Genome size variation in *Deschampsia cespitosa* sensu lato (Poaceae) in Eurasia

Plant Systematics and Evolution

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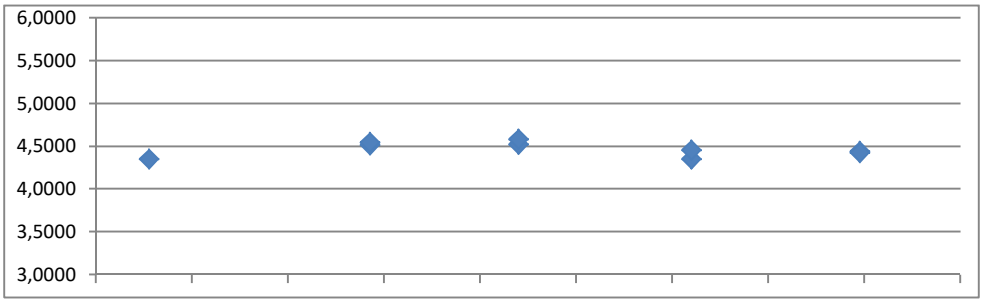
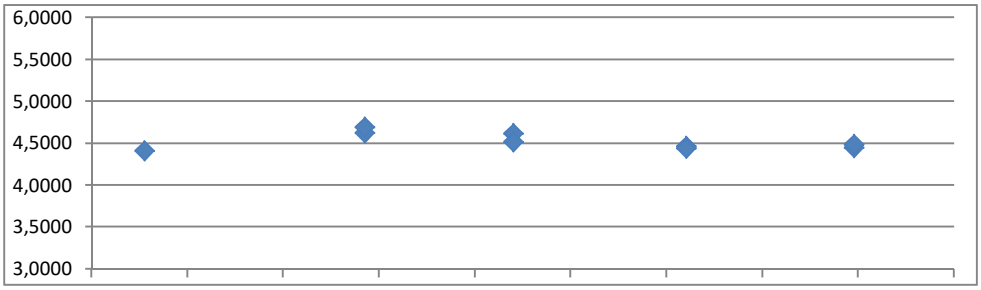
Online Resource 1. Performance test of two *Deschampsia cespitosa* samples in FCM analysis during five months.

The first analysis was performed with fresh material. The variation of 1 C values (pg) in the second and subsequent analyses under different drying conditions is shown in the following table and in the diagrams below. We have tested drying under warm/cold air conditions: wa - dried in warm air (2-3 days) and stored afterwards at room temperature; rt - dried and stored only at room temperature.

Date	Acc.nr	1C-value	S.D.	N	Material	Acc.nr	1C-value	S.D.	N	Material
29.09.2014	Rax 1	4,3488	0,0083	3	fresh	Rax 2	4,4076	0,0038	3	fresh
14.11.2014	Rax 1	4,5174	0,0072	3	wa	Rax 2	4,6244	0,0095	3	wa
14.11.2014	Rax 1	4,5422	0,0064	3	rt	Rax 2	4,6923	0,0081	3	rt
15.12.2014	Rax 1	4,5196	0,0028	3	wa	Rax 2	4,6161	0,0092	3	wa
15.12.2014	Rax 1	4,5822	0,0098	3	rt	Rax 2	4,5150	0,0117	3	rt
20.01.2015	Rax 1	4,3541	0,0148	3	wa	Rax 2	4,4649	0,0075	3	wa
20.01.2015	Rax 1	4,4575	0,0095	3	rt	Rax 2	4,4366	0,0154	3	rt
24.02.2015	Rax 1	4,4393	0,0094	3	wa	Rax 2	4,4481	0,0036	3	wa
24.02.2015	Rax 1	4,4218	0,0117	3	rt	Rax 2	4,4855	0,0117	3	rt



Performance Rax 1 (y-axis: 1C pg; x-axis: time)



Performance Rax 2 (y-axis: 1C pg; x-axis: time)

In relation to the fresh average (1C = 4.3782 pg) of the two samples all dried values were slightly higher with the mean ratio (dried/fresh) for measures on day 46 and 77 of 1.0452 ± 0.0147 which decreased to 1.0138 ± 0.009 for the values found day 113 and 148.

Using a small number of fresh materials (see Table 1) had a minor effect on statistics. Assuming also dry material would have been used for the 8 diploid European samples processed from fresh material may have added ca 3% (average of 1.4 and 4.5 % according to the storage intervalls in the test) to their genome size and an increase in the median of all European samples from 4.377 to 4.394 pg (1C). For the European tetraploids the median genome size of all samples of 4.314 pg would remain unchanged. Magnitudes of significances remain unchanged.