Longevity of clonal plants: why it matters and how to measure it

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INTRODUCTION

The life span of plants, as in any other organism, is a key demographic trait for understanding life history (Weiher et al., 1999), population dynamics (Harper, 1977; Silvertown and Lovett Doust, 1993) and evolutionary fitness (Silvertown, 1991). Extended longevity of plants is believed to enlarge persistence of populations and thus affects community stability and vegetation responses to present and future climate change (Steinger et al., 1996; Eriksson, 2000; Körner, 2003; Garcia et al., 2008; Morris et al., 2008).

Unfortunately, there are few reliable data on genet longevity and genet turnover rates in plants, because these are difficult to measure (Dietz and Schweingruber, 2002). Known maximum longevity ranges from a few weeks in annuals (e.g. Bliss, 1971; Sharitz and McCormick, 1973) to thousands of years in some clonal herbs and trees (Table 1; e.g. Wherry, 1972; Lynch et al., 1998; Brunda et al., 2008). This wide variation seems to be due to trade-offs between life span and other fitness traits and because the modular construction of plants and their indeterminate growth counteract intrinsic senescence. The broad range in longevity also implies that there are considerable differences in the timescale of population dynamics and in the selective forces acting on individual plants.

In clonal plants, temporal gaps between years with successful sexual recruitment were found to be highly variable in length, from zero to thousands of years (Eriksson, 1989). For example, in high alpine meadows, sexual reproduction can be hampered due to a lack of pollinators or from low temperatures that inhibit seed germination. In such habitats, clonality can enhance genet longevity considerably, it can compensate for the partial loss of genets due to disturbance, and thereby it can secure population persistence for long periods of time. In general, clonal reproduction allows plants to benefit from a potential two-fold fitness, persistence of the product of a single zygote plus repeated economical offspring production (Aarsen, 2008).

Persistent clonal reproduction of an individual not only enhances longevity, but it can also lead to genets inhabiting large areas, because clonal plants have a pronounced capacity to spread horizontally (Stöcklin, 1992; Herben and Hara, 1997; Hutchings and Wijesinghe, 1997). Therefore, many studies use size and annual size increments of a genet to measure its age (e.g. Vasek, 1980; Steinger et al., 1996; Reusch et al., 1998; Wescue et al., 2005), although size and age are not always linearly correlated. It is important to note that longevity of a genet is independent of ramet life span, and thus the spatial structure of all ramets belonging to the same genet is only an incomplete mirror of the life history of the entire genet. When genets become fragmented and when annual growth increments indicate high interannual variability, the relationship between size and age becomes particularly weak.
Table 1. Size (usually diameter) and longevity (in years) of clonal plants from the literature, separated into trees, shrubs, herbs, grasses, other species, and with an indication of the method used for size or age determination

(a) Clonal trees

<table>
<thead>
<tr>
<th>Species</th>
<th>Method to estimate the size of the clone</th>
<th>Size of clone [diameter (m, or as indicated)]</th>
<th>Estimated age of oldest genet (years)</th>
<th>Estimated age of youngest genet (years)</th>
<th>Reference(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Olea europaea</em> subsp. <em>laperrinei</em></td>
<td>Molecular markers</td>
<td>80 m^2 +</td>
<td>1000 +</td>
<td>–</td>
<td>Baali-Cherif and Besnard (2005)</td>
</tr>
<tr>
<td><em>Picea abies</em></td>
<td>Radiocarbon dating, statistical analysis</td>
<td>–</td>
<td>10 000 – 12 000</td>
<td>–</td>
<td>Kullman (2008)</td>
</tr>
<tr>
<td></td>
<td>Molecular markers and dendrochronological analysis</td>
<td>691-3 m^2</td>
<td>1800 +</td>
<td>100</td>
<td>Laberge et al. (2000)</td>
</tr>
<tr>
<td><em>Populus alba</em></td>
<td>Molecular markers</td>
<td>–</td>
<td>&gt;12 000</td>
<td>–</td>
<td>Brundu et al. (2008)</td>
</tr>
<tr>
<td><em>Populus tremuloides</em></td>
<td>Morphological analysis, aerial photographs</td>
<td>510</td>
<td>10 000 +</td>
<td>–</td>
<td>Kemperman and Barnes (1976)</td>
</tr>
<tr>
<td></td>
<td>Microsatellite divergence based on mutation accumulation</td>
<td>–</td>
<td>12 000</td>
<td>14</td>
<td>Ally et al. (2008)</td>
</tr>
<tr>
<td><em>Populus tremula</em></td>
<td>Molecular markers</td>
<td>16</td>
<td>152</td>
<td>2</td>
<td>Suvanto and Latva-Karjanmaa (2005)</td>
</tr>
</tbody>
</table>

(b) Clonal shrubs

<table>
<thead>
<tr>
<th>Species</th>
<th>Method to estimate the size of the clone</th>
<th>Size of genet [diameter (m, or as indicated)]</th>
<th>Annual growth rate (cm year^{-1})</th>
<th>Estimated age of oldest genet (years)</th>
<th>Estimated age of youngest genet (years)</th>
<th>Reference(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Calluna vulgaris</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>58</td>
<td>–</td>
<td>Mork (1946)</td>
</tr>
<tr>
<td><em>Dryas octopetala</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>108</td>
<td>–</td>
<td>Kihlman (1890)</td>
</tr>
<tr>
<td><em>Empetrum nigrum</em> ssp. <em>nigrum</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>140</td>
<td>–</td>
<td>Bell and Tallis (1973)</td>
</tr>
<tr>
<td><em>Erica carnea</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>82</td>
<td>–</td>
<td>Schweingruber and Poschlod (2005)</td>
</tr>
<tr>
<td><em>Juniperus sabina</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>67–70</td>
<td>–</td>
<td>Molisch (1929)</td>
</tr>
<tr>
<td></td>
<td>Molecular markers</td>
<td>795 m^2</td>
<td>1.8–6.8</td>
<td>770–2940</td>
<td>–</td>
<td>Wescue et al. (2005)</td>
</tr>
<tr>
<td><em>Lomatia tasmanica</em></td>
<td>Molecular markers, chromosome counts and radiocarbon dating</td>
<td>1200</td>
<td>–</td>
<td>43 600</td>
<td>–</td>
<td>Lynch et al. (1998)</td>
</tr>
<tr>
<td></td>
<td>Molecular markers</td>
<td>20 m^2</td>
<td>2.6</td>
<td>300</td>
<td>–</td>
<td>Escaravage et al. (1998)</td>
</tr>
<tr>
<td></td>
<td>Molecular markers</td>
<td>25 m^2</td>
<td>115</td>
<td>283 +</td>
<td>28</td>
<td>Pornon et al. (2000)</td>
</tr>
<tr>
<td><em>Salix arctica</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>150</td>
<td>–</td>
<td>Kraus (1873)</td>
</tr>
<tr>
<td><em>Vaccinium vitis-idaea</em></td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>109</td>
<td>–</td>
<td>Callaghan (1973)</td>
</tr>
</tbody>
</table>
### (c) Clonal herbs (except grasses and sedges)

<table>
<thead>
<tr>
<th>Species</th>
<th>Method to estimate the size of the genet</th>
<th>Size of genet [diameter (m, or as indicated)]</th>
<th>Annual growth rate (cm year(^{-1}))</th>
<th>Estimated age of oldest genet (years)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acantholimon diapensoides</td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>400</td>
<td>Agakhanyantz and Lopatin (1978)</td>
</tr>
<tr>
<td>Anemone nemorosa</td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>&gt;5</td>
<td>Shireffs (1985)</td>
</tr>
<tr>
<td>Calamagrostis epigejos</td>
<td>Comparative analysis of site history and genet size</td>
<td>50</td>
<td>–</td>
<td>370</td>
<td>Brzosko et al. (2002)</td>
</tr>
<tr>
<td>Convallaria majalis</td>
<td>Growth ring analysis</td>
<td>850</td>
<td>–</td>
<td>670 +</td>
<td>Oinonen (1969)</td>
</tr>
<tr>
<td>Cypripedium calceolus</td>
<td>Molecular markers</td>
<td>39 ramets</td>
<td>1 – 1.5</td>
<td>252</td>
<td>McCarthy (1992)</td>
</tr>
<tr>
<td>Gaylussacia brachycerium</td>
<td>Morphological analysis</td>
<td>1980</td>
<td>–</td>
<td>13 000 +</td>
<td>Wherry (1972)</td>
</tr>
<tr>
<td>Teucrium scorodonia</td>
<td>Morphological analysis</td>
<td>Several square metres</td>
<td>–</td>
<td>50–100</td>
<td>Hutchinson (1968)</td>
</tr>
<tr>
<td>Trifolium alpinum</td>
<td>Growth ring analysis</td>
<td>–</td>
<td>–</td>
<td>50</td>
<td>Schweingruber and Poschlod (2005)</td>
</tr>
</tbody>
</table>

### (d) Clonal grasses and sedges

<table>
<thead>
<tr>
<th>Species</th>
<th>Method to estimate the size of the genet</th>
<th>Size of genet [diameter (m, or as indicated)]</th>
<th>Annual growth rate (cm year(^{-1}))</th>
<th>Estimated age of oldest genet (years)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carex curvula</td>
<td>Comparative analysis of site history and genet size</td>
<td>50</td>
<td>–</td>
<td>400 +</td>
<td>Oinonen (1969)</td>
</tr>
<tr>
<td>Carex ensifolia ssp. arctisibirica</td>
<td>Molecular markers</td>
<td>1.6</td>
<td>0.04</td>
<td>2000</td>
<td>Steinger et al. (1996)</td>
</tr>
<tr>
<td>Carex stans</td>
<td>Molecular markers</td>
<td>7.4</td>
<td>–</td>
<td>Approx. 150</td>
<td>Jónsdóttir et al. (2000)</td>
</tr>
<tr>
<td>Festuca ovina</td>
<td>Morphological analysis, cross-pollination tests</td>
<td>8.25</td>
<td>0.3</td>
<td>1000 +</td>
<td>Harberd (1962)</td>
</tr>
<tr>
<td>Festuca rubra</td>
<td>Morphological analysis, cross-pollination tests</td>
<td>22.0</td>
<td>2.2</td>
<td>1000 +</td>
<td>Harberd (1961)</td>
</tr>
<tr>
<td>Holcus mollis</td>
<td>Morphological and phenological analysis, chromosome analysis</td>
<td>880</td>
<td>–</td>
<td>1000 +</td>
<td>Harberd (1967)</td>
</tr>
<tr>
<td>Sasa senanensis</td>
<td>Molecular markers</td>
<td>300</td>
<td>Approx. 100</td>
<td>75</td>
<td>Suyama et al. (2000)</td>
</tr>
<tr>
<td>Stipa pennata</td>
<td>Calendar age determination (Gatsuk et al., 1980)</td>
<td>–</td>
<td>–</td>
<td>Several decades</td>
<td>Vorontzova and Zaugolova (1985)</td>
</tr>
</tbody>
</table>

### (e) Clonal pteridophytes and marine species

<table>
<thead>
<tr>
<th>Species</th>
<th>Method to estimate the size of the genet</th>
<th>Size of genet [diameter (m, or as indicated)]</th>
<th>Annual growth rate (cm year(^{-1}))</th>
<th>Estimated age of oldest genet (years)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lycopodium annotinum</td>
<td>Comparative analysis of site history and genet size</td>
<td>Up to 250</td>
<td>–</td>
<td>250</td>
<td>Oinonen (1967)</td>
</tr>
<tr>
<td>Lycopodium complanatum</td>
<td>Comparative analysis of site history and genet size</td>
<td>250</td>
<td>–</td>
<td>850</td>
<td>Oinonen (1969)</td>
</tr>
<tr>
<td>Pteridium aquilinum</td>
<td>Comparative analysis of site history and genet size</td>
<td>489</td>
<td>–</td>
<td>1400</td>
<td>Oinonen (1967)</td>
</tr>
<tr>
<td>Zostera marina</td>
<td>Molecular markers</td>
<td>1015</td>
<td>43</td>
<td>1180</td>
<td>Parks and Werth (1993)</td>
</tr>
</tbody>
</table>

Methods include growth ring analysis, morphological analysis, radiocarbon dating, comparative analysis of site history, molecular markers and microsatellite divergence (see text for more explanation).
With this in mind, genet age seems to be difficult to measure, even when the spatial extension of a genet is known. Nevertheless, there have been many attempts to measure maximum longevity in clonal plants, either for curiosity or because it can serve as an indicator of population persistence.

Currently, there is considerable effort to find alternative methods to estimate longevity that are not based on genet size. For example, molecular divergence based on somatic mutations and cell-growth estimates (Ally et al., 2008) or the proportion of ramets to genets (variation due to somatic mutation vs. recombination; Mock et al., 2008) are being used. Also stage-based population or transition-matrix models can be useful tools to investigate life history, dynamics and individual longevity (Ehrleén and Lehtilä, 2002).

Here we critically review the present knowledge on genet longevity in clonal plants, which ranges from a few months up to several thousand years. We summarize and discuss the methods that have been used to estimate genet age and we examine their suitability. A comprehensive overview of published life-span data for clonal trees, shrubs, herbs and grasses is presented in Table 1. Next to the discussion on the recent progress in genet life-span determination and its importance, we examine the literature on the topic of somatic mutations and the role of genet longevity for population dynamics and community stability.

MAXIMUM LONGEVITY OF CLONAL TREES, SHRUBS, HERBS AND GRASSES

Genet life span, a fundamental aspect for understanding life history, is one of the highly attractive but least accessible traits in plants (Dietz and Schweingruber, 2002). Measurements of life span in plants that goes beyond the simple classification into annuals, biennials and perennials is available primarily for trees, in which counting the annual growth rings is a convenient and direct way to determine age (Ehrleén and Lehtilä, 2002). With dendrochronology the ‘oldest living tree’ was found in Nevada, USA, a bristlecone pine (Pinus longaeva) about 4800 years old (Schulman, 1958; Brown, 1996; Lanner and Connor, 2001). For trees that are able to reproduce clonally, genet longevity was found to exceed the maximum age of single tree stems considerably. With dendrochronological analysis, an age of about 300 years was determined for a Picea mariana tree in 1981 (Légère and Payette, 1981; Table 1c). Twenty years later, using molecular markers, a genet of the same species consisting of several stems was estimated to be more than 1800 years old (Laberge et al., 2000). Genets of Populus tremuloides were found to form large forest patches up to 80 ha based on morphological analyses and analyses of aerial photographs. From this, an estimated longevity of 10 000 years has been suggested by Kemperman and Barnes (1976). Analysis of microsatellite divergence based on mutation accumulation about 30 years later revealed an age of 12 000 years for this species (Ally et al., 2008). Radiocarbon dating applied to fossil wood resulted in extreme life-span estimates for several clonal species (e.g. Picea abies, Kulman, 2008; Lomatia tasmanica, Lynch et al., 1998).

Genet age of non-trees has long been ignored in the literature, for example in biological floras (but see Poschlod et al., 1996). Only in the second half of the 20th century did researchers start to determine the life span of shrubs, herbs and grasses. Direct measurements of morphological structures, such as via herbchronology, usually account for maximum ages of only a few decades, for example 50 years for the clonal herb Trifolium alpinum (Schweingruber and Poschlod, 2005; Table 1c). With more recent methods, which will be described below, longer genet life spans have been reported in shrubs, herbs and grasses (e.g. Escaravage et al., 1998; Stehlík and Holderegger, 2000; Wesche et al., 2005), indicating that these life forms can reach maximum ages of one to several hundreds of years and, in some cases, thousand years (Table 1b–e). Hence, there is no indication from the available literature that genets of shrubs, herbs or grasses have potentially lower life spans than trees, but plant life forms of shrubs, herbs and grasses that can be safely attributed to a single genet are usually much younger than the massive outliving stems of trees.

Maximum age estimates may be in part a product of curiosity. Scientifically, they are an indication of the slowest possible genet turnover rate in a population. Moreover, they tell us more about adult survival relevant for an understanding of the life history and demography of a species (Silvertown et al., 1993; Franco and Silvertown, 1996). However, the maximum longevity ever recorded for a species depends on the sampling effort taken and of the methods used, making it difficult to compare the data.

METHODS TO MEASURE LIFE SPAN IN PLANTS

Direct methods

The following direct methods have been used to determine the life span of clonal plants. (1) Analysis of annual growth rings, a widely used method usually applied to stems of trees, can also be applied to herbs and shrubs that have primary root systems or woody stems with visible growth rings (herbchronology; Zoller, 1949; Dietz and Ullmann, 1997; Schweingruber and Dietz, 2001; Dietz and Fattorini, 2002). Schweingruber and Poschlod (2005) determined the life span of many species with this method and included a critical evaluation of the method. Growth ring analysis is relatively quick, and makes comparisons among successional stages or ecosystems easily possible (Dietz and Ullmann, 1998; Kuen and Erschbamer, 2002; Erschbamer and Retter, 2004; Jönsson, 2004; Von Arx and Dietz, 2005; Perkins and Parks, 2006; Kuss et al., 2008). With this method, for example, it was found that Vaccinium myrtillus ramets were significantly younger on ski pistes in the Swiss Alps than in control plots (Rixen et al., 2004). (2) Radiocarbon (C14) dating is usually applied to organic remains of archaeological sites (e.g. Vasek, 1980; Kullman, 2008), but is relatively expensive. These first two methods are only reliable for clonal plants when the oldest parts of the genet are still in place and can be identified. Another disadvantage is that these two methods normally result in single age estimates not useful for population demographic analysis. (3) Growth-form or phenological analysis based on annual morphological markers (e.g. Troll, 1937; Harberd, 1967; Kemperman and Barnes, 1976; Kulman and Kulman, 1991; García and Antor, 1995;...
Jäger et al., 1997) is used to study growth strategies, age-related patterns, size and age distribution or survivorship curves. By counting annual growth increments, Callaghan (1980) estimated an age of 21 years for a genet of the clonal plant Lycopodium annotinum (Table 1e). (4) Permanent plot research involves long-lasting research efforts, but yields highly reliable age determinations (e.g. Bärlocher et al., 2000; Erschbamer and Winkler, 2005). This method is especially appropriate for use in geophytes, such as orchids, which may disappear from above ground for years (Tamm, 1948, 1956; Inghe and Tamm, 1985). (5) Age determination by colour band analysis in grassstrees allows for the reconstruction of fire history (Ward et al., 2001; Colangelo et al., 2002).

Less known and seldomly applied methods include (6) comparative analysis of site history (Oinonen, 1967), (7) age state determination (Rabotnov, 1950; Gatsuk et al., 1980; Kawano, 1985; Vorontzova and Zaugolnova, 1985) and (8) chromosome analysis (Harberd, 1967).

Only rarely has a life span longer than 200 years been found with the above listed direct methods (Table 1). The main drawback is that only surviving and connected plant structures can be measured and attributed, with certainty, to a particular genet. Therefore, direct measurements systematically underestimate the longevity of clonal plants.

**Indirect estimates of age**

The size or diameter of a genet can be divided by a measure of mean annual size increment (Suvanto and Latvakarjanmaa, 2005), yielding an indirect estimate of its age. Several maximum age estimates are based on this method (e.g. Steinger et al., 1996; Reusch et al., 1998). Clonal plants covering large areas can intermingle with other genets and the longer they survive, the more likely they are to become fragmented or to partially die. This hampers easy recognition of entire genets by eye. To overcome these difficulties, some scientists have used genet-specific morphological markers or self-incompatibility tests to detect the size of genets and to determine their age. Harberd (1962, 1967; Table 1d), for example, reported extremely large sizes and old ages for Festuca rubra (diameter 220 m) and Holcus mollis (880 m) based on self-incompatibility tests. Barsoum et al. (2004) identified genets by excavation of root connections, but this method is strongly invasive and causes biases when roots graft naturally or connections are lost over time. Today, the use of DNA fingerprinting techniques, discussed further below, facilitates precise genet identification.

The accuracy of such indirect age estimates largely depends on the reliability of the annual size increment measurement. Size increments can be highly variable among individuals depending on ontogenetic development, successional stage, competitive and nutritional conditions, and environmental factors. The larger and older a genet is, the more critical it is to estimate its expansion rate over the entire life span. Age estimates are therefore generally less accurate than estimates of genet size, and also because the relationship between size and age is not always linear in clonal plants. Therefore, age estimates of genets should include such putative variation, but this is rarely the case (but see Vasek, 1980).

**The use of DNA fingerprinting**

Although the methods used to measure the size of clonal plants, discussed above, may be doubtful or might not recognize the total size of large genets, modern molecular analysis of leaf samples now allows for a better identification of entire genets. In recent decades, genet identity has been revealed by genetic markers such as allozymes (e.g. Stehlik and Holderegger, 2000) and DNA fingerprinting techniques such as microsatellites (e.g. Suvanto and Latva-Karjanmaa, 2005), random amplification of polymorphic DNAs (e.g. Laberge et al., 2000) or amplified fragment length polymorphisms (e.g. Escaravage et al., 1998). With molecular markers, individuals can be distinguished, allowing spatially explicit sampled plant material to be assigned to genets. Based on the use of a defined sampling distance, genet size can be determined and then divided by a measure of annual growth increment to obtain age information. Using DNA fingerprinting, the oldest genet occurring in a population of the alpine clonal dwarf shrub Rhododendron ferrugineum was estimated to be 300 years (Escaravage et al., 1998; Table 1b) and a genet of the alpine grassland species Carex curvula was found to be an estimated 2000 years old (Steinger et al., 1996; Table 1d).

The use of DNA fingerprinting techniques has the advantage that a large number of markers can be developed easily and at low cost (Jones et al., 1997; Mueller and Wolfenbarger, 1999). Further advantages include the possibility to sample over large spatial scales and that it causes minimal impact on populations. Unfortunately, there is still some ambiguity associated with two types of molecular assignment errors: misidentification of genetically similar ramets as one genet and misidentification of dissimilar fingerprints as genetically distinct individuals (Widen et al., 1994). Repeated samples coming from the same genet but from different ramets do not always have identical fingerprints. This may result from somatic mutations, from contamination in the laboratory, or from scoring errors that may happen during data analysis (Arens et al., 1998; van der Hulst et al., 2000; Douhovnikoff and Dodd, 2003). Bias introduced by scoring errors has been underestimated until recently (Pompon et al., 2005; Arnaud-Haond et al., 2007; Bonin et al., 2007), but it is now accepted how crucial it is to apply repeatability tests and statistical tools to critically evaluate error probability in molecular fingerprinting studies (Lasso, 2008).

In crop science, DNA fingerprinting has achieved importance because this technique is used to identify genetic relationships between cultivars and establishes pedigree reconstructions. Thereby, the life span of several cultivars was revealed, for example grapes (Vitis vinifera). For the clonally propagated and economically important grapevine cultivar ‘Albarino’, from north-western Spain, which is being used in a recent breeding programme, was given an estimated age of 200–300 years (Alonso et al., 2007). ‘Rouge du Pays’, presently cultivated in the Valais (Switzerland), was already mentioned in a manuscript from the year 1313 (Vouillamoiz et al., 2003), suggesting an even longer life expectancy for grapevine cultivars.

The crop plant vanilla (Vanilla planifolia) is propagated only vegetatively in many areas due to a lack of pollinators. On islands in the Indian Ocean, where the plants have been
cultivated since the early 1800s, almost all accessions were found to constitute a single and probably very old genet (Bory et al., 2008; Lubinsky et al., 2008).

Overall, molecular size determination in clonal plants has led to better insights into population size and age structure owing to the extensive and qualitative genet detection. However, its accuracy can be impaired by genetic assignment errors due to somatic mutations and scoring mistakes. Therefore, efforts to improve the molecular assignment are necessary for reliable results.

**Demographic approaches to longevity**

Increasingly, studies are using size- or stage-structured matrix models to estimate demographic properties of long-lived plants (Callaghan, 1976; Erschbamer, 1994; Erschbamer and Winkler, 1995; Molau, 1997; Erschbamer et al., 1998; Diemer, 2002; Nicolé et al., 2005; Weppeler et al., 2006). Such models are usually based on ramet dynamics but are nevertheless helpful because they allow us to overcome the difficulties of the long observation periods necessary to understand population processes in clonal plants (Watkinson and Powell, 1993). Demographic data of long-lived clonal plants at the genet level are still scarce (Menges, 2000), and very few studies have used matrix models and population viability analysis techniques to investigate genet longevity and population persistence. A notable exception is the work of Colling and Matthies (2006) on Scorzonera humilis, which revealed low mortality of adult genets and a life expectancy of several decades.

In a few cases, the transition probabilities between plant size stages or age stages in matrix models were used to estimate life span or population age distribution (Cochran and Ellner, 1992; Barot et al., 2002). For Silene acaulis, for example, a size-based projection-matrix model revealed a life expectancy of more than 300 years for genets (Morris and Doak, 1998). Ehrlén and Lehtilä (2002) reviewed population matrix models for 71 herbaceous perennials and calculated species life spans ranging from 4 to approx. 1000 years, whereby more than half of the studied species had a life expectancy over 35 years. Their results agree reasonably well with previously published age estimates for long-lived plant species. However, most matrix models for clonal plants used in their study (86%) were based on ramet data. It is important to recognize that understanding the life history of clonal plants should involve investigations at the genet level, too (Harper, 1977; Cook, 1985; de Steven, 1989; Eriksson, 1993; Fair et al., 1999; Tanner, 2001; Araki et al., 2009), although ramet dynamics may be used as an indirect measure of genet fitness, population growth and persistence (Caswell, 1985; Eriksson and Jerling, 1990; Weppeler et al., 2006). For example, Eriksson (1994) predicted that clonal populations of Potentilla anserina, Rubus saxatilis and Linnaea borealis consisting of more than 250 ramets are able to persist much longer than 50 years despite a negative population growth rate.

A challenge will be to employ demographic techniques on genet data obtained by molecular genotyping studies to make more accurate predictions at the genet level. For example, in a combined demographic–molecular approach to study growth patterns, reproduction and spatial expansion at the ramet level, it was possible to reveal spatio-temporal patterns at the genet level, and thus the characteristics particularly relevant to clonal life histories and population viability (Araki et al., 2009; see also de Steven, 1989; Torimaru and Tomaru, 2005).

**Somatic mutations and life span measurements**

The use of genetic divergence generated by somatic mutations is a novel approach to measure genet size and to estimate life span (Heinze and Fussi, 2008). It is based on the fact that constant division of mitotic cells in clonal plants leads to the accumulation of somatic mutations over time (‘somatic mutation theory of clonality’, Klekowski, 1997). With this method, Gil et al. (2004; Table 1a) were able to date the origin of an Ulmus procera genet back to the time of the Romans, with some of its ramets growing as far apart as in Spain and Britain. The effective vegetative propagation and the deliberate plantation of this elm variety by humans explain the large distance between its ramets. In Populus tremulooides, molecular divergence detected by microsatellites was related to clone age with the help of demographic models of ramet and genet dynamics (Table 1a; Ally et al., 2008). The resulting age estimates were up to 12 000 years, indicating that genet size of Populus tremulooides actually is not related to their life span. The formation of extra petals due to somatic mutations in buttercup (Ranunculus repens) was the key to establish a quick method to estimate the age of meadows by Warren (2009). Based on the frequency of this phenotypic change in buttercup of pastures of known age, he established a relationship between phenotypic change and meadow age. There is a similar link between increased frequency of pollen abortion and genet age for several clonal species (Harberd, 1967; Brighton et al., 1983). However, thus far, somatic mutation rates have rarely been used for life span estimates, because somatic mutations cannot yet be detected efficiently (Gil et al., 2004), and because somatic mutations are difficult to distinguish from allelic variation (Heinze and Fussi, 2008). Moreover, molecular divergence, due to somatic mutations, may differ between species (Klekowski and Godfrey, 1989), among populations (Gill et al., 1995) and among genets (Schaal and Leverich, 1996), probably because somatic mutations may occur in response to environmental stress. In genets of Pinus longaeva ranging in age from 23 to 4713 years, no age-related accumulation of somatic mutations was detected at all (Lanner and Connor, 2001), while molecular divergence was found in distinct ramets of wild olive trees about 1000 years old (Baali-Cherif and Besnard, 2005). The incertitude concerning measured rates of somatic mutations remains a main concern for the precision of indirect life span estimates.

**Senescence and ageing in clonal plants**

Clonal plants are considered to be immortal and several extreme life spans reported seem to confirm this. Senescence, defined here as the apparent weathering or a highly regulated deteriorative process (Leopold, 1975; see also Munné-Bosch, 2008), has indeed never been observed...
Longevity and population persistence of clonal plants

Among the many traits enhancing population persistence, longevity of genets is, by far, the most important (Weih et al., 1999). Even populations that have a negative population growth rate are able to persist for long time periods due to the slow turnover rates of genets. The low extinction probability of genets results in a high persistence of well-established populations, which is typical for most clonal plant species (Helm et al., 1996). Eriksson (1996, 2000) assessed the causal relationship between long-lived remnant populations and their function within their ecosystem. He suggests that remnant populations increase community and ecosystem stability as well as ecosystem resilience. First, this is due to vegetative recruitment that can directly buffer environmental variation experienced by a clonal population. Second, community resilience is increased by the continuous maintenance of similar habitat conditions created by the populations themselves, by balanced nutrient cycling and by enhanced (re-)colonization after disturbances. This phenomenon of positive species interactions stabilizing communities is also known as facilitation, an important process in community organization (Bertness and Leonard, 1997; Bruno et al., 2003).

Arctic and alpine permanent vegetation types, such as grasslands and dwarf-shrub heaths, have been found to be very stable communities that have not been affected by past and recent climate changes (Grabherr and Nagy, 2003). The main reason for this appears to be the longevity of the mainly vegetatively reproducing members of such communities, reinforcing the hypothesis that long-lived clonal plants can enhance community and ecosystem resilience, thereby slowing vegetation change as a consequence of global warming (Guisan and Thuiller, 2005). On the other hand, analysis of available observational data has also revealed range expansions for several clonal species towards higher altitudes or latitudes (Pauli et al., 1996; Walther et al., 2002). Plant responses to artificially applied climate change included increased flowering, increased senescence of old modules and altered internal resource ratios (Carlsson and Callaghan, 1994; Callaghan et al., 1997; Grabherr et al., 2000). The indirect consequences were an increased rate of genet turnover and an increase of youger age-classes, indicating changes in population dynamics and structure. But more empirical data on current changes and the potential buffering of environmental variation by clonal plants will be necessary to make safe predictions about the future fate of old clonal populations when climate change is accelerating. Moreover, there is a need for studies that investigate population demography and viability. There are many age estimates for single genets, but there is only limited information on the variability of genet size and age at the population level that can form a basis for studies on the dynamics and persistence of clonal plant populations (Ponnor et al., 2000; van Kleunen et al., 2001; Erschbamer and Winkler, 2005; Scheepens et al., 2007). Depending on competitors and the success of seedling recruitment in dense populations, genets within a clonal population can differ considerably in size or age.

The level of genetic diversity is another important issue for the population viability of clonal plants. High genetic diversity can enable adaptation to changing climates, which in turn increases the persistence of populations. Asymmetric competition among differently sized genets can result in self-thinning, diversity loss and, in extreme cases, a monoclonal stand (Harberd, 1962; 1967; Oinonen, 1967; Williams, 1975). However, because clonal plants grow horizontally rather than in height, competition among genets is often found to be symmetric and genet diversity is maintained (Soane and Watkinson, 1979; Hartnett and Bazzaz, 1985; Cain, 1990; de Kroon et al., 1998).
1992; Hara, 1994; van Kleunen et al., 2001). Low sexual recruitment has long been reported to be a common feature of clonal plant populations (Eriksson, 1989; Schmid, 1990), but their size and age structure seem to be strongly shaped by sexual recruitment patterns (Kudoh et al., 1999; Weppner et al., 2006; Stöcklin et al., 2009). Molecular studies of clonal plants found on average similar high levels of genetic diversity in clonal populations as in other plant species, indicating that seed recruitment does at least occasionally occur (Nybom, 2004) and that low levels of seedling recruitment in clonal plants are compensated for by the longevity of genets. In several populations of Rhododendron ferrugineum, next to very large and old individuals of about 260–300 years, many small and probably young genets were found (see Table 1; Escaravage et al., 1998; Pormon et al., 2000). Repeated seedling recruitment was also detected in populations of Ranunculus repens (Soane and Watkinson, 1979), Calystegia collina (Wolf et al., 2000), in the rare orchid species Cypridipedium calceolus (Brzosko et al., 2002; Table 1c) and in populations of Uvularia perfoliata (Kudoh et al., 1999), Studies that combine the estimation of maximum age with an investigation of genet size and age structure and a demographic analysis of ramet growth and seedling recruitment will help us to better understand population persistence, and will allow inferences to be made about their fate.

CONCLUSIONS

Our knowledge of plant longevity remains limited, particularly for clonal species. Methods to measure clonal plant age are either not appropriate, laborious or have inherent uncertainties. However, life span estimates of genets achieved by indirect methods, demographic approaches and the use of somatic fingerprints have increased our empirical knowledge considerably and thereby understanding of the structural and demographic properties of clonal plant populations. Maximum age estimates range from a few to several thousands of years and are an indicator for the slowest possible genet turnover rate and for population persistence. New molecular tools, used to estimate age indirectly, allow the investigation of size and age structure of whole populations instead of single genets and also on larger scales. Plant size estimates based on molecular fingerprinting can be critically evaluated with statistical methods, improving their accuracy. Because this is less the case for estimates of annual growth increments over hundreds or even thousands of years, age estimates are generally less accurate than estimates of genet size. Nevertheless, together with information on demography at the ramet and genet level, molecular data on whole populations provide a better tool to evaluate species life history and population viability.

Next to maximum longevity, genet size and age structure, demography and genet diversity will be important for predicting population persistence in clonal plants and their ability to enhance community stability and ecosystem resilience under global change.

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