



Title	Genet dynamics and its variation among genets of a clonal plant <i>Convallaria keiskei</i>
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1 **Title: Genet dynamics and its variation among genets of a clonal plant *Convallaria***

2 ***keiskei***

3 **Abstract**

4 In clonal plant populations, a number of genetically identical ramets form a genet. While  
5 coexisting ramets potentially perform independently, their behaviours not only depend on  
6 ages and sizes but are also constrained by genetic background. In this study, genet dynamics  
7 and its variability among neighbouring genets were investigated based on the ramet  
8 demography of each genet in *Convallaria keiskei*. Genet dynamics were first formulated as  
9 a matrix model with the two components of clonal growth (clonal reproduction) and  
10 survival-transitions between ramet size classes. Then, a statistical estimation of the matrix  
11 elements was established using three datasets: aboveground demographic censuses,  
12 belowground directional rhizome connections and genetic identification of ramets. Finally,  
13 genet growth rates reflecting both the changes of clonal growth and ramet size growth were  
14 estimated and compared for fundamental demographic elements among genets. Over three  
15 years of aboveground annual censuses of a  $28 \times 2$  m plot, 2021 ramets were identified as  
16 belonging to 28 genotypes. Belowground excavation detected 515 clonal fragments. Genet  
17 growth rate of three dominant genets varied with medians of 1.13, 1.02 and 1.05; 95%  
18 credible intervals of the posterior distributions did not overlap between the genet with the  
19 largest median and the others. The variation was caused primarily by differences in clonal  
20 growth rather than survival-transitions between size classes. Clonal growth by branching  
21 was rarer than at the tips but contributed to the maintenance of the genet. Therefore, both  
22 clonal growth frequencies and connecting patterns of ramets caused the variation of genet  
23 dynamics and established genets persist for a long time through the positive growth rates,  
24 which would contribute to maintain a population. We also conclude that fundamental  
25 demographic elements relating to clonal growth traits (the features of individual genets)  
26 strongly impact genet dynamics.

27 **Introduction**

28 Plants with the ability to produce offspring via clonal organs, such as rhizomes, stolons  
29 and tubers, are called clonal plants (Klimeš et al. 1997, Whigham 2004, Silvertown 2008).  
30 A remarkable characteristic of clonal plants is horizontal expansion and multiplication by  
31 developing clonal organs (Klimeš et al. 1997, Herben and Klimešová 2020). This ability  
32 generates interesting and complex life-histories with two life cycles – seedling  
33 recruitment and clonally recruited offspring (Jackson et al. 1985, van Groenendael and  
34 de Kroon 1990). A number of genetically identical sub-units (ramets) exist simultaneously  
35 and have the potential to perform independently from each other; these constitute a  
36 genetic individual called a genet (Abrahamson 1980, Tuomi and Vuorisalo 1989, Eriksson  
37 1993, Tanner 2001). A clonal plant thus possesses a hierarchical structure of ramets,  
38 genets and populations.

39 Demographic analysis is an effective approach to understanding the population  
40 dynamics and life-history of organisms (Abrahamson 1980, Silvertown et al. 1993,  
41 Franklin et al. 2021). A basic approach is to determine three fundamental demographic  
42 elements of individuals in a population: reproduction, survival and growth. Many  
43 mathematical modelling approaches set the individual as the basic unit (e.g. Caswell 2001  
44 and references therein). In the case of clonal plants, both ramets and genets can be treated  
45 as individuals; the formation of clonal ramets is sometimes treated as reproduction of  
46 ramets (clonal reproduction) and sometimes as growth of a genet (clonal growth)  
47 (Hartnett and Bazzaz 1985, Fair et al. 1999, Eriksson and Bremer 1993). Many studies  
48 have mainly analysed ramet demography by using ramet-based data, and have offered  
49 useful predictions for changes in dynamics such as biomass, ground cover and population  
50 expansion (e.g. Cain and Damman 1997, Ehrlén and Lehtilä 2002, Decruyenaere and Holt

51 2005). Genet-based studies, on the other hand, treat genet recruitment as reproduction by  
52 seeds, and genet growth as the incrementation of the ramet number and/or occupied area  
53 (e.g. Fair et al. 1999, Suzuki et al. 2006, Kouassi et al. 2014). However, the origin of  
54 clonal offspring ramets has so far not been considered in studies. If demographic  
55 characteristics differ from one genet to another, considering the variations among genets  
56 may improve understanding of population dynamics of clonal plants (Barsoum et al. 2004,  
57 Franklin et al. 2021). In addition, the demographic variation among ramet ages and sizes  
58 may differently impact on the dynamics of each genet. Thus, determining the fundamental  
59 demographic elements for ramets with considering clonal growth as well as growth,  
60 survival and transition of each ramet per genet and comparing them among genets, would  
61 shed light on understanding the life-history strategy of clonal plants.

62 It is sometimes hard to determine demographic traits such as reproduction (seed  
63 and clonal growth), growth and survival of ramets per genet because of ecological and  
64 genetic features of clonal plants. First, in order to deal with genets, we have to know  
65 which genet each ramet belongs to. Although genet distribution can be distinguished by  
66 the clumping structure for plants forming genet patches (Kouassi et al. 2014, Kawai and  
67 Kudo 2018), it is impossible to identify genets at a glance for plants spreading via  
68 structures that intermingle with each other. DNA analysis is an alternative tool now  
69 available for identifying genetic relations between ramets (e.g. Reusch 2006, Suzuki et al.  
70 2006, Matsuo et al. 2018). Second, in order to explore features of ramets producing  
71 offspring, it is necessary to detect which ramets perform clonal growth and produce  
72 offspring ramets. Clonal growth can be treated as reproduction by the mother ramet and  
73 largely depends on the situation of the mother ramet and the reproductive ability of the  
74 genets in such plants as the stoloniferous herb *Rubus* (Lambrecht-McDowell and

75 Radosevich 2005) and the pseudo-annual herb *Uvularia perfoliata* (Huber et al. 2004).  
76 However, the mother ramet of newly emerged offspring may not be identifiable from  
77 aboveground plant structures, especially in clonal plant species that use underground  
78 organs for clonal growth and have long life spans. Ease and required approach of  
79 observation largely depend on the architecture of the clonal organs and on expansion  
80 frequency (Franklin et al. 2021). If the directional connection of mother to daughter is  
81 directly observable, exact information about mother-daughter pairs can be obtained and  
82 variability in clonal recruitment from mother ramets may be analysed in addition to such  
83 demographic traits as survival and growth (e.g. leaf area incrementation and stem height  
84 expansion) of mother ramets.

85 *Convallaria keiskei* is a perennial clonal herb species that can expand widely on  
86 the forest floor (Ohara et al. 2006, Araki et al. 2007). It has stoloniform rhizomes, i.e.  
87 underground stems (Bell 2008), elongating during the growing season. The distal end of  
88 the rhizome containing the apical meristem becomes erect and grows vertically forming  
89 a new ramet, while rhizomes gradually die from the basal end (Supporting information).  
90 The resulting linear structure is thus oriented from an older to the youngest end in a  
91 rhizome fragment (Araki and Ohara 2008, Logofet 2016). Since most rhizomes are  
92 maintained for several years and older ones often persist as more fragmented pieces in  
93 soil, destructive excavation provides not only a snap-shot of belowground connections  
94 but also a record of growth history; that is, the directional connections of the belowground  
95 rhizome may be used as a source of information for reconstructing the expanding state of  
96 a genet over the previous few years. On the other hand, ramets usually live for years and  
97 produce new ramets repeatedly even if they are disconnected from each other (Supporting  
98 information; Araki and Ohara 2008). However, as identifying all ramet members of an

99 expanding and fragmented genet is impossible because of vigorous clonal expansion,  
100 statistical estimation from sampled data is inevitable.

101 In this study, we aimed to reveal the life-history strategy of herbaceous clonal  
102 plants having stoloniform rhizomes by investigating the variation of genet dynamics in a  
103 population, based on the ramet demography of clonal recruitment and survival-transition.  
104 We addressed the following questions: 1) do genet growth rates, composed of clonal  
105 growth and ramet size growth, vary among genets?; 2) what demographic traits of ramets  
106 cause any variation?; 3) do less frequent clonal growth patterns such as branching  
107 contribute to the genet dynamics, and if so, to which degree compared with frequent  
108 expansion at a clonal fragment tip?

109 To this end, we first formulated genet dynamics as a matrix model. After  
110 establishing a statistical estimation of the elements of the matrix using three datasets  
111 (aboveground behaviour, belowground directional rhizome connection and genetic  
112 identification of ramets), we quantitatively estimated genet growth rates and compared  
113 these between genets for a *C. keiskei* population. In particular, we estimated the  
114 consecutive clonal growth probability over years, which also indicates how long it takes  
115 for a *C. keiskei* genet to expand over a given distance. Finally, we discuss the belowground  
116 ecology of this plant, an aspect that has repeatedly been highlighted in the population  
117 ecology of clonal plants (Janovský et al. 2017, Klimešová et al. 2021).

118

## 119 **Methods**

### 120 **Study species**

121 *Convallaria keiskei* (Asparagaceae) is a perennial herb, distributed across Japan  
122 (Hokkaido, Honshu and Kyushu), Sakhalin Island, Korea, China and eastern Siberia

123 (Utech and Kawano 1976). An aerial shoot of sheath leaves is elongated aboveground and  
124 develops one or two leaves in late April to May. An inflorescence also develops and  
125 flowering takes place in late May to June (Ohara et al. 2006). The aerial shoots die down  
126 during September and October, leaving only belowground organs over winter (Supporting  
127 information). In the following season the aerial shoots grow again from the basal organs  
128 that persist for years, thus ramets of *C. keiskei* emerge at almost the same position  
129 (Supporting information). *Convallaria keiskei* propagates clonally by growing  
130 stoloniform rhizomes belowground. A rhizome starts to elongate in spring and forms a  
131 new ramet that expands a shoot at the tip next season in autumn. Rhizomes gradually  
132 decay and are usually maintained for several years in the soil. Therefore, ramets are  
133 separated physically every year, resulting in an average of 1.86 ramets connected in a  
134 clonal fragment. This indicates that the rhizomes primarily function to produce new  
135 ramets rather than provide physiological integration to transport resources. This  
136 configuration has been described as ‘developmentally-programmed division of labour’  
137 (*sensu* Alpert and Stuefer 1997) or ‘division of labour in time’ (Jonsdottir and Watson  
138 1997), based on the type and degree of functional specialization.

139

#### 140 **Study site**

141 The study was carried out in a windbreak forest (143° 10' N, 42° 40' E) in Nakasatsunai,  
142 eastern Hokkaido, Japan. The forest is several kilometres long and fragmented by roads  
143 and agricultural fields. Planted *Larix leptolepis* is the most dominant tree, followed by  
144 naturally established *Quercus dentata* and *Betula platyphylla*. In 2001, a study plot (100  
145 × 90 m) with grid points plotted every 5 m (total 21 × 19 = 399 points) and characterized  
146 by *x* and *y* coordinates, was established on the forest floor. Genotypes of the ramets

147 nearest to each grid point were identified using allozyme analysis over the whole plot  
148 (Araki et al. 2007). In 2005, a new, long rectangular plot ( $28 \times 2$  m) was established for  
149 the present study within the original plot (coordinates  $x = 20-48$ ,  $y = 50-52$ ). Fifty-six  $1$   
150  $\times 1$  m subplots were also laid out in the plot.

151

### 152 **Aboveground demographic census**

153 Aboveground demographic censuses were performed in June and July from 2005 to 2007.  
154 In the first year, all aerial shoots observed in the  $28 \times 2$  m plot were carefully marked and  
155 mapped. For each shoot, the number of leaves was counted and the length of the longest  
156 leaf (leaf size) was measured. The fate of leaves and successive changes in leaf number  
157 and size at marked shoots were recorded and re-measured until 2007. Newly emerged  
158 shoots (NEW) within the plots were additionally marked and measured. Marked shoots  
159 that did not emerge aboveground in following years might be either 1) dead or 2) living;  
160 in the latter case they were recorded as 'unemerged (UEM)' for that year (Araki et al.  
161 2009).

162

### 163 **Genetic identification**

164 Leaf tissues of all ramets appearing in 2005 and newly emerging in 2006 and 2007 within  
165 the  $28 \times 2$  m plot were collected after they were measured. Collected leaves were frozen  
166 until analysis. To minimize the damage to plants, we collected only  $\sim 1$  cm<sup>2</sup> of tissue from  
167 each leaf. DNA was extracted using CTAB methods, and 5 ng of the extracted DNA was  
168 then amplified using a set of six labelled primer pairs targeting highly polymorphic DNA  
169 microsatellite loci according to previously reported protocols (GeneBank accession  
170 numbers AB251398, AB251399, AB251400 and AB251401; Araki et al. 2006). Size



171 separation of the PCR products was carried out using capillary electrophoresis on an ABI  
172 3100 genetic analyzer (Applied Biosystems, Thermo Fisher Scientific). Size scoring of  
173 banding patterns and genotyping were performed using a semi-automated method and the  
174 program GENESCAN (Applied Biosystems). Identical genotypes were classified as  
175 members of the same clone if the probability of a particular multilocus genotype occurring  
176 by free recombination was very small. The error likelihood of falsely ascribing genotypes  
177 to the same genet,  $P_{\text{gen}}$ , was calculated according to Parks and Werth (1993). Since the  
178 chance of obtaining the same multilocus genotypes by recombination was smaller than  
179 1%, the results (all  $P_{\text{gen}} < 0.001$ ) overall affirmed that the used primers were highly  
180 polymorphic microsatellite markers and that all identical genotypes could be considered  
181 members of the same clone.

182

### 183 **Belowground rhizome connection**

184 In order to explore rhizome connections between ramets in the soil, all subterranean  
185 organs in fourteen of the  $1 \times 1$  m subplots (coordinates  $x = 30\text{--}42$ ,  $y = 50\text{--}52$ ) within the  
186  $28 \times 2$  m plot were completely dug up in September 2007. Only the area where ramets  
187 and underground organs could be stably excavated was used in this experiment. All plant  
188 organs of elongating or senescent rhizomes with established aboveground shoots, new  
189 apical buds and remaining old tissues were carefully taken out, so as to maintain rhizome  
190 connections between ramets for direct observation. When a rhizome extended beyond the  
191 plot, the subterranean organs were excavated as far as possible towards the end of the  
192 rhizome connections. Some rhizomes ended or started with decayed or interrupted tips  
193 and were classified as ‘interrupted rhizomes’.

194 We defined a set of connected subterranean organs and shoots as a ‘fragment’

195 unit. Observing rhizome connections in a fragment enabled us to identify pairwise  
196 connections and the direction of rhizomes elongating from mother to daughter ramets  
197 (Araki and Ohara 2008). These observations were first sketched and then digitized in the  
198 form of a table in which each row corresponded to one pairwise connection from a mother  
199 to a daughter ramet.

200 In *C. keiskei*, rhizome elongation takes place during the spring to autumn  
201 growing season and daughter ramets emerge in the subsequent year. Thus, new buds  
202 found in September 2007 indicate clonal growth in 2007 and newly emerged shoots in  
203 June 2007 reflect the clonal growth in 2006. A further eight of the  $1 \times 1$  m subplots in  
204 2008 and three in 2009 were similarly excavated. The remaining areas in the plot proved  
205 impractical to dig up because of heavy grass cover and typhoon damage.

206

### 207 **Modelling genet dynamics**

208 In order to examine the genet dynamics of *C. keiskei*, we applied a matrix model which  
209 has been widely applied in population dynamics studies of perennial plant species  
210 (Caswell 2001, Salguero-Gómez et al. 2015). In this model, individuals are categorized  
211 into ‘growth stages’. Let  $i$  and  $j$  denote the stages ( $i, j = 1, \dots, I$  where  $I$  indicates the  
212 number of stages). The model consists of a diagonal matrix of survival,  $\mathbf{S} = (S_j)$ , a  
213 transition matrix,  $\mathbf{T} = (T_{ij})$  and a reproductive matrix,  $\mathbf{R} = (R_{ij})$ . The diagonal element  $S_j$   
214 indicates the survival probability per year of an individual that belongs to stage  $j$ .  $T_{ij}$   
215 indicates the transition probability that an individual in stage  $j$  is transmitted to stage  $i$   
216 conditionally for survival at stage  $j$ .  $R_{ij}$  indicates the expected number of offspring in stage  
217  $i$  produced by an individual of stage  $j$ . The population matrix  $\mathbf{A}$  is then defined as  $\mathbf{A} = \mathbf{TS}$   
218  $+ \mathbf{R}$

219           Supposing that in year  $t - 1$ , there are  $n_j$  individuals in stage  $j$ . Denoting them by  
220 vector  $\mathbf{n}_{t-1} = (n_1, \dots, n_I)^T$  ( $T$  indicating transposition), the expected number of individuals  
221 in year  $t$  can be written as:

$$222 \quad \mathbf{n}_t = \mathbf{A}\mathbf{n}_{t-1} = (\mathbf{TS} + \mathbf{R}) \mathbf{n}_{t-1}.$$

223           Applying this population dynamics modelling framework, we developed a genet  
224 dynamics model in which the population was replaced by a genet, individuals by ramets  
225 in the genet, and reproduction was obtained from clonal growth. When a matrix model is  
226 applied in population ecology under the stationary assumption (i.e. matrix  $\mathbf{A}$  is invariant  
227 across years), the largest real eigenvalue of  $\mathbf{TS} + \mathbf{R}$ , which is often denoted by  $\lambda$ , is  
228 generally interpreted as the intrinsic growth rate of the population. Thus, in the case of  
229 genet dynamics, it expresses the genet growth rate.

230           The partial derivative of  $\lambda$  with respect to each matrix element is called  
231 sensitivity and has been commonly applied in population ecology in order to examine  
232 effects of a small change in each matrix element on the largest eigenvalue  $\lambda$ . There is a  
233 convenient formula (Caswell 2001);

$$234 \quad \frac{\partial \lambda}{\partial a_{ij}} = \frac{v_i u_j}{\sum_k v_k u_k}$$

235 in which  $\mathbf{u}$  and  $\mathbf{v}$  respectively indicate the right and left eigenvector of the largest  
236 eigenvalue  $\lambda$ .

237

### 238 *Growth stage*

239 A new rhizome regularly extends from the internode that is the nearest to a shoot, which  
240 finally develops a new bud at the tip (Fig. 1a, 2, Supporting information). In terms of  
241 ramet behaviour this mean that a new ramet is produced from a ramet at the tip of a clonal  
242 fragment (Araki and Ohara, 2008). Rhizomes also occasionally extend to shoots from

243 internodes other than the nearest, resulting in rhizome ‘branching’. Thus, if a new ramet  
244 is formed from a non-tip ramet, it was treated as ‘branching’ clonal growth in this study.  
245 It was hypothesized that clonal growth occurred at different rates between tip and non-tip  
246 ramets and between newly born and older ramets. We therefore classified ramets  
247 according to I) age and position, followed by II) size.

248 I) Three classes were defined for age-position in a fragment:

249 1-y-tip: ramet at the tip of a fragment and appearing in that year, age = 1.

250 2-y-tip: at the tip of a fragment and appearing before that year, age  $\geq 2$ .

251 Non-tip: at an intermediate position of a fragment and appearing before that year, age  $\geq$   
252 2.

253 II) Ramets were first grouped into two size categories according to the number of leaves:

254 (1) one-leaf (1L), and (2) two or more (rarely three or four) leaves (2L). Ramets in the 2L  
255 category were then further divided according to leaf length:  $< 10$ ,  $10\text{--}15$ ,  $15\text{--}20$  and  $\geq 20$

256 cm. Ramets in 1L were not subdivided by leaf length because of a smaller variance in leaf  
257 length (Araki et al. 2009). Ramets were thus categorized into a total of 15 stages (1-y-tip

258 1L, 2L-  $< 10$ , ..., 2L-  $\geq 20$ ; 2-y-tip 1L, 2L-  $< 10$ , ..., 2L-  $\geq 20$ ; non-tip 1L, 2L-  $< 10$ , ...,  
259 2L-  $\geq 20$ ). Hereafter, the age-position is denoted by  $h$  and the size class by  $k$  ( $k = 1, \dots, K$

260 = 5) as  $_k^h$ .

261

### 262 *Structure of the matrix model*

263 Examples of the transition patterns of surviving ramets and those of recruiting new ramets  
264 by clonal growth are shown in Fig. 1a. If a ramet at the 1-y-tip age-position performs

265 clonal growth, it transitions to non-tip (ramet A in pattern 1-1); otherwise, it transitions to

266 2-y-tip (ramet A in pattern 1-2). If a ramet at the 2-y-tip age-position conducts clonal

267 growth, it transitions to non-tip (ramet B in pattern 2-1); otherwise, it stays at the 2-y-tip  
268 (ramet B in pattern 2-2). A ramet at the non-tip remains in this position (ramet C in pattern  
269 3) regardless of its clonal growth (branching). These transitions are illustratively  
270 summarized as blue arrows in Fig. 1b. The position of a daughter ramet is always at the  
271 1-y-tip (red arrows in Fig. 1b).

272 For simplicity, it was assumed that the size of a daughter ramet was not affected  
273 by the stage, i.e. either by the age-position or size category, of the mother. Let  $N_k$  be the  
274 probability that a daughter belongs to size class  $k$ . Let  $E_l^h$  and  $C_l^h$  be the expected number  
275 of daughters and the probability that a mother recruited a new ramet via clonal growth  
276 (clonal reproduction), when the mother belongs to age-position  $h$  and size class  $l$ ,  
277 respectively. The expected number of daughters in size class  $k$  produced by a ramet in  
278 age-position  $h$  and size class  $l$ ,  $R_{kl}^h$ , can then be written as  $R_{kl}^h = N_k E_l^h C_l^h$  (right matrix in  
279 Fig. 1c).

280 When a ramet in size class  $l$  survives with the probability  $S_l$ , it transitions to size  
281 class  $k$  with probability  $T_{kl}$  (left matrix in Fig. 1c). Genet dynamics of *C. keiskei* are thus  
282 modelled in the matrix model framework as illustrated in Fig. 1c. In the following, the  
283 left blue  $15 \times 15$  matrix is referred to as  $\mathbf{T}_{SC}$  (this matrix is formed by not only  $T_{kl}$  but  
284 also  $S_l$  and  $C_l^h$ ) and the red right matrix as  $\mathbf{R}$ . The largest real eigenvalue of the matrix  
285  $\mathbf{T}_{SC} + \mathbf{R}$  is referred to as ‘genet growth rate’ that integrates clonal growth and ramet size  
286 growth.

287

## 288 **Statistical estimation of matrix elements**

289 Statistical estimation of  $C_l^h$ ,  $N_k$ ,  $E_l^h$ ,  $S_l$  and  $T_{kl}$  was carried out separately for each genet.

290 In the following we therefore do not explicitly indicate genet identity. Because we applied

291 the matrix model that assumes stationarity, all data were pooled across years. The  
292 estimations were conducted in a Bayesian modelling framework separately for the five  
293 parameter sets. Some additional technical details are described in the Supporting  
294 information.

295 Information regarding whether a ramet in age-position  $h$  and size class  $l$  in year  
296  $t$  produced a daughter ramet was obtained from three annual censuses of shoots, as well  
297 as from the belowground information such as the rhizome connections between ramets  
298 from excavated fragments. Focusing on the tip parts, how a series of shoots were observed  
299 during the censuses, and on the fragments excavated in 2007, we classified connection  
300 patterns incorporating above- and belowground information into eight groups (Fig. 2).  
301 For example, if a ramet newly born in 2007 (defined as year  $t$ ) was positioned in front of  
302 a ramet born in 2006 (year  $t - 1$ ), this indicated that the latter ramet performed clonal  
303 growth in the summer of 2006 (year  $t - 1$ ) at the 1-y-tip position. If an apical bud was  
304 observed in front of the former, this showed that a 1-y-tip ramet performed clonal growth  
305 in the 2007 summer (pattern-1). If the ramet did not have a bud, it belonged to pattern-2.  
306 This classification was performed for every branch in a fragment (when branching clonal  
307 growth was performed, a new ‘branch’ appeared in the fragment; throughout the paper,  
308 ‘branching’ is used to represent a clonal growth while a “branch” indicates a part of one  
309 fragment). We then counted the numbers of branches of the eight patterns. Fragments  
310 excavated in 2008 and 2009 were similarly classified (in these cases, the excavated year  
311 was defined as year  $t$  and the longest series begins with year  $t - 3$ ).

312 For branching clonal growth ( $C^{\text{non-tip}}$ ), the numbers of triplets consisting of a  
313 mother ramet, an old daughter and a new bud (or new ramet) and those of potential non-  
314 tip ramets of branching clonal growth were counted (these were not classified into size

315 classes). When we counted new daughter ramets belonging to the size class  $k$ , if some  
316 newly emerged shoots connected to dead ramets or to interrupted rhizomes, they were  
317 excluded because such ramets were probably not newly born (Supporting information).  
318 The numbers of new buds were counted if a ramet produced a bud.

319         Following Araki et al. (2007), if a ramet observed in 2005 appeared neither in  
320 2006 nor 2007, it was classified as dead from 2005 to 2006. Subsequently, some of these  
321 ramets were excavated and found to be alive. They were re-labelled as surviving ramets.  
322 Mortality from 2006 to 2007 and later was not considered. We counted the numbers of  
323 surviving and dead ramets for each size class. We also counted the numbers of ramets that  
324 were transmitted from size class  $l$  to  $k$ , conditional on survival.

325         To evaluate uncertainty caused by these limited count data, we applied a  
326 Bayesian approach. This was done separately for  $C_l^h$ ,  $N_k$ ,  $S_l$  and  $T_{kl}$ , while for  $E$  the  
327 average number of new buds was used, because most of the existing ramets produced just  
328 one daughter ramet and two or more were rare (Supporting information). For  $C_l^{1-y\text{-tip}}$  and  
329  $C_l^{2-y\text{-tip}}$ , a generalized linear model (GLM) was applied. Using flat prior distributions, we  
330 produced random samples from the posterior distributions of the coefficients in the GLM  
331 by Markov chain Monte Carlo (MCMC) simulation and transformed them to those of  $C_l^{1-}$   
332  $y\text{-tip}$  and  $C_l^{2-y\text{-tip}}$  (further details are provided in the Supporting information). For  $C^{non\text{-tip}}$ ,  
333  $N_k$ ,  $S_l$  and  $T_{kl}$ , flat conjugate prior distributions were applied. Random samples were drawn  
334 from the (binomial or multinomial) posterior distributions (details are provided the  
335 Supporting information).

336

### 337 **Matrices and genet growth rate**

338 By randomly combining random samples from the posterior distributions of  $\{C_l^h\}$ ,  $\{N_k\}$ ,

339  $\{S_l\}$ ,  $\{T_{kl}\}$  and the fixed value for  $E$ , we produced 10000 matrices ( $\mathbf{T}_{SC} + \mathbf{R}$ ) and for each  
340 computed the largest real eigenvalues showing the genet growth rate.

341 In order to examine which component ( $\mathbf{T}_{SC}$  or  $\mathbf{R}$ ) contributed to determining the  
342 differences in the growth rates between the genets, if any, we produced another two  
343 matrices: in matrix (1), let clonal growth ( $\{C_l^h\}$ ,  $\{N_k\}$ ,  $E$ ) be common to the genets; in  
344 matrix (2), let the survival and transition ( $\{S_l\}$ ,  $\{T_{kl}\}$ ) be common to the genets. For (1),  
345 by pooling the three genets' data on clonal growth, random samples from the posterior  
346 distribution for  $\{C_l^h\}$  and  $\{N_k\}$  were produced by respectively MCMC and by using the  
347 conjugate prior. The mean numbers of buds for the three genets were used for  $E$ .  
348 Combining this with the random samples of  $\{S_l\}$  and  $\{T_{kl}\}$  for each genet, we then  
349 produced 10,000 matrices and computed eigenvalues for the three genets. For (2), by  
350 pooling the three genets' data on survival and transition, we produced 2000 random  
351 samples of  $\{S_l\}$  and  $\{T_{kl}\}$ . We then combined them with the random samples from clonal  
352 growth ( $\{C_l^h\}$ ,  $\{N_k\}$ ) for each genet to produce 10000 matrices, and computed  
353 eigenvalues for the three genets. If the posterior distributions of eigenvalues vary from  
354 the original ones only for (1), it implies that inter-genet differences had effects on clonal  
355 growth but little influence on survival and transition, and vice versa.

356 To examine the contribution of branching, we set the branching probability to 0  
357 for the 10000 matrices and calculated the eigenvalues for each genet. If the posterior  
358 distribution decreases, it indicates a contribution of branching to the maintenance of that  
359 genet.

360 Finally, we conducted a sensitivity analysis. In this case, the commonly used  
361 formula was considered insufficient due to the need to know the partial derivatives of  $\lambda$   
362 with respect to  $C_l^h$  and the others. We derived suitable formulae (Supporting information)



363 and calculated sensitivity for each of the 10,000 matrices.

364

## 365 **Results**

### 366 **Genet identification**

367 Of 2114 ramets in the 28 × 2 m plot, 2021 were identified and grouped into 28 genotypes.

368 There were four dominant genotypes with respectively 809, 152, 648 and 367 ramets;

369 hereafter genets e-1, e-2, e-3 and e-4, respectively. Nineteen genotypes were represented

370 by only one ramet, and the other five were represented by 2-13 ramets. The four dominant

371 genets were also found in the 5 m lattice of the original 100 × 90 m plot (Araki et al.,

372 2007).

373

### 374 **Aboveground shoot demography**

375 A total of 1525, 1868 and 2113 ramets were found in the 28 × 2 m plot in 2005, 2006 and

376 2007, respectively. The numbers of ramets counted during the three annual censuses of

377 aboveground shoots are summarized for the four dominant genets in Table 1. In the four

378 genets, 108 to 701 ramets emerged every growing season. More new ramets (NEW) were

379 found in 2006 than in 2007 and the number of ramets increased from 2005 to 2006 for all

380 the genets (Table 1). New ramets mostly emerged clonally with two leaves 15-20 cm in

381 length in genets e-1 and e-3, and with two leaves 10-15 cm in length for genet e-2

382 (Supporting information). Recruitment rates of ramets per genet were calculated as 8-

383 20% based on ramet numbers existing in the previous year and newly emerged in the

384 current year. The four genets were distributed to form clonal patches except in a section

385 of intermingled parts where the range of genet e-2 overlapped with genets e-1 and e-3

386 (Supporting information).

387

388 **Belowground rhizome connection and fragments**

389 The *C. keiskei* parts dug up from 2007 to 2009 contained 943 living ramets (including  
390 638 censused ramets and ramets connecting to a fragment but located outside the plot)  
391 and 139 buds. Old tissues of 58 remains from dead ramets were also found in fragments.  
392 These were also separated into 515 fragments. The numbers of branches varied from 2  
393 (56 fragments) or 3 (19 fragments) to more (the maximum was 9 followed by 8, one  
394 fragment for each), while 431 fragments had no branches. The biggest fragment, in genet  
395 e-2, contained 34 living or dead ramets and buds with 9 branches (Supporting  
396 information). This fragment also contained the longest series of 11 ramets and a new bud  
397 at the tip, indicating that this genet was born at least 10 years ago. The average was 2.21  
398 ramets per fragment. The dominant genets, e-1, e-2 and e-3, had 307, 57 and 125  
399 fragments, respectively (Table S1b), with a total of 478, 152 and 279 living ramets (genet  
400 e-4 was not found in this area).

401           Among 210 newly emerged ramets in 2006 and 2007, 46.2% were connected to  
402 dead tissues or not connected to anything (isolated), implying that these were not newly  
403 born but had not emerged in the previous censuses and that the recruitment rates of 8-  
404 20% were overestimated.

405

406 **Features of clonal growth in each genet**

407 Table 2 shows the number of fragments associated with each connection pattern which  
408 informs the occurrence of clonal growth in certain ages and positions in the 2006 and  
409 2007 growing seasons. Pattern-4 and -6 in Fig. 2 were dominant connection patterns in  
410 genets e-1 and e-3, while pattern-6 was less frequent in genet e-2. Most fragments

411 belonged to pattern-8. Based on these data combined with those of fragments excavated  
412 in 2008 and 2009, we classified all fragments, separately for every branch, and counted  
413 the number of successful and unsuccessful clonal growth occurrences for each stage  
414 (Supporting information). Ramets at the 1-y-tip position exhibited higher clonal growth  
415 frequencies than those at the 2-y-tip, especially in genet e-2 with 38.5% versus 11.3% and  
416 marginally in genet e-1 with 38.8% versus 32.2% and in genet e-3 20.4% versus 20.3%  
417 (these were further examined with Bayesian modelling, below). The average branching  
418 frequency was 3.4, 3.1 and 1.4% for genets e-1, e-2 and e-3, respectively (Supporting  
419 information). The numbers of buds per mother ramet ranged from one (91.9%) to three  
420 (1.6%), with a mean of 1.10, 1.00 and 1.12 for genets e-1, e-2 and e-3, respectively  
421 (Supporting information).

422

### 423 **Survival and transitions of ramets between size classes**

424 The observed numbers of ramets that did or did not change size class, the numbers of  
425 surviving and dead ramets from 2005 to 2007 and the numbers of new ramets for each  
426 size class are summarized in the Supporting information. In the 2L category, most ramets  
427 remained in the same size class or transitioned to a larger size class, whereas more than  
428 half of the 1L ramets grew to the 2L size classes. This tendency did not differ between the  
429 three genets (Supporting information). Surviving and newly born ramets from genets e -  
430 1 and e-3 were mostly within the 2L 15-20 cm size class and those from genet e-2 were  
431 within the 2L 10-15 cm size class (Supporting information).

432

### 433 **Matrix and genet growth rate**

434 By randomly combining 2000 samples from the posterior distributions of  $C_l^h$  (Supporting

435 information; some of 95% credible intervals of  $C_l^h$  overlapped between genets and  
436 between 1-y-tip and 2-y-tip),  $N_k$  (Supporting information),  $S_l$  (Supporting information),  
437  $T_{kl}$  (Supporting information) and the fixed value of  $E$ , we produced 10000 matrices for  
438 each genet. Intrinsic growth rates (the largest real eigenvalues) for the three genets,  
439 derived from the largest real eigenvalues, were differently distributed (Fig. 3a). Genet e-  
440 1 tended to show higher growth rates (99.8% across 10000 matrices were highest, median  
441 = 1.13) and genet e-2 was the lowest for 77.7% (median = 1.02). The 95% credible  
442 interval of genet e-1 did not overlap with those of genets e-2 and e-3 (median = 1.05).  
443 The interval of genet e-2 was relatively wide, presumably because of the smaller sample  
444 size, and overlapped even to include the median of e-3. These patterns suggest that genet  
445 growth rates varied among genets. It is also noteworthy to point out that the tendency of  
446 these growth rates were consistent with changes of observed numbers of ramets from  
447 2006 to 2007 (Table 1): 1.00 (genet e-1), 0.96 (genet e-2) and 0.98 (genet e-3).

448 Figure 3b–c compares how the posterior distributions of eigenvalues were  
449 affected when either clonal growth ( $C_l^h$ ,  $N_k$ ,  $E$ ) or survival and transition ( $S_l$ ,  $T_{kl}$ ) of ramets  
450 was unified over genets. The difference between genets e-1 and e-3 was reduced when  
451 the clonal growth data were pooled (Fig. 3b). On the other hand, when the survival and  
452 transition data were pooled, the difference between genets e-1 and e-3 was largely  
453 unaffected (Fig. 3c), and the differences to genet e-2 were reduced. This implies the  
454 effects of clonal growth and suggests much weaker influences of survival-transition on  
455 the genet growth rates.

456 If no branching was assumed, the medians of posterior distributions of  
457 eigenvalues declined in all three genets by 4.7–9.0% (Fig. 4), among which genet e-1  
458 showed the largest decline. This result suggests that branching ramet recruitment

459 significantly contributes to maintaining genet dynamics despite the clonal growth  
460 probabilities being lower than those at fragment tips. The sensitivity of  $C^{non-tip}$  also  
461 exhibited much higher values than  $C^{1-y-tip}$  and  $C^{2-y-tip}$  (Supporting information). While Fig.  
462 4 shows an extreme case when the branching never occurs, the sensitivity expresses  
463 changes of the largest eigenvalue by a (infinitesimally) small change of the branching  
464 probability. The consistent results between the two support the definite contribution of  
465 branching to the maintenance of the genets.

466

## 467 **Discussion**

### 468 **Variation of genet dynamics**

469 We here proposed a ‘genet dynamics’ approach, exploring the fundamental elements for  
470 ramet demography of genets in a clonal plant species by deriving demographic  
471 information from ramet connections in clonal fragments. To this end, we defined the  
472 intrinsic growth rate of a genet using the maximum real eigenvalue of a matrix model  
473 reflecting clonal growth and survival-transitions depending on age-position and size of  
474 each ramet in the genet (Fig. 1). It was quantitatively detected that genet growth rates  
475 varied between dominant genets with closely adjacent locations in a natural population  
476 (Fig. 3, Supporting information). The differences resulted from the different probabilities  
477 and contributions of such demographic traits as clonal growth, ramet size growth and  
478 branching to the genet growth rates depending on genets (Fig. 3b-c, 4).

479         Demographic variations between genets have been reported within experimental  
480 populations (Geber et al. 1992, Cheplick 1997, Prati and Schmid 2000), between genet  
481 patches in a population (Falinska 1995, Kawai and Kudo 2018) and between populations  
482 of clonal plant species (Nantel and Gagnon 1999, Barsoum et al. 2004). Differences in

483 genet performance are caused by such factors as genetic variation, age of establishment  
484 and environmental heterogeneity (Prati and Schmid 2000, Pan and Price 2002, Timerman  
485 and Barrett 2019). Investigation of genet dynamics after simultaneous death in dwarf  
486 bamboo, a monocarpic clonal plant, revealed that more productive genets survived and  
487 spread initially, replacing less productive ones (Matsuo et al. 2018, Tomimatsu et al.  
488 2020). Kawai and Kudo (2018) detected different ramet productivity between genets  
489 located in different snow melt habitats. In the present study, we investigated already  
490 established adjacent genets and the area where ramets of some genets were intermingled  
491 (Supporting information). The assumption was that genetic variation would sometimes  
492 interact with environmental conditions and/or differences of ages to contribute to genet  
493 dynamics variations. Indeed, genet e-1 was found distributed over a large area of about  
494  $15 \times 25$  m (see Araki et al. 2009), implying a relatively long time since establishment,  
495 and showed the highest genet growth rate (Fig. 3).

496

#### 497 **Ramet demography for population and genet dynamics**

498 To understand population dynamics, demographic traits of individuals in a population are  
499 generally investigated (Silvertown et al. 1993, Menges and Dolan 1998, Logofet 2016).  
500 As for clonal plant populations, recruitment, mortality and growth of ramets were  
501 explored based on ramet census, from which annual variations of ramet numbers and  
502 biomass, frequencies of clonal recruitment per ramet and contributions to a population  
503 were estimated (Tanner 2001). In the case of *Rubus*, clonal growth has the greatest impact  
504 on population growth rates, suggesting a significant contribution of clonal growth to  
505 population development (Lambrecht-McDowell and Radosevich 2005). Guàrdia et al.  
506 (2000) used a matrix model to conclude that clonal growth contributed less population

507 growth in *Achnatherum calamagrostis* while the population growth rate was higher than  
508 1.0. Growth and survival of ramets in the certain size class caused the different dynamics  
509 between populations in *Helianthus divaricatus* (Nantel and Gagnon 1999).

510 Genet growth rates were also observable as an increase in numbers and area  
511 occupied by ramets of a certain genet. For example, de Witte and Stöcklin (2010)  
512 measured changes in genet sizes from plant morphology. Reusch (2006) monitored  
513 changes in the lattice point numbers for each genet to assess genet growth in a seagrass  
514 population. If not all ramet members are identifiable and multiple genets are intermingled  
515 with one another, statistical inference of genet growth rates from sampled data is required;  
516 the present study established a statistical method for this purpose (Fig. 1, 2). In this study,  
517 we found that ramets located at the tip of a fragment more frequently produced offspring  
518 (Supporting information). This clonal growth seems to support genet maintenance rather  
519 than contribute to genet expansion, because the rhizomes expanded in all directions,  
520 forming a complex clonal structure. Moreover, clonal growth of non-tip ramets showed  
521 higher sensitivity (Supporting information), suggesting that clonal growth of older ramets  
522 was also important to maintain genets. This implies that in genets containing older ramets,  
523 e.g. larger genets, branching clonal growth has a greater impact on genet growth and  
524 longevity. Thus, once a genet occupies a certain area, it would be able to survive for a  
525 long time.

526

### 527 **Applications of belowground information**

528 Estimation of the elements in the matrix model was achieved using both data from  
529 aboveground censuses and information from belowground directional connection of  
530 ramets (Fig. 2). We were able to classify excavated fragments into eight patterns, although

531 belowground organs exhibited very complex structures. Belowground information is as  
532 important as aboveground data for advancing studies on plant species (Klimešová et al.  
533 2018, Ott et al. 2019), and integrating both types of data demands novel approaches suited  
534 to particular data and species characteristics. For example, Wildová et al. (2007)  
535 excavated to parameterize the architecture of belowground clonal organs as well as  
536 aboveground performances, which showed different impact on population and  
537 community structure between aboveground and underground traits among species. From  
538 belowground excavation after two annual censuses, Araki and Ohara (2008) also derived  
539 preliminary insight of ramet reproductive demography that ramets perform clonal growth  
540 before repeated flowering. In contrast to these approaches, the present study investigated  
541 directional rhizome connections of ramets (Fig. 2) and estimated consecutive clonal  
542 growth rates at tips (Fig. S3) to understand clonal growth strategy of genet as well as  
543 ramet. This growth rate also enables prediction of genet distribution and thus sizes for a  
544 given period. In fact, genet e-1 covered a  $15 \times 25$  m area (see Araki et al. 2007) and  
545 occupied over more than half the area of the  $28 \times 2$  m plot (Fig. S1). Based on the distance  
546 between ramets (average 22.7 cm in Araki and Ohara 2008), combining the distributions  
547 of rhizome lengths and turning angles enables calculation of the number of years needed  
548 to attain the expansion of a given genet size as it fits the reality.

549

#### 550 **From genet demography to population dynamics**

551 Population dynamics can also be estimated from demographic traits of genets. If a genet  
552 growth rate was smaller than 1.0, we could predict the reduction of ramets in that genet  
553 and its disappearance, using the stationary assumption in the matrix model. All studied  
554 genets of *C. keiskei* showed growth rates greater than 1.0, and few dead ramets were found



555 during the experimental period. In our study plot, nine of 19 seedlings with one leaf  
556 shorter than 10 cm found in 2005 did not emerge in 2006 and 2007. These findings can  
557 provide evidence of birth and death of genets, but there were no observations of genets  
558 with two or more ramets disappearing. The employed statistical analysis incorporated  
559 only growth but not the birth and death of genets. Suzuki et al. (2006) estimated genet  
560 mortality in *Festuca rubra* from ramet demographic data and genet identification by  
561 applying spatial theory using the probabilities of genet identity of ramets, as described in  
562 Harada et al. (1997).

563

#### 564 **Conclusion**

565 Fundamental demographic elements are important in understanding life-history  
566 characteristics of species. This study formulated genet growth rates in terms of both clonal  
567 growth and ramet size growth per genet in a population. Genet dynamics and associated  
568 variability between genets were statistically investigated using a matrix model of ramet  
569 demography within each genet. The structure and growth pattern of the rhizome of *C.*  
570 *keiskei* include continuous clonal growth at the tip end of the rhizome and spatial spread.  
571 However, once a genet was established, clonal growth at the tip as well as growth of non-  
572 tip ramets contributed to genet maintenance rather than expansion. Consequently,  
573 dominant genets with positive genet growth rates would tend to persist for a long period,  
574 contributing to population maintenance in this herbaceous clonal plant.

575

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731 **Figure legends**

732 **Figure 1.** Schematic representation of the life-history transition of ramets in a genet in a  
733 clonal perennial plant species, *Convallaria keiskei*.

734 (a) Examples of transition patterns of mother ramets from year  $t - 1$  to  $t$ . (b) All transition  
735 patterns of ramets. Blue components show the position and age transitions of ramets, red  
736 components indicate ramet recruitment through clonal growth. The survivals are not  
737 shown for simplicity. (c) Matrix for genet dynamics. Details of the symbols in the matrix  
738 elements are described in the text.

739 **Figure 2.** Eight clonal fragment patterns found in *Convallaria keiskei* and obtained  
740 information about clonal growth occurring in year  $t - 1$  and  $t$  in each fragment.

741 Years of aboveground growth were obtained from the 2005 (correspond to year  $t - 2$ ) to  
742 2007 (correspond to year  $t$ ) censuses and rhizome connections were derived from  
743 belowground excavation in 2007. The two right columns show the transition probability  
744 of clonal growth by focal (mother) ramets. Years and arrows in parentheses indicate birth  
745 years of offspring (right side of the arrow) and connections between the focal ramets (left  
746 side of the arrow). In case of year  $t - 1$  season of the column, year  $t$  at the right side of the  
747 arrow means clonal growth and no number is no clonal growth. In case of year  $t$  season,  
748 year  $t + 1$  at the right side of the arrow means clonal growth and no number is no clonal  
749 growth.

750 **Figure 3.** Posterior distributions of growth rates of the three dominant genets.

751 (a) When clonal growth and the survival-transition data were separated according to  
752 genets, (b) when clonal growth data were pooled and the survival-transition data were  
753 separated according to genets, and (c) when the survival-transition data were pooled and  
754 clonal growth data were separated by genet.

755 **Figure 4.** Posterior distributions of growth rates of the three dominant genets, with and  
756 without branching. Genets (a) e-1, (b) e-2 and (c) e-3.

757

#### 758 **Supplemental information**

759 **Appendix I:** Technical details in the statistical estimation of matrix elements in Methods

760 **Appendix II:** Summary of data

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

763 **Table S1b.** The number of clonal fragments of each fragment size (number of ramets  
764 in a fragment) in the three dominant genets.

765 **Table S1c.** The number of triplets consisting of one mother and one older daughter  
766 ramets and one new bud (Branching) and of non-tip ramets potentially branching clonal  
767 growth (Non-tip) in the three dominant genets.

768 **Table S1d.** The number of ramets having one, two or three new buds in the three  
769 dominant genets.

770 **Table S1e.** The number of ramets transmitted from size class  $k$  (rows) to  $l$  (columns)  
771 in the three dominant genets. Genets (1) e-1, (2) e-2 and (3) e-3.

772 **Table S1f.** The number of survival and dead ramets in each size class in three dominant  
773 genets from 2005 to 2006 in the three dominant genets.

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

775 **Appendix III:** Supporting results

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

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

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

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

787 **Table S2e.** Medians and 95% credible intervals (in parentheses) of the posterior  
788 distributions of the probabilities that ramets moved between size classes in the three  
789 dominant genets. Genets (1) e-1, (2) e-2 and (3) e-3.

790 **Table S2f.** Medians and 95% credible intervals (in parentheses) of the sensitivity for  
791 the clonal growth probabilities in each size class in the three dominant genets.

792 **Figure S1.** Morphological characteristics of underground organs and state of the field  
793 survey of *Convallaria keiskei*. A rhizome fragment connecting ramets and elongating  
794 at the tip (b) and the underground organ of a shoot (a); aboveground shoots in the study  
795 plot in the following year of making ramets (c, d). Sheath leaves start to expand  
796 aboveground (c) and fully expanded leaves of the existing ramets with pink tag and  
797 newly appearing one with orange tag (d).

798 **Figure S2.** A map of ramet distribution in a  $28 \times 2$  m plot for a *Convallaria keiskei*  
799 population. The X axis of  $X = 0-28$  corresponds to  $X = 20-48$  and Y axis of  $Y = 0-2$   
800 is  $Y = 50-52$  in the text. The ramets appeared at least once for the study periods were  
801 plotted.

802 **Figure S3.** The clonal growth probability of 1-y-tip and 2-y-tip ramets in each size  
803 class for the three dominant genets. Medians (solid line) and 95% credible intervals  
804 (dashed line) of the posterior distributions are shown. Genets (a) e-1, (b) e-2 and (c) e-  
805 3.

Table 1. Summary of census data of ramets in four genets in 2005, 2006 and 2007. The total number and number of surviving (SUR), newly emerged (NEW) and unemerged (UEM) ramets were calculated for each genet. Dashes indicate that data were neither calculated nor estimated.

\*Numbers in parentheses represent recovering ramets that did not emerge in the previous year.

†Numbers in parentheses represent unemerged ramets in the second successive year.

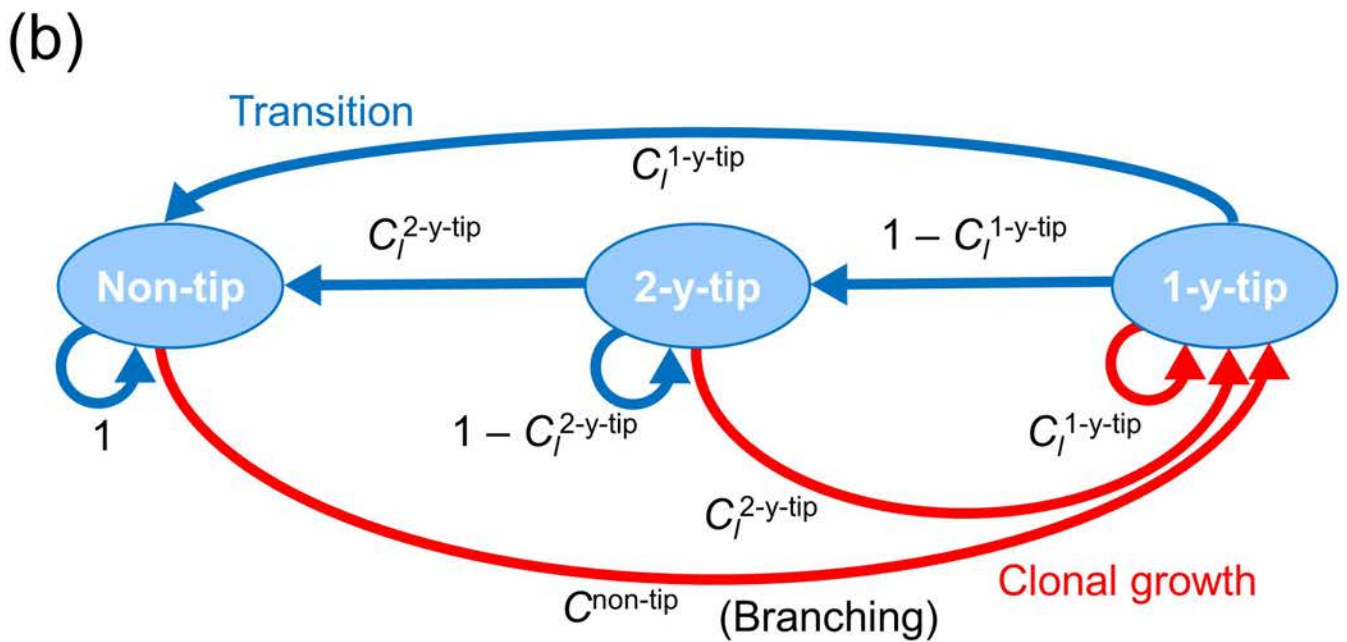
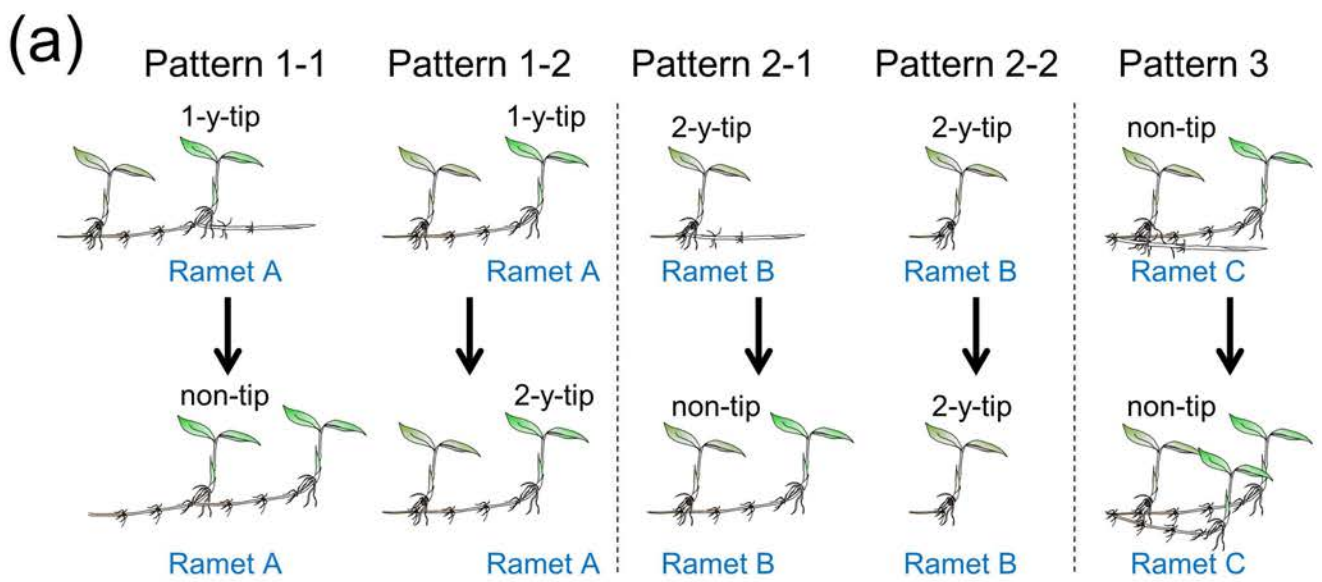
Genet ID	Year	No. of ramets			
		Total	SUR	NEW*	UEM†
e-1	2005	600	—	—	—
	2006	701	581	120	19
	2007	700	603	97 (8)	98 (11)
e-2	2005	108	—	—	—
	2006	137	104	33	4
	2007	131	119	12 (1)	18 (3)
e-3	2005	477	—	—	—
	2006	550	451	99	26
	2007	538	448	90 (16)	102 (10)
e-4	2005	236	—	—	—
	2006	297	227	70	9
	2007	319	255	64 (3)	42 (6)

808

Table 2. Number of fragments observed in the three genets and the total of each clonal fragment pattern. Patterns correspond to those illustrated in Figure 2.

Pattern*	Genet			Total
	e-1	e-2	e-3	
1	5	3	2	10
2	8	4	4	16
3	4	3	0	7
4	18	6	9	33
5	7	1	2	10
6	21	2	12	35
7	5	0	0	5
8	32	16	39	87

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(c) Survival and transition **T** and Clonal growth (reproduction) **R** matrices.

**Survival and transition **T****

year  $t$ , size class  $k$

		year $t - 1$ , size class $l$		
		1-y-tip	2-y-tip	Non-tip
1-y-tip		0	0	0
2-y-tip		$T_{kl}S_l$ $(1 - C_l^{1-y-tip})$	$T_{kl}S_l$ $(1 - C_l^{2-y-tip})$	0
Non-tip		$T_{kl}S_l C_l^{1-y-tip}$	$T_{kl}S_l C_l^{2-y-tip}$	$T_{kl}S_l$

**Clonal growth (reproduction) **R****

year  $t - 1$ , size class  $l$

		year $t - 1$ , size class $l$		
		1-y-tip	2-y-tip	Non-tip
1-y-tip		$N_k E_l^{1-y-tip}$ $C_l^{1-y-tip}$	$N_k E_l^{2-y-tip}$ $C_l^{2-y-tip}$	$N_k E_l^{non-tip}$ $C^{non-tip}$
2-y-tip		0	0	0
Non-tip		0	0	0

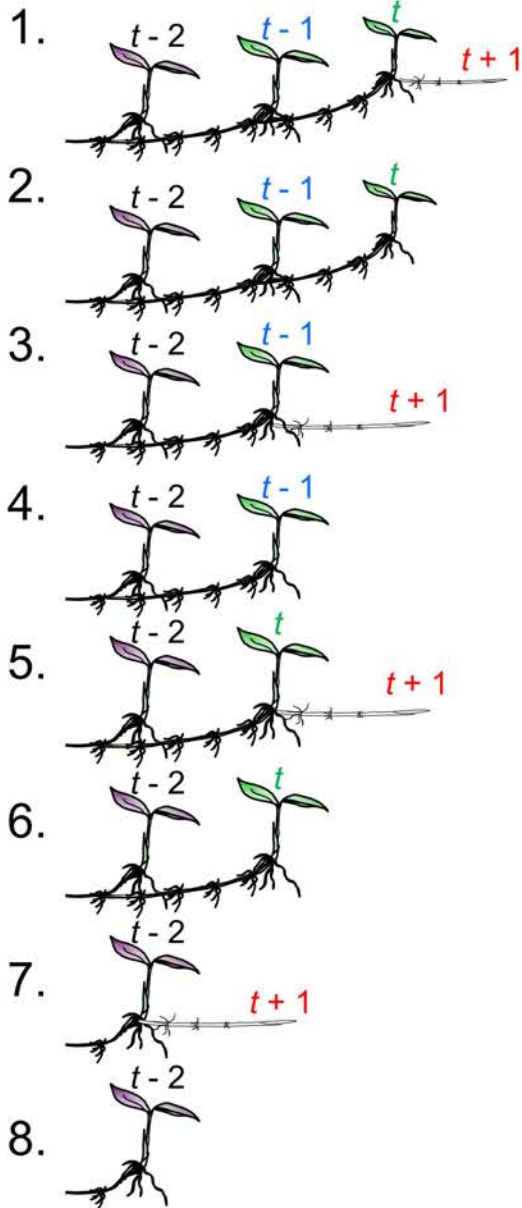
+

# Clonal growth

year  $t - 1$

year  $t$

Pattern



$$C_j^{1\text{-y-tip}} \\ (t-1 \rightarrow t)$$

$$C_j^{1\text{-y-tip}} \\ (t \rightarrow t+1)$$

$$C_j^{1\text{-y-tip}} \\ (t-1 \rightarrow t)$$

$$1 - C_j^{1\text{-y-tip}} \\ (t \rightarrow)$$

$$1 - C_j^{1\text{-y-tip}} \\ (t-1 \rightarrow)$$

$$C_j^{2\text{-y-tip}} \\ (t-1 \rightarrow t+1)$$

$$1 - C_j^{1\text{-y-tip}} \\ (t-1 \rightarrow)$$

$$1 - C_j^{2\text{-y-tip}} \\ (t-1 \rightarrow)$$

$$C_j^{2\text{-y-tip}} \\ (t-2 \rightarrow t)$$

$$C_j^{1\text{-y-tip}} \\ (t \rightarrow t+1)$$

$$C_j^{2\text{-y-tip}} \\ (t-2 \rightarrow t)$$

$$1 - C_j^{1\text{-y-tip}} \\ (t \rightarrow)$$

$$1 - C_j^{2\text{-y-tip}} \\ (t-2 \rightarrow)$$

$$C_j^{2\text{-y-tip}} \\ (t-2 \rightarrow t+1)$$

$$1 - C_j^{2\text{-y-tip}}$$

$$1 - C_j^{2\text{-y-tip}}$$



