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## Electronic Supplementary Material

### Genet dynamics and its variation among genets of a clonal plant *Convallaria keiskei*

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## Appendix I

### Technical details in statistical estimation

#### S1.1 Logistic regression model for estimating clonal growth $C_j^h$

In order to estimate  $C_j^{1\text{-y-tip}}$  and  $C_j^{2\text{-y-tip}}$ , pooling the four growing seasons (2006 summer to 2009 summer), the logistic regression model was applied in which covariates were age-positions and sizes classes and the objective variable was the presence/absence of clonal growth:

$$y = 1 / \{1 + \exp(a^1 x^1 + a^2 x^2 + a_1 x_1 + \dots + a_5 x_5)\}$$

where  $x^1$  and  $x^2$  were dummy variables of age-position (1-y-tip and 2-y-tip, respectively),  $x_1, \dots, x_5$  were those for the five size classes, and  $a^1, a^2, a_1, \dots, a_5$  were free parameters;  $a^1$ : 1-y-tip,  $a^2$ : 2-y-tip,  $a_1$ : 1L,  $a_2$ : 2L-<10,  $a_3$ : 2L-10–15,  $a_4$ : 2L-15–20,  $a_5$ : 2L- $\geq$ 20. Because one was redundant,  $a^1$  was fixed at 0.  $C_j^h$  is given by, for example,  $C_{1L}^{1\text{-y-tip}} = 1 / \{1 + \exp(a_2)\}$ ,  $C_{2L-10-15}^{2\text{-y-tip}} = 1 / \{1 + \exp(a^2 + a_2)\}$ , and so on.

#### S1.2 Clonal growth $C_j^h$ when some information was missing

When size information was missing, depending on missing patterns, we used the following dummy variables for the size classes.

If we had no size information in year  $t$  but had in year  $t - 1$  (size class  $k$ ), we used the dummy variable as  $x_j = T_{jk}$ .

If there was no size information in year  $t$  and  $t - 1$  but had in year  $t - 2$  (size class  $k$ ), we used the dummy variable as  $x_j = (\mathbf{T}^2)_{jk}$ .

If there was no size information in year  $t$  but had in year  $t + 1$  (size class  $i$ ), we used the dummy variable as  $x_j = T_{ij} / \sum_l T_{lj}$ , i.e., the conditional probability given size class  $i$  in the subsequent year.

If there was no size information in year  $t$  but had in year  $t - 1$  (size class  $k$ ) and  $t + 1$  (size class  $i$ ), we used the dummy variable as  $x_j = T_{ij} T_{jk} / \sum_l T_{il} T_{lk}$ .

These modifications were for the following cases. Some ramets were not present in a census (year  $t$ ) but observed in the previous and the subsequent years (year  $t - 1$  and/or  $t + 1$ ). This happened probably when an aboveground shoot emerged after the census in year  $t$ , or that ramet did not produce a shoot. Because we stopped the annual census in 2007, there was no plant size information in 2008 and 2009.

### S1.3 Clonal reproduction $C_j^h$ when birth year was not identifiable

When the birth year was unknown (either 2008 or 2009), for simplicity, the same probability (0.5) was given to the two cases. This happened for new ramets in 2009.

### S1.4 Excluded cases from statistical analysis

We found isolated ramets (no rhizome was connected) and almost isolated ones (only interrupted rhizome(s) was connected). There are two possibilities; (1) at the tip and the rhizome from the mother was disappeared, (2) at the non-tip and all the rhizomes were disappeared. Because we did not have any evidence to distinguish the two, these were excluded from the logistic regression. In addition, we found new 14 buds on fragments that had no living shoot (only with interrupted rhizome or a dead ramet). These were not used in the logistic regression (S1.1), either.

Note: The clonal growth frequency of the isolated ramets was 3.2% (5 over 154, genets and size classes were pooled), which was smaller than that of almost isolated ramets (7.0%, 10 over 142), and these were smaller than that of 2-y-tip (Fig. S2 in Appendix III), but higher than branching (Table S2b). These might suggest the capability of clonal growth for a long period with slowly decreasing rates for *C. keiskei*.

### S1.5 Bayesian estimation

In order to evaluate sampling bias caused by small sample size, Bayesian statistics was applied. For the distribution of newly born ramets (**N**) and the elements in each column of the transition matrix (**T**), the multi-nominal distribution and the flat conjugate Dirichlet prior were applied. For the branching probabilities ( $C^{\text{non-tip}}$ ) and the survival (**S**), we applied the binomial distribution and the flat conjugate Beta prior. 2,000 random samples were produced from each posterior distribution (Table S2c for **N**, Table S2b for  $C^{\text{non-tip}}$  and Table S2d for **S**, Table S2e for **T**).

For the coefficients of the logistic regression of the clonal growth (the equation in S1.1), we used flat priors of wide range (-10, 10) with constrain  $a_2 \leq a_3 \leq a_4$ ,  $a_3 \leq a_5$ , which means that for ramets with two leaves (2L), larger ramets tended to reproduce more frequently and the largest two classes ( $a_4$ ,  $a_5$ ) may have similar probabilities.

The Markov chain Monte Carlo (MCMC) of the Metropolis-Hastings algorithm updated by random walk was conducted with initial values at 0. From the total 65,000 MCMC iterations, the first 5,000 iterations were discarded as a burn-in period, and every 30 was chosen to produce 2,000 MCMC samples (Table S2a). 2,000 random samples of  $C_j^h$  were produced by transforming them as  $C_{1L}^{1-y\text{-tip}} = 1/\{1 + \exp(a_2)\}$ ,  $C_{2L-10-15}^{2-y\text{-tip}} = 1/\{1 + \exp(a^2 + a_2)\}$ , and so on (Fig. S2).

**Appendix II:** Summary of data.

**Table S1a** The numbers of tip ramets performing clonal growth or not, in each age-position and the size class of the three dominant genets.

Genet	Clonal growth	1-y-tip						2-y-tip						None <sup>†</sup>	Total
		1L	2L				None*	1L	2L				None*	None*	
			< 10 cm	10 - 15 cm	15 - 20 cm	20 cm <			< 10 cm	10 - 15 cm	15 - 20 cm	20 cm <			
e-1	No	9	2	7	17	1	14	6	1	19	42	11	43	1	172
	Yes	2	0	3	9	2	17	3	1	4	16	10	23	1	90
e-2	No	2	2	9	0	0	3	1	2	20	12	2	10	0	63
	Yes	0	1	1	5	0	3	1	0	2	1	0	2	0	16
e-3	No	15	0	1	10	1	0	12	0	16	24	17	79	8	175
	Yes	3	0	0	3	1	4	2	0	0	8	4	17	5	42

\* No size information

† Age undetectable

**Table S1b** The number of clonal fragments of each fragment size (number of ramets in a fragment).

Genet	No. of ramets in a fragment*															Total
	1	2	3	4	5	6	7	8	9	10	11	15	18	22	34	
e-1	180	53	39	19	8	3	1	3	0	0	1	0	0	0	0	307
e-2	29	9	3	6	1	3	2	0	1	1	0	1	0	0	1	57
e-3	63	26	11	6	4	4	3	4	0	1	0	0	1	2	0	125

\*Total ramet number including living ramets, new buds and dead parts.

**Table S1c** The numbers of triplets consisting of a mother ramet, an old daughter and a new bud/ramet (Branching) and those of potential non-tip ramets of branching clonal growth (Non-tip) of the three dominant genets.

Genet	Branching	Non-tip
e-1	13	378
e-2	5	161
e-3	5	351

**Table S1d** The numbers of ramets having one, two or three buds for three dominant genets.

Genet	Number of buds		
	1	2	3
e-1	71	4	2
e-2	13	0	0
e-3	30	4	0

**Table S1e** The numbers of ramets transmitted from size class  $i$  (rows) to  $j$  (columns) for the three dominant genets. Genets (a) e-1, (b) e-2 and (c) e-3.

(1) Genet e-1

Size class	1L	2L			
		< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm
1L	22	12	16	12	1
< 10 cm	6	7	9	4	0
2L	18	10	114	58	13
15 – 20 cm	37	1	110	344	59
≥ 20 cm	10	2	10	152	106
Total	93	32	259	570	179

(2) Genet e-2

Size class	1L	2L			
		< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm
1L	0	0	4	0	0
< 10 cm	0	3	4	1	0
2L	3	6	83	19	3
15 – 20 cm	6	1	35	41	0
≥ 20 cm	0	0	0	8	3
Total	9	10	126	69	6

(3) Genet e-3

Size class	1L	2L			
		< 10 cm	10 - 15 cm	15 - 20 cm	≥ 20 cm
1L	42	7	29	19	4
< 10 cm	2	4	1	0	0
2L	16	5	78	46	12
15 – 20 cm	44	3	55	262	56
≥ 20 cm	8	0	10	103	60
Total	112	19	173	430	132

**Table S1f** The numbers of survival and dead ramets in each size class for three dominant genets from 2005 to 2006.

Genet	Fate	Size class				
		1L	2L			
			< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm
e-1	Survival	55	18	147	290	59
	Death	1	0	3	1	0
e-2	Survival	2	5	68	30	1
	Death	1	0	0	0	0
e-3	Survival	54	16	109	217	50
	Death	2	2	2	2	2

**Table S1g** The numbers of new ramets in each size class for three dominant genets.

Genet	Size class				Total	
	1L	2L				
		< 10 cm	10 – 15 cm	15 – 20 cm		≥ 20 cm
e-1	30	3	45	68	11	157
e-2	3	3	13	8	0	27
e-3	51	2	18	63	10	144
Total	84	8	76	139	21	328

**Appendix III:** Supporting results.

**Table S2a** Medians and 95% credible intervals (in parentheses) of the posterior distributions of the coefficients in the logistic regression (GLM) for clonal growth probabilities.

Genet	2-y-tip	All positions		1-y-tip		
	All sizes	1L	2L, < 10 cm	2L, 10 – 15 cm	2L, 15 – 20 cm	2L, ≥ 20 cm
e-1	0.430	0.700	1.904	0.984	0.332	-0.483
	(-0.16, 0.98)	(-0.21, 1.78)	(0.96, 3.58)	(0.36, 1.73)	(-0.21, 0.90)	(-1.39, 0.45)
e-2	2.050	0.320	2.716	1.460	-0.958	0.348
	(0.54, 3.68)	(-2.10, 3.63)	(1.15, 5.54)	(0.21, 3.05)	(-2.58, 0.51)	(-3.18, 2.52)
e-3	0.050	1.507	6.334	2.734	0.954	1.242
	(-0.81, 0.92)	(0.63, 2.60)	(2.98, 9.65)	(1.31, 4.71)	(0.10, 1.85)	(-0.03, 2.58)
Parameter*	a <sup>2</sup>	a <sub>1</sub>	a <sub>2</sub>	a <sub>3</sub>	a <sub>4</sub>	a <sub>5</sub>

\*Corresponded to parameters defined in S1.1 of Appendix I.

**Table S2b** Medians and 95% credible intervals (in parentheses) of the posterior distributions of the probabilities of branching via non-tip ramets for the three dominant genets.

Genet	Posterior distribution		
	Median	2.5%	97.5%
e-1	3.7%	2.1%	5.9%
e-2	3.5%	1.4%	7.3%
e-3	1.7%	0.7%	3.4%

**Table S2c** Medians and 95% credible intervals (in parentheses) of the posterior distributions of new ramets in each size class for the three dominant genets.

Genet	Size class				
	1L	2L			
		< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm
e-3	0.3478 (0.28 - 0.42)	0.0178 (0.00 - 0.05)	0.1257 (0.08 - 0.18)	0.4307 (0.35 - 0.51)	0.0716 (0.04 - 0.12)
e-2	0.1148 (0.04 - 0.26)	0.1186 (0.04 - 0.25)	0.4375 (0.28 - 0.60)	0.2776 (0.15 - 0.44)	0.0227 (0.00 - 0.11)
e-1	0.1893 (0.14 - 0.25)	0.0222 (0.01 - 0.06)	0.2833 (0.22 - 0.36)	0.4249 (0.35 - 0.5)	0.0736 (0.04 - 0.12)

**Table S2d** Medians and 95% credible intervals (in parentheses) of the posterior distributions of the probabilities that ramets survive in each size class for the three dominant genets.

Genet	Size class				
	1L	2L			
		< 10 cm	10 – 15 cm	15 – 20cm	≥ 20 cm
e-1	0.971 (0.91 - 1.00)	0.963 (0.82 - 1.00)	0.976 (0.94 - 0.99)	0.994 (0.98 - 1.00)	0.989 (0.94 - 1.00)
e-2	0.613 (0.21 - 0.93)	0.888 (0.51 - 1.00)	0.990 (0.95 - 1.00)	0.977 (0.89 - 1.00)	0.716 (0.18 - 0.99)
e-3	0.951 (0.88 - 0.99)	0.862 (0.66 - 0.96)	0.976 (0.94 - 0.99)	0.988 (0.97 - 1.00)	0.951 (0.87 - 0.99)

**Table S2e** Medians and 95% credible intervals (in parentheses) of the posterior distributions of the probabilities that ramets moved between size classes for the three dominant genets.

(1) Genet e-1						
Size class	1L	2L				
		< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm	
1L	0.234 (0.16 - 0.32)	0.349 (0.20 - 0.50)	0.063 (0.04 - 0.10)	0.022 (0.01 - 0.04)	0.009 (0.00 - 0.03)	
< 10 cm	0.069 (0.03 - 0.13)	0.215 (0.10 - 0.35)	0.037 (0.02 - 0.06)	0.008 (0.00 - 0.02)	0.004 (0.00 - 0.02)	
10 – 15 cm	0.191 (0.13 - 0.28)	0.293 (0.17 - 0.45)	0.435 (0.37 - 0.49)	0.103 (0.08 - 0.13)	0.075 (0.04 - 0.12)	
2L	15 – 20 cm	0.387 (0.30 - 0.48)	0.046 (0.01 - 0.15)	0.420 (0.36 - 0.48)	0.599 (0.56 - 0.64)	0.326 (0.26 - 0.40)
	≥ 20 cm	0.109 (0.06 - 0.18)	0.072 (0.02 - 0.18)	0.041 (0.02 - 0.07)	0.267 (0.23 - 0.30)	0.583 (0.51 - 0.65)

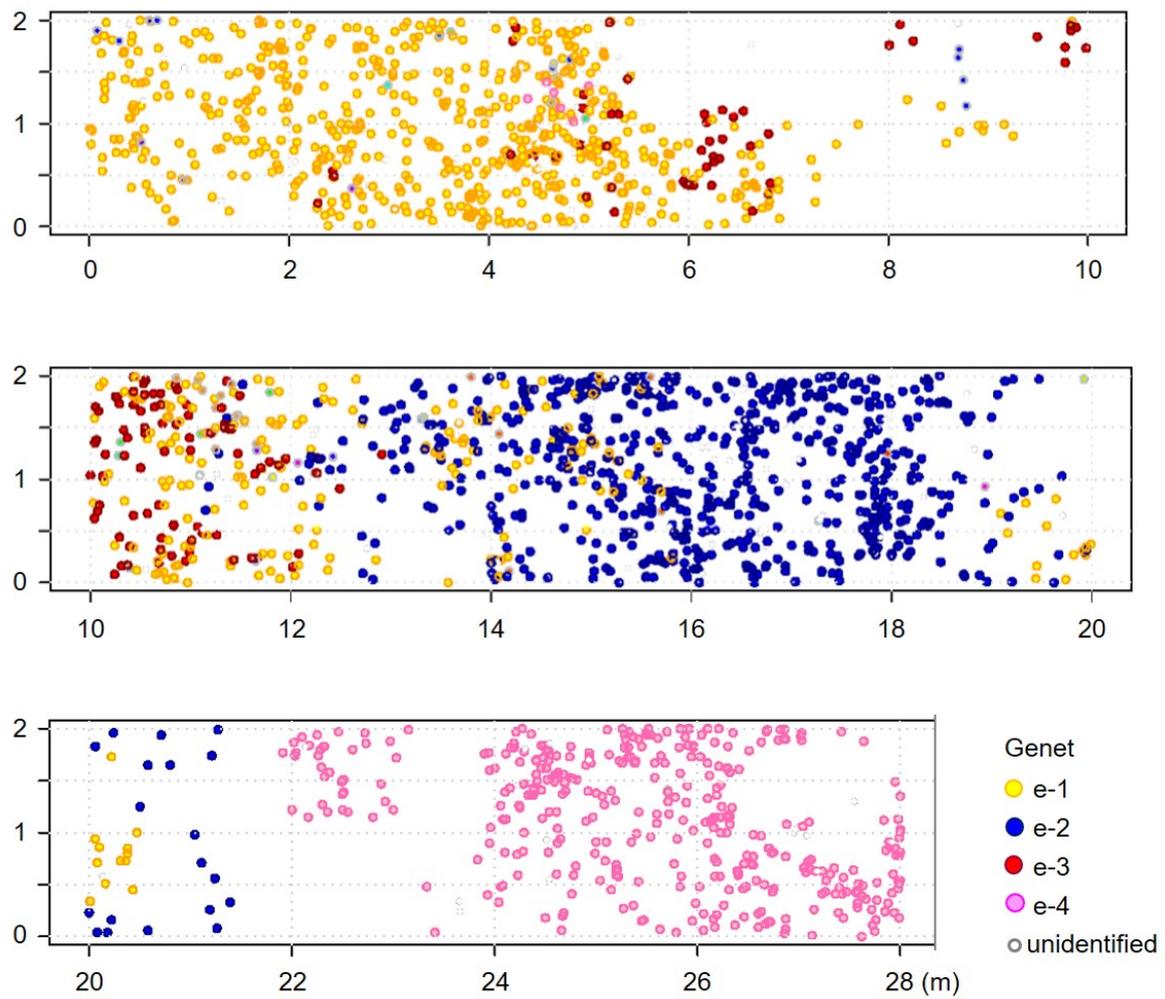
  

(2) Genet e-2						
Size class	1L	2L				
		< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm	
1L	0.051 (0.00 - 0.24)	0.051 (0.00 - 0.24)	0.036 (0.01 - 0.08)	0.009 (0.00 - 0.05)	0.065 (0.00 - 0.31)	
< 10 cm	0.052 (0.00 - 0.24)	0.256 (0.08 - 0.51)	0.036 (0.01 - 0.08)	0.024 (0.00 - 0.07)	0.068 (0.00 - 0.3)	
10 – 15 cm	0.285 (0.09 - 0.54)	0.459 (0.22 - 0.70)	0.642 (0.56 - 0.72)	0.268 (0.18 - 0.37)	0.355 (0.13 - 0.65)	
2L	15 – 20 cm	0.503 (0.25 - 0.75)	0.118 (0.02 - 0.34)	0.274 (0.20 - 0.35)	0.568 (0.46 - 0.68)	0.065 (0.00 - 0.31)
	≥ 20 cm	0.053 (0.00 - 0.24)	0.052 (0.00 - 0.25)	0.005 (0.00 - 0.03)	0.117 (0.06 - 0.21)	0.354 (0.13 - 0.65)

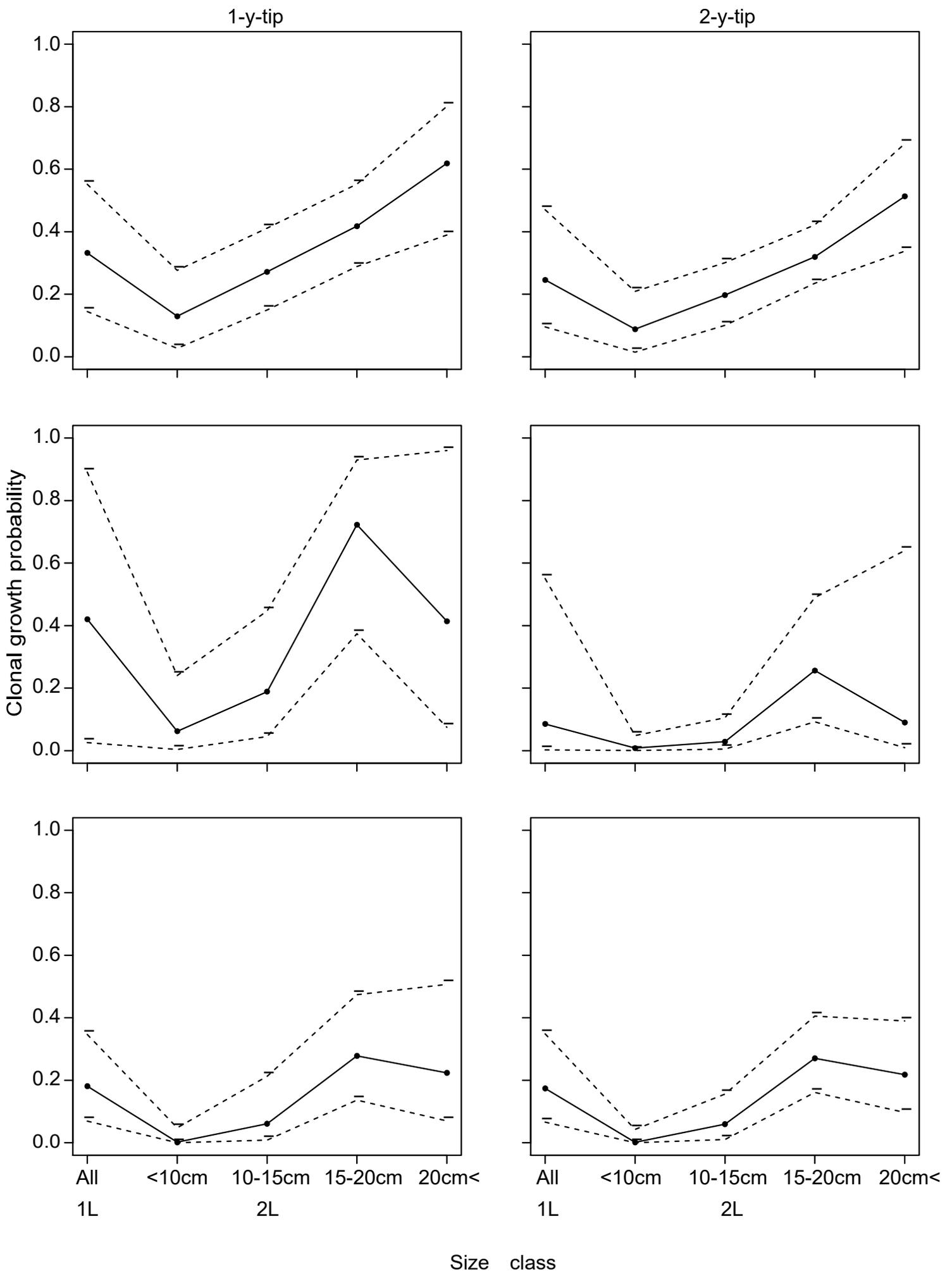
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(3) Genet e-3

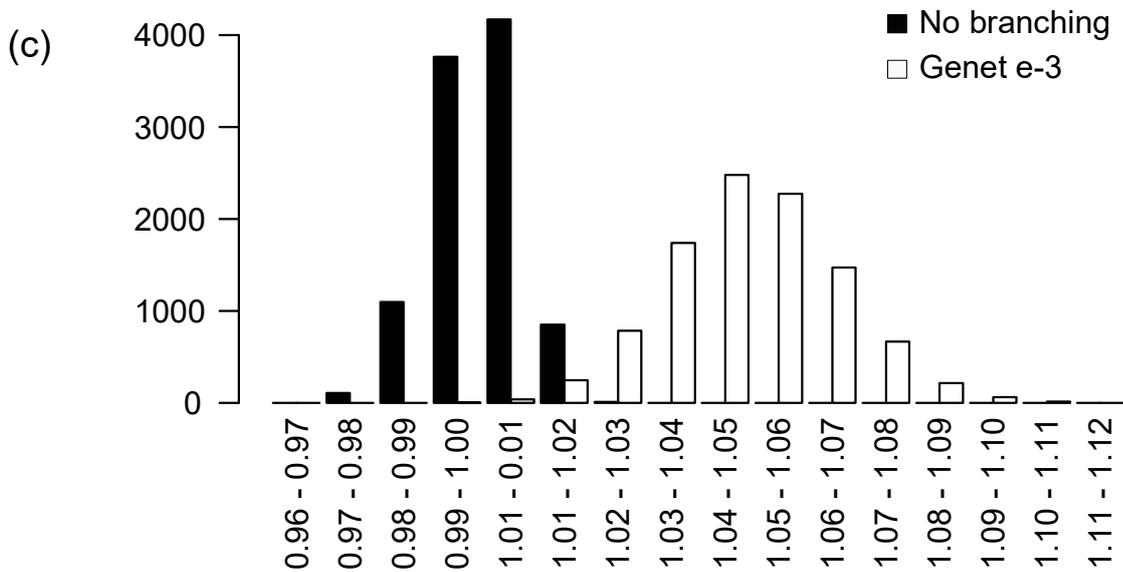
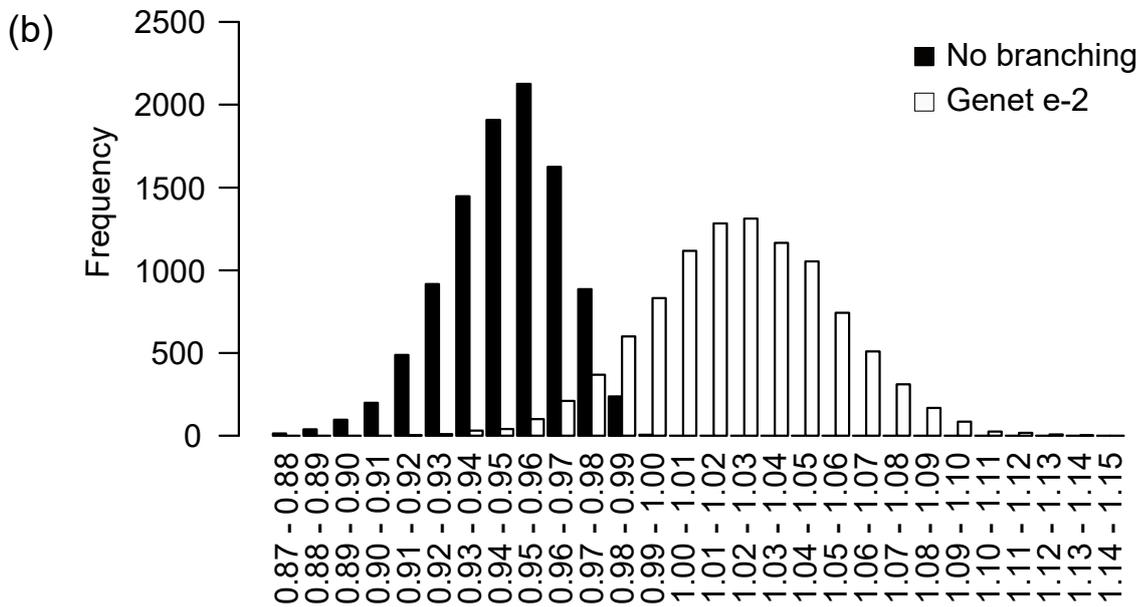
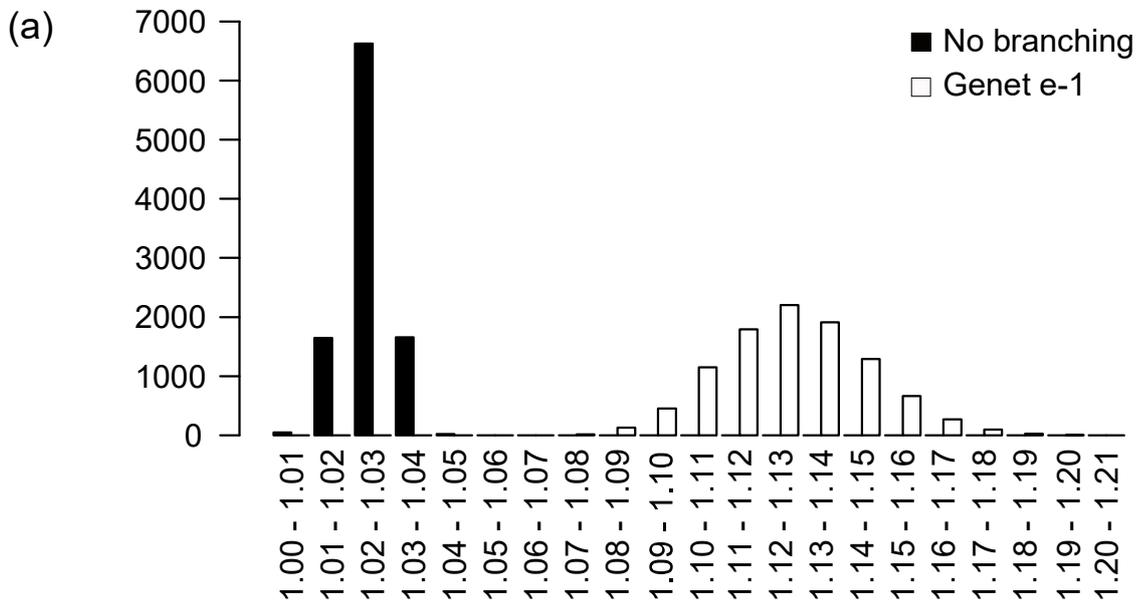
Size class	1L	2L			
		< 10 cm	10 – 15 cm	15 – 20 cm	≥ 20 cm
1L	0.367 (0.28 - 0.45)	0.326 (0.16 - 0.53)	0.166 (0.12 - 0.22)	0.045 (0.03 - 0.07)	0.034 (0.01 - 0.07)
< 10 cm	0.024 (0.01 - 0.06)	0.199 (0.08 - 0.39)	0.010 (0.00 - 0.03)	0.002 (0.00 - 0.01)	0.005 (0.00 - 0.03)
10 – 15 cm	0.144 (0.09 - 0.21)	0.239 (0.11 - 0.43)	0.444 (0.37 - 0.52)	0.108 (0.08 - 0.14)	0.092 (0.05 - 0.15)
2L 15 – 20 cm	0.384 (0.30 - 0.48)	0.157 (0.05 - 0.35)	0.314 (0.25 - 0.38)	0.604 (0.56 - 0.65)	0.414 (0.34 - 0.5)
≥ 20 cm	0.075 (0.04 - 0.13)	0.030 (0.00 - 0.16)	0.060 (0.03 - 0.10)	0.239 (0.20 - 0.28)	0.446 (0.37 - 0.53)



**Figure S1.** A map of ramet distribution in a 28 × 2 m plot in a *Convallaria keiskei* population.



**Figure S2.** The clonal growth probability of 1-y-tip and 2-y-tip ramets in each size class for three dominant genets. Medians (solid line) and 95% credible intervals (dashed line) of the posterior distributions are shown. Genets (a) e-1, (b) e-2 and (c) e-3.



**Figure S3.** Posterior distributions of growth rates of the three dominant genets with and without branching for three dominant genets. Genets (a) e-1, (b) e-2 and (c) e-3.