Title: Comparative metabolomics and molecular phylo-genetics of melon (*Cucumis melo*, Cucurbitaceae) biodiversity

Authors: Moing et al.

Journal: Metabolites

Supplementary figures, S1-S4

A)
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CLUSTAL O(1.2.4) multiple sequence alignment


PI435288        AGCAAGCGTAAAATTTTCCAGGTAAAAAGCTAGGATCCRGTATAAACCGATATAAACGAA        60
FAQ             AGCAAGCGTTCAATTTTCCAGCTAAAGGGGTAGGATCCGRTATAGGCCGATACAAACGTG        60
PMR45           AGCAAGCGCAAAATTTTCCACCTCGTGGGCTAGGATTTAGTAAAAACCGACACAAAGGTA        60
HBJ             AAATGGCGCAAAATTTTCCACCTCGTGGGCTAGGATTTAGTAAAAACCGATATAAACGAA        60
BES             AAATGGCGCAAAATTTTCCAGCTAAAGGGCTAGGATTTAGTAAAAACCGATATAAACGAA        60
OHG             AAATGGCGCTCTATTCCTTAGCTAAAAAGCTCGGACCCGRCAAAAAYSRRTRTMWRCGAA        60
FRC             AAATGGCACTCTATTCCTTAGCTAAAAAGCTCGGACCCGRCAAAAACCGATATAAACGAA        60
BSK             AAATGGCGCTCTATTCCTTAGCTAAAAATCTCGGACCCGGCAAAAACCGATATAAACGAA        60
PI149169        TATAARYGCAMAATTTTCCACCTCGTAATCTCAAGTCYGGTGCAGACCGATACAAACGAA        60
STA             AGCAAGCGCACTATTCCTTACCTCGTGGGCTAGGATCCGGTATAGGCCGATATAAACGAA        60
CRE             AGCAAGCGCAAAATTTTCCACCTCGTGAGCTAGGATCCGGTAAAAACCGATATAAACGAA        60
PI334107        TATAAATGCAAAATTTTCCACCTCGTGAGCTAGAATCCGGTAAAAACCGATATAAACGAA        60
PI201581        TATAAATGCAAAATTTTCCACCTCGTGAGCTAGGATCCGGTAAAAACCGATATAAACGAA        60
PSR             AAATGGCGCAAAATTTTCCACCTCGTGAGCTAGGATCCGGTAAAAACCGATATAAACGAA        60
HDG             AAATGGCGCAAAATTTTCCACCTCGTGAGCTAGGATCCGGTAAAAACCGATATAAACGAA        60
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PI435288        ACTAGCTCAAGCGSYGWYRGTTAATAGGCCCGCCATTGACTATGWMCWWGGSTGRY        116
FAQ             ACTATTCCAAGCAGCGTCGGGTAATAGGCCCGCCATTGGTCACATCCATGGCTGAT        116
PMR45           ACTATTCCAAGCRCCGTCGGGTGATAAGCCCGCCATTGACTATGATCATCGGTGGC        116
HBJ             ACTATTCCAAGCGCCGTCGGGTRATARGCCCGCCATTGACTATGWMCWWCGGTGGC        116
BES             TCCATTCCAAGCAGCGTCGRGTRATARGCCCGCCATTGACTATGTACTTCGGTGGC        116
OHG             ACTAGCTCAATTGSCCTCAGTGAGAGGATATAATGGCAACTATGTGTAACGGTGGC        116
FRC             ACTAGCTCAATCGGCGTCAGTGAGAGGATCYGCYRKYRACTACGTGTAACGGTGGC        116
BSK             ACTAGCTCAATCGGCGTCAGTGAGAGGATCCGCCATTGACTACGTGTAACGGTGGC        116
PI149169        WCYATTCCGATCGGCGTCAGTTAATAGGCATAATGGCAACTATGTACTTCAGTGGC        116
STA             ACTAGCTCAAGCGGYGTYAGTTAATAGGCATAATGGCAACTATGTACTTCGGTGGC        116
CRE             ACTATTCCAAGCGGCGTCAGTGAGAGGATATAATGGCAACTATGATCATCGGTGGC        116
PI334107        ACTAGCTCAAGCGGCGTCAGTGAGAGGATATAATGGCAACTATGATCATCGGTGGC        116
PI201581        ACTAGCTCAAGCGGCGTCAGTGAGAGGATATAATGGCAACTATGATCATCGGTGGC        116
PSR             ACTAGCTCAAGCGGCGTCAGTGAGAGGATATAATGGCAACTATGATCATCGGTGGC        116
HDG             ACTAGCTCAAGCACCGTCGGTGAGAGGATATAATGGCAACTATGATCATCGGTGGC        116
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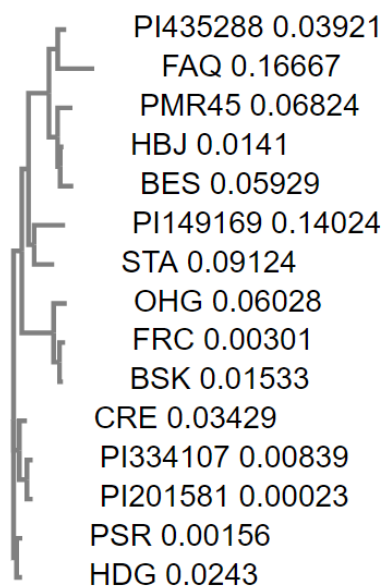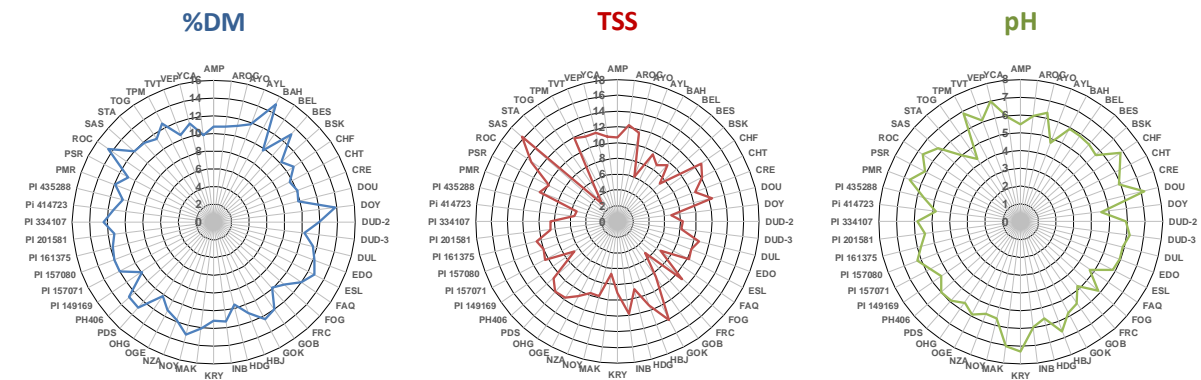
B)

Figure S2. Classification of the seven accessions not included in the GBS analysis. A) Clustal alignment of the 116bp haplotype of the seven accessions together with GBS-analyzed closely related accessions. B) Phylogenetic tree developed by Neighbor-Joining method. Clustal Omega: https://www.ebi.ac.uk/Tools/msa/clustalo/

a)

Overview (n=52)	DM content (%)	TSS (°Brix)	pH
Mean	11.50	9.72	5.89
Min	9.60	3.00	4.27
Max	15.00	16.20	7.31
CV (%)	10.42	26.16	11.02

b)

Figure S2. Variability of the 52 melon accessions for fruit quality global measurements: fruit flesh percent dry matter (%DM), and fruit juice total soluble solids (TSS) and pH. CV, coefficient of variation. a) radar plots for the 52 accession samples. b) overview.
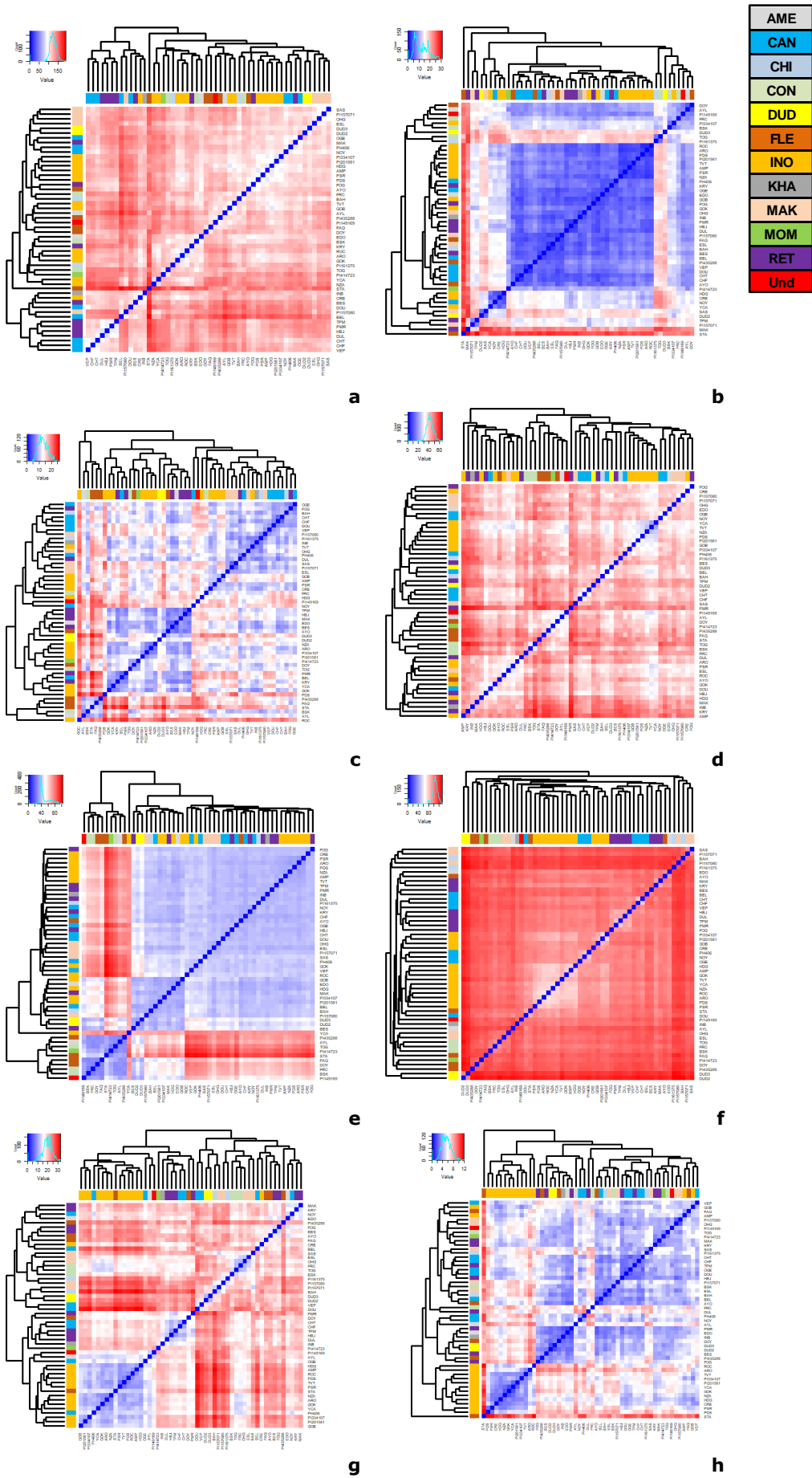
a

b

c

d

e

f

g

h

Figure S3. Hierarchical clustering analysis of the 52 melon accession samples based on each analytical platform for fruit flesh with Euclidian distance and complete linkage. Each subfigure represent an accession dendrogram with heatmaps for accession x accession distances. The colored bar close to the dendrogram indicates accession groups. The distribution of distances is presented on the upper left side of each subfigure. a) GC-MS of polar extracts; b) ^{1}H-NMR profiles of polar extracts; c) ^{1}H-NMR fingerprints of polar extracts; d) ^{1}H-NMR fingerprints of semi-polar extracts; e) DI-MS of semi-polar extracts; f) LC-QTOF-MS of semi-polar extracts; g) SPME-GCMS of volatile compounds; h) ICP-MS of micronutrients.
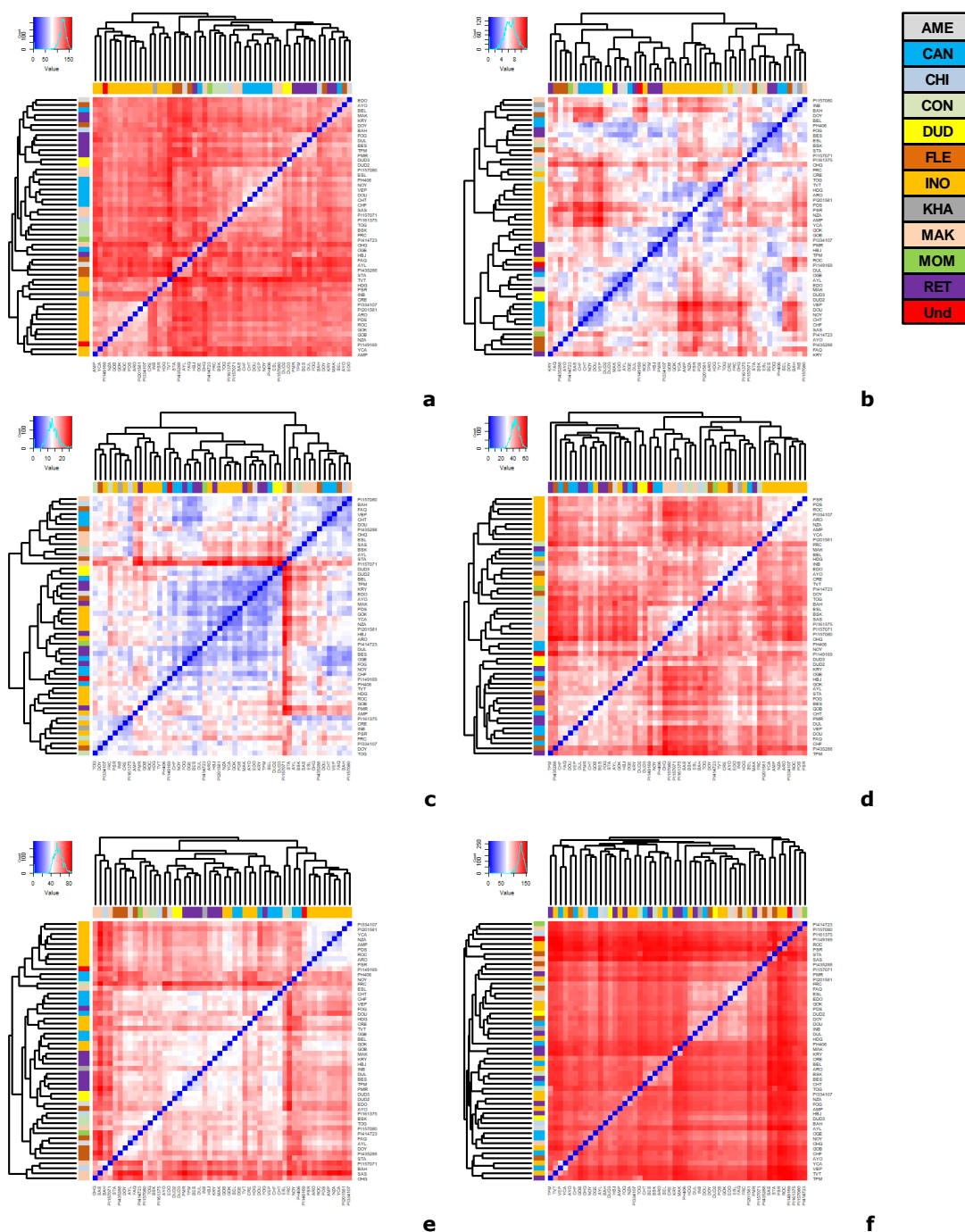
Figure S4. Hierarchical clustering analysis of the 52 melon accession samples based on each analytical platform for fruit peel with Euclidian distance and complete linkage. Each subfigure represent an accession dendrogram with heatmaps for accession x accession distances. The colored bar close to the dendrogram indicates accession groups. The distribution of distances is presented on the upper left side of each subfigure. a) GC-MS of polar extracts; b) ^{1}H-NMR profiles of polar extracts; c) ^{1}H-NMR fingerprints of polar extracts; d) ^{1}H-NMR fingerprints of semi-polar extracts; e) DI-MS of semi-polar extracts; f) LC-QTOF-MS of semi-polar extracts