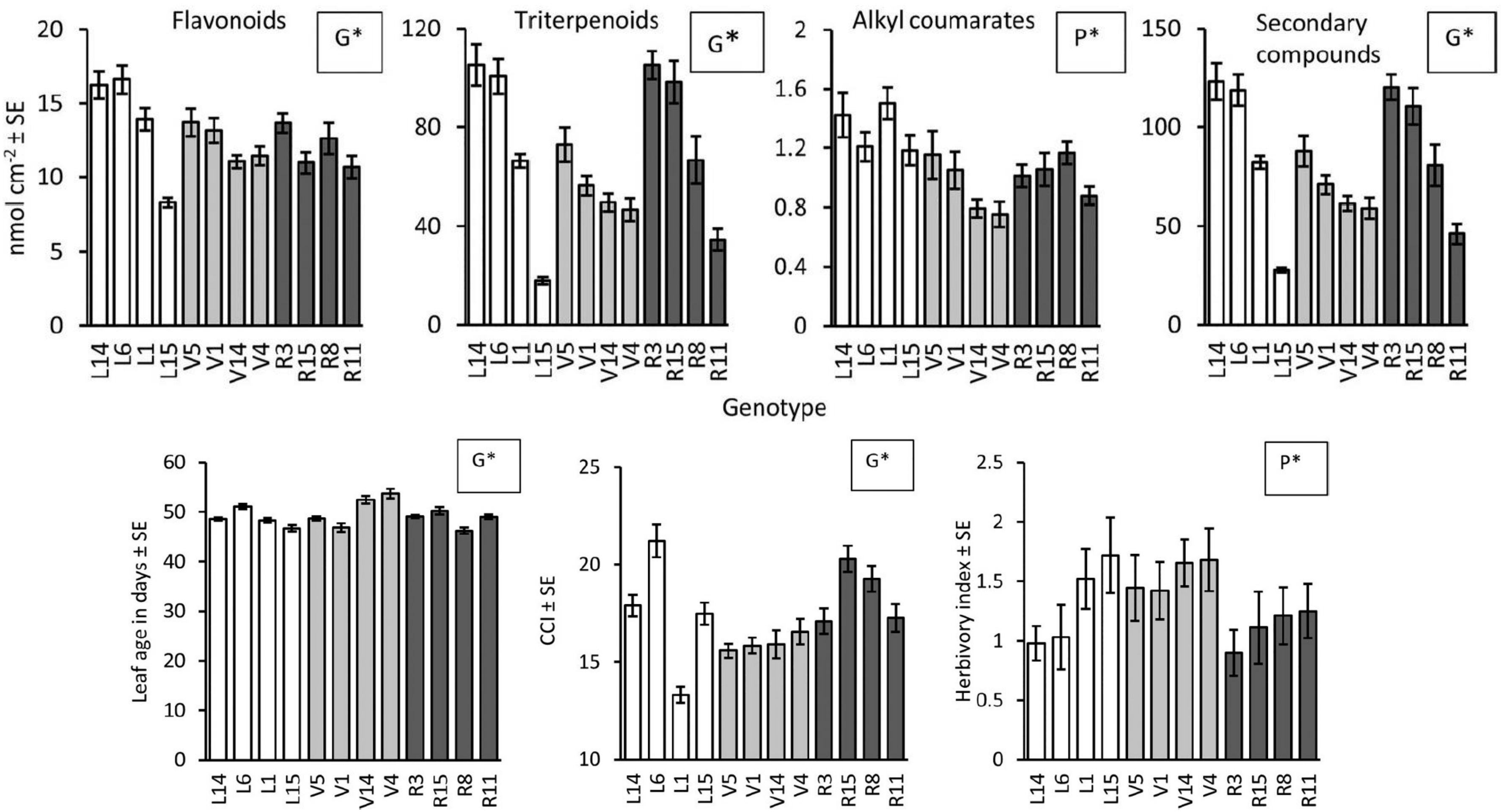


Table 2. Correlation coefficients between herbivory indices during early summer, midsummer, and early summer and midsummer combined and the contents of secondary metabolite groups.

Secondary metabolites	Herbivory index: Early summer	Midsummer	Early summer + midsummer
Triterpenoids	–0.198*	–0.087	–0.183*
Flavonoids	–0.213*	–0.033	–0.136
Alkyl coumarates	–0.092	0.079	–0.021
β-Sitosterol	–0.039	–0.089	–0.072
Total	–0.249**	–0.084	–0.180

Note: The relationship between herbivory indices and leaf surface secondary metabolites was determined by Spearman correlation: *, $p < 0.05$; **, $p < 0.01$. Herbivore surveys were performed in May and July in 2011 and 2012, and leaf surface secondary metabolite contents was determined in June 2013. Early summer, midsummer, and early and midsummer combined were calculated from the means of 2011–2012.

Thank you

This is groupwork:

Elina Oksanen
Laure Fauch
Sarita Keski-Saari
Maya Deepak
Lars Granlund
Antti Tenkanen

Actively looking for collaboration with researchers and companies

ACADEMY OF FINLAND

NATIONAL PLANT PHENOTYPING INFRASTRUCTURE

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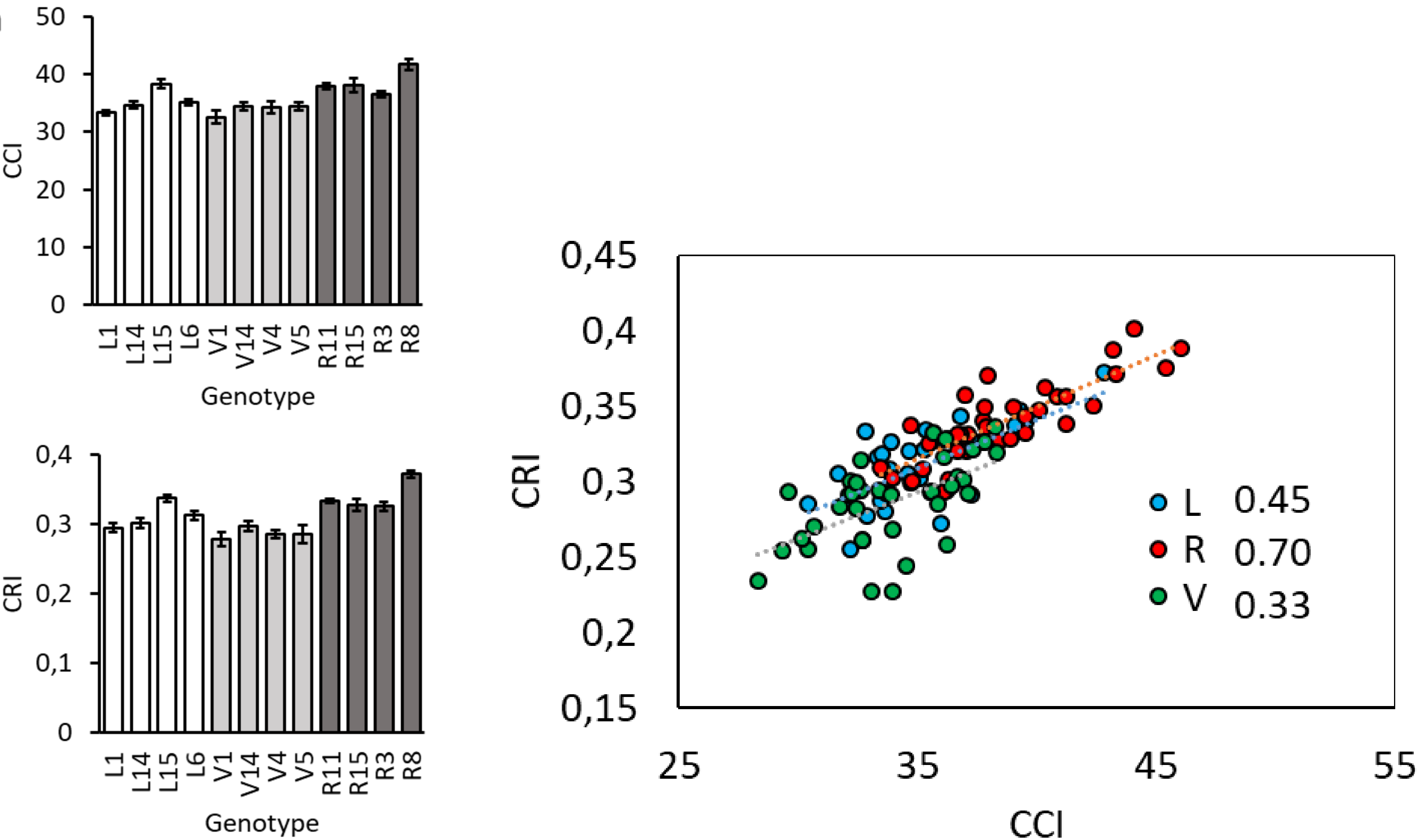
a


CCI
50
40
30
20
10
0
L1 L14 L15 L6 V1 V14 V4 V5 R11 R15 R3 R8
Genotype
CRI
0,4
0,3
0,2
0,1
0
L1 L14 L15 L6 V1 V14 V4 V5 R11 R15 R3 R8
Genotype
CRI
0,45
0,4
0,35
0,3
0,25
0,2
0,15
25
35
45
55
CCI
L 0.45
R 0.70
V 0.33