

Supplementary information

Figure S1. Global distribution of lingonberry in different parts of the world



Figure S2. Mechanism of DNA methylation using Methylation Sensitive Amplification Polymorphism (MSAP) assay

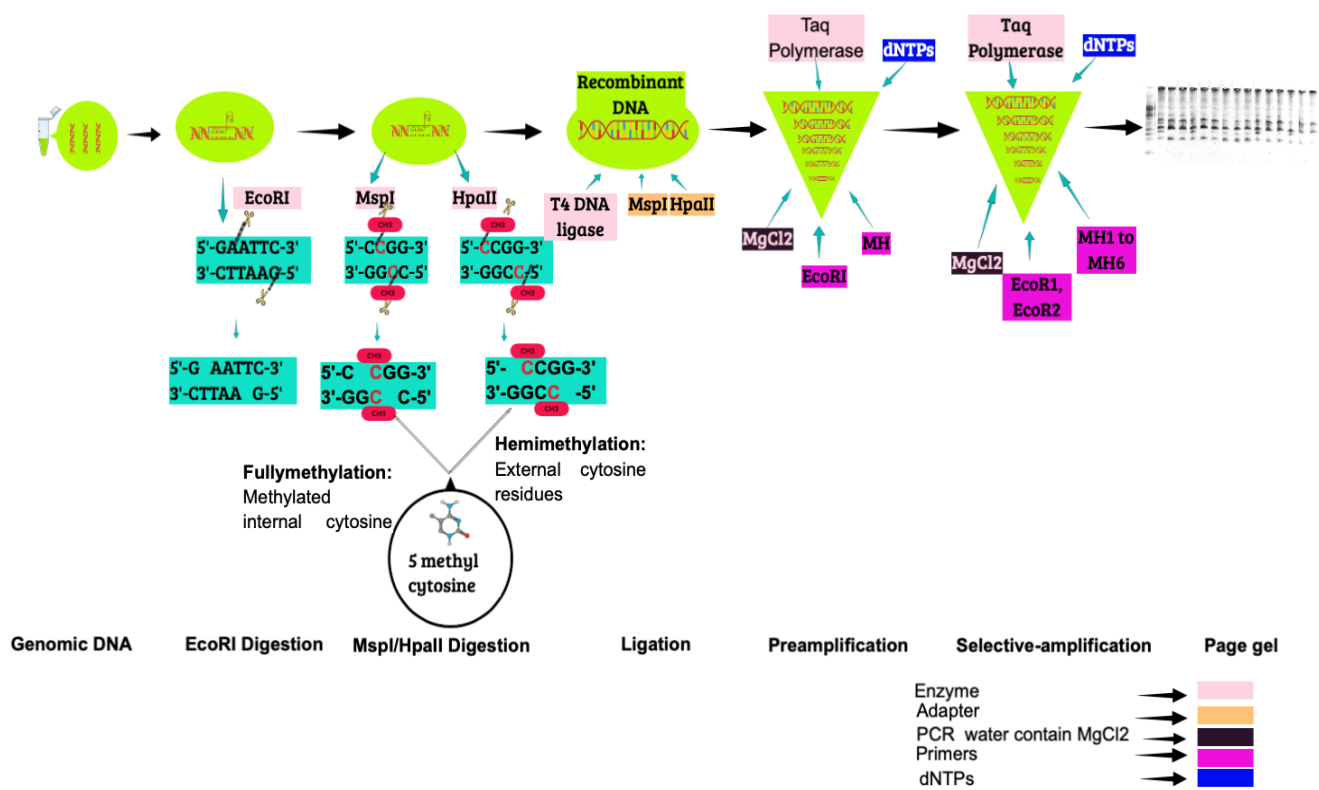


Table S1. Sequences of adapters and primers performed in MSAP assay

Adapters:	
EcoRI:	5'- CT GTA GAC TGC GTA CC -3'
	3'- CA TCT GAC GCA TGG TTAA -5'
MspI-HpaII:	5'- GA TCA TGA GTC CTG CT -3'
	3'- AG TAC TCA GGA CGA GC -5'
Pre-selective primers:	
EcoRI:	5'- GAC TGC GTA CCA ATT CA -3'
MspI-HpaII (MH):	5'- ATC ATG AGT CCT GCT CGG -3'
Selective primers:	
EcoRI 1:	5'- GAC TGC GTA CCA ATT CAC G -3'
EcoRI 2:	5'- GAC TGC GTA CCA ATT CAC T -3'
MH1:	5'- ATC ATG AGT CCT GCT CGG AAT -3'
MH2:	5'- ATC ATG AGT CCT GCT CGG ACT -3'
MH3:	5'- ATC ATG AGT CCT GCT CGG TCC -3'
MH4:	5'- ATC ATG AGT CCT GCT CGG AAC C -3'
MH5:	5'- ATC ATG AGT CCT GCT CGG CGA A -3'
MH6:	5'- ATC ATG AGT CCT GCT CGG TAG C -3'

Table S2. Summary of total number of bands, number and percentage (%) of DNA methylation events detected by methylation sensitive amplification polymorphism (MSAP) technique using twelve selective primer combinations in five samples of lingonberry.

Those samples were derived from cutting cultivar Erntedank (ED) and micropropagation methods (NC node culture and LC leaf culture). NC1 node culture derived in vitro-grown shoots from liquid media, NC2 node culture derived in vitro-grown shoots from semi-solid media, NC3 node culture derived greenhouse-grown plant and LC1 leaf culture derived greenhouse-grown plant.

Combinations of Selective Primers		NC1			NC2			NC3			LC1			ED		
		fmet	hmet	nmet	fmet	hmet	nmet	fmet	hmet	nmet	fmet	hmet	nmet	fmet	hmet	nmet
Ecor1-G AAT	MH1-	3	3	6	3	2	6	2	1	7	3	3	7	3	3	8
Ecor2-T AAT	MH1-	5	4	6	4	6	7	5	5	8	9	6	4	5	7	4
Ecor1-G ACT	MH2-	0	1	5	2	2	4	4	4	4	1	2	4	2	2	3
Ecor2-T ACT	MH2-	4	3	9	4	2	10	8	4	6	3	9	1	5	1	9
Ecor1-G TCC	MH3-	3	4	7	2	4	8	3	3	7	4	4	7	3	3	4
Ecor2-T TCC	MH3-	2	2	4	4	2	3	3	2	5	3	8	2	2	4	2
Ecor1-G AAC C	MH4-	4	4	4	2	3	6	3	3	6	5	6	4	6	6	3
Ecor2-T AAC C	MH4-	4	2	7	4	3	5	3	2	8	5	7	7	3	2	6
Ecor1-G CGA A	MH5-	1	2	9	2	3	7	0	1	9	2	3	6	4	2	6
Ecor2-T CGA A	MH5-	3	4	2	4	4	4	2	4	6	6	7	2	6	4	2
Ecor1-G TAG C	MH6-	3	3	4	3	4	4	0	0	7	3	3	4	3	3	4
Ecor2-T TAG C	MH6-	5	5	1	2	3	6	3	3	7	2	4	6	0	0	6
Total bands of 3 set of methylated sites (fmet, hmet and nmet)		37	37	65	36	38	70	36	32	80	46	62	54	42	37	57
Total bands of in vitro-grown shoots and greenhouse-grown plant		139			144			148			162			136		
Total methylation (%) of in vitro-grown shoots and greenhouse-grown plant		56.92	56.92	46.76	51.42	54.28	48.61	45.00	40.00	54.05	85.18	114.81	33.33	73.68	64.91	41.91
Total methylated polymorphisms of in vitro-grown shoots and greenhouse-grown plant		51			52			46			80			64		

Table S3. Data were performed for expressing the relationship between cytosine methylation and secondary metabolites

Propagated Plants	Fmet	Hmet	Nmet	TPC	TPrC	TFC	TAC
NC 1	56.9200	56.9200	46.7600	3.7913	0.0034	2.3293	0.0350
NC 2	51.4200	54.2800	48.6100	2.4827	0.0018	2.7103	0.0427
NC 3	45.0000	40.0000	54.0500	7.5850	0.0025	2.7103	0.0357
LC 1	85.1800	114.8100	33.3300	7.5843	0.0013	1.6760	0.0353
ED	73.6800	64.9100	41.9100	7.5843	0.0049	2.9557	0.0350