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First *vs.* second rotation of a poplar short rotation coppice: Above-ground biomass productivity and shoot dynamics

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ABSTRACT

Within the global search for renewable energy sources, woody biomass from short rotation coppice (SRC) cultures is a valuable option. So far there is a shortage of large-scale field yield data to support stakeholders. We investigated an operational-scale SRC plantation (POPFULL) with 12 poplar genotypes in Flanders during its first two biennial rotations. By inventorying shoot numbers and diameters, combined with allometric relationships, productivity related data were derived after each growing season. We observed significant variation in biomass yield and productivity-related characteristics among the 12 poplar genotypes, of which two recently selected. Genotype Hees (*Populus deltoides* × *Populus nigra*) and Skado (*Populus trichocarpa* × *Populus maximowiczii*, selected in 2005) reached the highest productivity among genotypes, i.e. 16 Mg ha^{-1} y^{-1} of dry matter (DM) yield in the second rotation, which was more than double than the poorest performing genotype Brandaris (a pure *P. nigra*). However, with many small shoots genotype Hees had a different growth strategy than Skado that resprouted with few, thicker and higher shoots. Biomass production increased from a plantation average of 4.04 Mg ha^{-1} y^{-1} of DM in the first (establishment) rotation to 12.24 Mg ha^{-1} y^{-1} in the second rotation. Mean height growth raised from 2.08 m y^{-1} during the first rotation to 2.99 m y^{-1} during the second rotation. The influence of the first coppicing on tree mortality was negligible. Monitoring of subsequent rotations over the plantations' lifetime — which counts for SRC bioenergy cultures in general — is essential to evaluate productivity in the long term.

1. Introduction

Short rotation coppice (SRC) cultures can be a potential option to meet the increasing demand for woody biomass as a renewable energy source [1–3]. Despite the fact that the amount of research on SRC plantations is increasing, data on the productivity are so far rather scarce and limited to small experimental-scale plantations. Studies have shown that small-scale plantations tend to overestimate biomass production values [4–6]. As Searle and Malins [5] concluded when reviewing energy crop yields, more realistic yield data from

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commercial-scale SRC fields are needed for stakeholders to set targets for the support of bioenergy.

The success of an SRC plantation largely depends on its sustainability and biomass yield, which is on its turn for a major part dependent on the choice of the genotypic materials next to management practices and site conditions [7−9]. To decrease cultivation risks as diseases, insects or pests, it is necessary to use a sufficiently broad genetic diversity among the planted genotypes. At the same time it is important to examine how much genetic variation is available in particular traits in order to determine the selection efficiency of a certain trait in future breeding and selection programs [10,11]. The advantage of the genetic variation is often challenged by the demand of industry for uniform biomass quality (e.g. importance of shoot or stem size for harvesting; wood quality for processing). Therefore, more comparative data are needed for different genotypes, especially for the more recently produced genotypes, and over different rotations under larger scale operational conditions. It has already been shown that weed control during the establishment year is of crucial importance in SRC plantations, regardless of genotypes or site conditions [12−14]. Besides weed problems, diseases as rust infections are a common cause of tree mortality [15]. Nearly all poplars (*Populus* spp.) and all willow species (*Salix* spp.) − both in the *Salicaceae* family − have vigorous regrowth after coppicing [16,17]. Poplars resprout after coppicing with 5−25 shoots per coppiced tree. Due to self-thinning, the number of sprouted shoots reduces with up to 75% within the first growth year. Shoot mortality occurs mostly among the smallest shoots, in favor of the largest shoots whose dominance increases. From a scientific point of view (understanding shoot population dynamics, biomass productivity determinants) as well from an applied perspective (yield, uniformity in size of shoots to be harvested) the changes between different rotations in biomass productivity and in shoot dynamics need to be examined in more detail.

In 2010 an operational-scale SRC plantation for bioenergy purposes was established with 12 poplar genotypes in Flanders. The plantation was studied during the first (single-stem) biennial rotation and the second biennial rotation after coppice (2010−2014). This study is part of an ambitious large-scale project (POPFULL [18]) aiming to make a full greenhouse gas balance and to investigate the economic and energetic efficiency of a SRC culture with poplar. Within the context of the POPFULL project, the objectives of this study were: (i) to quantify the biomass production of the plantation during both rotations; (ii) to determine the impact of coppicing on productivity and related productivity characteristics; and (iii) to study the variation among the 12 poplar genotypes over the four years and to assess the first yield data of a number of recently (2005) selected and released poplar genotypes.

2. Materials & methods

2.1. Site description and plant material

The POPFULL SRC site is located in Lochristi, Belgium (51°06′44″ N, 3°51′02″ E). The climate is temperate oceanic with a long-term mean annual temperature and precipitation of 9.5 °C and 726 mm, respectively (Royal Meteorological Institute of Belgium [19]). According to the Belgian soil classification the site is part of the sandy region with poor natural drainage [20]. The groundwater table fluctuates throughout the year between 0 cm and −140 cm below ground level, being on average 100 cm higher during winter than during summer [21,22]. The 18.4 ha site was a former agricultural area consisting of croplands (62%) and extensively grazed pasture (38%). An area of 14.5 ha (excluding the headlands that remained unplanted) was planted on 7−10 April 2010 with 12 selected and commercially available poplar and three willow genotypes. The poplar genotypes represented different species and interspecific hybrids of *Populus deltoides* Bartr. (ex Marsh.), *Populus maximowiczii* Henry, *Populus nigra* L., and *Populus trichocarpa* Torr. & Gray (ex Hook.). The present study focuses on the poplar genotypes only; details on the origin and the parentage of the 12 genotypes are shown in Table 1.

Six of the 12 genotypes were bred by and obtained from the Institute for Nature and Forestry Research in Geraardsbergen (Belgium). Genotype Robusta originates from an open-pollinated *P. deltoides* tree, first commercialized by the nursery Simon-Louis Frères (Metz, France). The other five genotypes were bred by "De Dorschkamp" Research Institute for Forestry and Landscape Planning in Wageningen (The Netherlands) and, as Robusta, obtained from the Propagation Nurseries in Zeewolde (The Netherlands). Preceding the planting, soil preparation included ploughing (40−70 cm depth), tilling and the application of a pre-emergent herbicide treatment. Using an agricultural leek planting machine, the 25-cm-long dormant and unrooted cuttings were planted in a double-row planting scheme with alternating inter-row distances of 0.75 m and 1.50 m and a distance of 1.10 m between trees within the rows, corresponding to a tree density of about 8000 ha^{-1}. The plantation was designed in large (0.16−0.61 ha) monoclonal blocks of eight double rows wide that covered the two types of former land use (cropland and pasture). The minimum of two and maximum of four replicated blocks of each genotype, with row lengths varying from 90 m to 340 m, were based on the available number of cuttings and on the spatial configuration of the site.

During the first months after planting intensive weed control − mechanical, chemical and manual − was applied to decrease competition for light and nutrients (details in Ref. [12]). Otherwise, plantation management was extensive, without fertilization or irrigation. After two years of growth (2010 and 2011), i.e. at the end of rotation 1 (R1), the plantation was harvested for the first time on 2−3 February 2012 with commercially available SRC harvesters (described in Ref. [23]). From then on, trees continued to grow as a coppice culture with multiple shoots per stool in the following biennial rotation, i.e. rotation 2 (R2). The second harvest took place on 18−20 February 2014, partly manually and partly by mechanical SRC harvesters (described in Ref. [24]).

2.2. Shoot diameter and mortality

Tree mortality, number of shoots per tree and shoot diameter were assessed as the main productivity characteristics in winter − during the dormant stage − at the end of each growing season (GS). For reasons of spatial

Table 1 – Place of origin, botanical and parental characteristics of the twelve poplar (Populus) genotypes studied (adapted from Verlinden et al. [32]). D = Populus deltoides, M = Populus maximowiczii, N = Populus nigra, T = Populus trichocarpa.

Genotype	Parentage	Section	Place of origin	Gender	Year of cross/commercialization
Bakan[a]	T × M	Tacamahaca	(Washington US × Oregon US) × Japan	♂	1975/2005
Skado[a]	T × M	Tacamahaca	(Washington US × Oregon US) × Japan	♀	1975/2005
Muur[a]	D × N	Aigeiros	(Iowa US × Illinois US) × (Italy × Belgium)	♂	1978/1999
Oudenberg[a]	D × N	Aigeiros	(Iowa US × Illinois US) × (Italy × Belgium)	♀	1978/1999
Vesten[a]	D × N	Aigeiros	(Iowa US × Illinois US) × (Italy × Belgium)	♀	1978/1999
Ellert[b]	D × N	Aigeiros	Michigan US × France	♂	1969/1989
Hees[b]	D × N	Aigeiros	Michigan US × France	♀	1969/1989
Koster[b]	D × N	Aigeiros	Michigan US × The Netherlands	♂	1966/1988
Robusta[c]	D × N	Aigeiros	Eastern US × Europe	♂	1885-1890/1895
Grimminge[a]	D × (T × D)	Aigeiros × (Tacamahaca × Aigeiros)	(Michigan US × Connecticut US) × (Washington US × (Iowa US × Missouri US))	♂	1976/1999
Brandaris[b]	N	Aigeiros	The Netherlands × Italy	♂	1964/1976
Wolterson[b]	N	Aigeiros	The Netherlands	♀	1960/1976

[a] Genotypes bred by the Institute for Nature and Forestry Research (INBO, Geraardsbergen, Belgium).
[b] Genotypes bred by Research Institute for Forestry and Urban Ecology "De Dorschkamp" (Wageningen, The Netherlands).
[c] Genotype originating from an open-pollinated P. deltoides tree, first commercialized by the nursery Simon-Louis Frères (Metz, France).

representativeness, measurements were carried out in one entire row (between 80 and 310 trees) within each monoclonal block. Mortality was determined as the relative amount of missing trees in a row. Missing trees were counted, which could be done accurately since trees were planted on regular within-row distances. Before the first coppice (during GS1 and GS2), the majority of trees had one single shoot (or stem). Shoot diameters were measured for every tree in the row. For the second rotation (GS3 and GS4), when trees had a coppice structure, the number of shoots per tree was counted for every tree in the row and shoot diameters were measured for every fifth tree in the row. Shoot diameters were measured with a digital caliper (Mitutoyo, CD-15DC, UK, 0.01 mm precision) at 22 cm above soil level (according to [25]) after GS1 and GS2, and at 22 cm above the stump insertion height for coppiced trees in GS3 and GS4. Shoots with a diameter at 22 cm height (D) smaller than 5 mm were ignored from the inventory (neither counted, nor measured). The stem basal area at 22 cm height of each tree was subsequently calculated as the sum of the basal areas of all shoots within the tree.

2.3. Above-ground biomass and tree height

For each genotype allometric relationships were established linking above-ground woody (dry) biomass to shoot diameter. These genotypic allometric relationships were determined twice, once after R1, in December 2011 and a second time after R2, in January 2014. Based on the shoot diameter distribution after GS2, ten shoots per genotype were selected for destructive harvest, covering the widest possible diameter range. Following a diameter measurement at 22 cm height (D), the shoot was harvested at 15 cm above soil level, the mean harvesting height of the plantation (cfr. [23]). Dry biomass (DM) of each shoot was determined by oven drying in the laboratory for 10 days at 70 °C. Biomass values were plotted against diameter and fitted as $DM = a \cdot D^b$ for each of the 12 genotypes (with 'a' and 'b' regression coefficients; cfr. [25,26]). Genotypic means for woody biomass production were derived from the allometric equations combined with the shoot diameter inventory data. This procedure was repeated after GS4 (at the end of R2), with eight harvested shoots per genotype. Shoots were cut at 7 cm above the insertion point with the stump. For the trees of which shoot diameters were measured (ca. 20% of the trees per block), the biomass of every shoot was estimated using the allometric relationship. The estimated shoot DM per block was then averaged to obtain an above-ground biomass value for a theoretical 'average shoot' per block. This value was multiplied with the number of shoots per tree to estimate DM of trees of which the shoot diameters were not measured. For trees of which the shoot diameters were measured, shoot biomass was summed per tree to obtain tree biomass. Considering the inventory data as spatially representative for the blocks – and for the plantation as a whole – a mean tree DM value was calculated per monoclonal block. Using the planting distances, the attained biomass production values were converted to area based values [Mg ha^{-1}] (DM) at the end of each rotation. Genotypic values were calculated taking into account the (relative) area coverage of the multiple blocks for each genotype.

After GS1, tree height was measured for all trees included in the inventory, using a telescopic rule (Nedo mEssfix-S, NL, 1 mm precision). For GS2-GS4 tree height was determined indirectly through a linear relationship with diameter applied to the diameter inventories. At the time of harvesting the length of the shoots — that were used to establish the allometric relationships with biomass (see supra) — was measured with a tape measure (1 mm precision). Plotting these lengths against shoot diameter at 22 cm per genotype resulted in linear relationships (all with $R^2 > 0.87$). Subsequently the height of the trees included in the diameter inventories was estimated applying these linear equations, where the length of the thickest shoot was taken as the tree height.

2.4. Total plantation yield

We used three different approaches to assess the overall yield of the entire SRC plantation. As a first approach the detailed DM estimations made-up at the monoclonal block level were scaled-up to the level of the plantation (planted area of 14.5 ha). The (relative) area coverage of the different genotypes was taken into account. In a second approach, the total mass of wood production was determined at the chipping stage. The mass of the harvested woodchips was quantified in tractor trailers on a standard truck weighbridge (Delaere, IT 8000) at the biomass handling company (SME Groep Mouton;

www.groepmouton.be). At the chipping stage moisture content of the wood was determined by oven-drying a sample of woodchips. For the first harvest (after R1), weighing was performed immediately after harvest, i.e. with fresh wood of 56% moisture (wet mass basis). After the second harvest (at the end of R2), the harvested shoots remained on the field for two months for natural air drying up to 38% moisture content at the time of chipping. During the second harvest, the weight of the harvested shoots was also assessed during harvesting on the trailer of the harvesting machine (type: *Stemster MKIII -Nordic Biomass* pulled by a *JD 8520T* tractor) as a third approach [24].

2.5. Statistical analysis

Genotypic differences in the productivity-related characteristics were analyzed by applying a non-parametric Kruskal—Wallis test with factor 'genotype', followed by pairwise comparison (Mann-Whitney U test) to elaborate the variation among genotypes. Related-samples Wilcoxon singed rank tests were implemented to check whether certain productivity characteristics differed in consecutive years and/or rotations, both per genotype and per parentage separately, as well as for all genotypes pooled. The latter tests were applied using only those trees for which (diameter) measurements were actually performed in both consecutive years or rotations. Tests were repeated with the factor 'parentage'. Whereas all
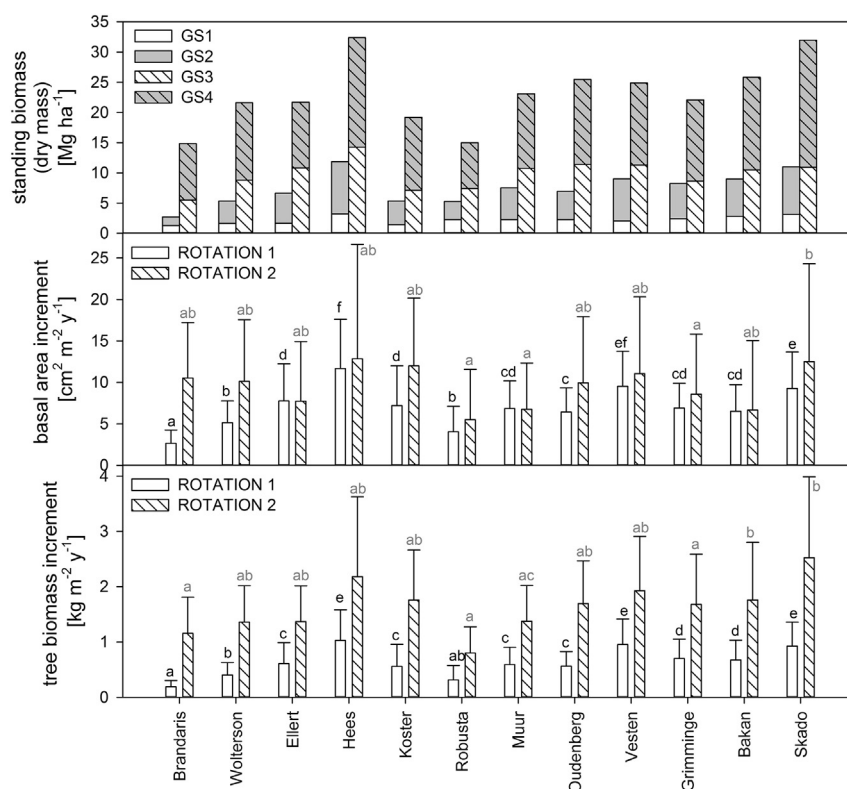
Fig. 1 — **Genotypic means of standing above-ground woody biomass at the end of each growing season (GS) in two biennial rotations. The middle and lower panels show the increment of basal area (at 22 cm height above the soil) of individual trees (middle panel) and of above-ground woody tree biomass (lower panel) from the end of the first growing season (GS) to the end of the second GS of both rotations. Error bars indicate standard deviation of the mean. Identical letters indicate homogeneous groups resulting from the pairwise comparisons following the Kruskal—Wallis test.**

above mentioned analyses were performed with data at tree level, a Wilcoxon singed rank test looking at differences in mortality was performed at block level. All analyses were performed in SPSS (Version 20, SPSS Inc., Chicago, IL, USA). A P-value smaller than 0.05 was considered significant.

3.   Results

The standing biomass at the end of each rotation, taking into account the mortality, is shown in Fig. 1 (upper panel) for each genotype. The plantation mean of the standing above-ground biomass was 2.33 (GS1), 8.09 (GS2), 10.16 (GS3) and 24.48 Mg ha^{-1} of DM (GS4). The first − establishment − rotation yielded 4.04 Mg ha^{-1} y^{-1} of DM, which tripled to 12.24 Mg ha^{-1} y^{-1} of DM in the following biennial rotation. Over both rotations, a mean yield of 8.14 Mg ha^{-1} y^{-1} of DM was produced. From the planted area of 14.5 ha, a total plantation DM yield of 103 Mg was harvested at the first harvest in February 2012 as quantified during the chipping stage. Our first approach via the diameter inventory data resulted in a value of 117 Mg of DM for the total plantation yield (Table 2). At the second harvest, the total plantation yield was 357 Mg of DM, as weighed at the time of chipping. The quantification via the diameter inventory yielded 355 Mg of DM while the third approach via weighing on the harvesting machine resulted in an overall biomass productivity of 346 Mg of DM.

The end-of-season genotypic means of all productivity-related characteristics are shown in Fig. 2. Boxplots show the diameter distribution of all shoots included in the inventory after GS2 and GS4, i.e. at the timing of coppicing (Fig. 3). Whereas the mean D decreased in R2 compared to R1, the overall D range increased from up to 78 mm at the end of R1 to up to 98 mm at the end of R2. The basal area increment, as represented by the slope of the lines in Fig. 2 (panel d), was significantly larger (Table 3, Fig. 1) during R2 than during R1. Besides the much higher number of shoots per tree in R2 than in R1, also the diameters of the thickest shoot per tree were higher in R2 (Fig. 1, Table 3). The biomass proportion of the thickest shoot significantly increased over R2 for all genotypes (Fig. 2 panel f, Table 3), indicating an increasing dominance of the thickest shoot. The thickest shoot was 95%–96% of the total tree biomass in R1 (GS1-GS2); in R2 the proportion was on average 44% in GS3 and increased to 58% in GS4. The number of

shoots per tree decreased overall with 0.42 shoots from GS3 to GS4 (Table 3), although there was no clear trend in this change. For half of the genotypes the number of shoots slightly decreased from GS3 to GS4, whereas for others the number of shoots increased or did not change (Table 3). The observed increase in the number of shoots from GS3 to GS4 for some genotypes is explained by the measuring protocol for shoots with D smaller than 5 mm. These tiny shoots were ignored during the inventories because of their marginal importance in the overall biomass. Shoots that fell below the 5 mm threshold in GS3 were included in GS4 as D exceeded this lower D-limit. The stem basal area increment and the tree biomass increment were significantly higher in R2 than in R1, except for genotype Koster (Table 3). The insignificant result for genotype Koster is probably due to the lower number of data points. It should be noted that Table 3 shows results based on analyses of a restricted number of data points (viz. those trees that were measured in both consecutive years), whereas Fig. 1 shows data based on measurements and/or estimations of all inventoried trees. This explains why results apparently differ between Table 3 and Fig. 1. At the end of the first growing season after coppicing (GS3) the stem basal area was on average larger than the stem basal area reached after the two previous growing seasons (Fig. 2, Table 3). The individual tree biomass showed a similar pattern. In the course of R1 individual tree biomass increased from 0.36 kg to 1.25 kg of DM. During one single season after coppicing (GS3) 1.58 kg of DM per tree was produced which increased to 3.78 kg after GS4. Hence, coppicing significantly increased individual tree biomass. With an average of 15% the mortality after the first growing season was rather high, but it remained nearly unchanged during the following growing seasons. At plantation scale, the mortality had increased with 0.8% up to GS2, and increased with 0.5% up to GS3, one year after coppice (Fig. 2, Table 3). Tree height reached mean values of 2.39 m and 4.15 m after GS1 and GS2 respectively; after coppice resprouted trees grew up to 4.19 m and 5.97 m height after GS3 and GS4, respectively.

The diameter of the thickest shoot per tree was lowest for the P. nigra genotypes, whereas the P. trichocarpa × P. maximowiczii genotypes (T × M) showed the thickest shoots. Details of genotypic differences are shown in Table 4. During R1 most of the trees − for all the genotypes − were single-stem. Both T × M genotypes (Skado and Bakan) typically regrew after coppice with one apical dominant shoot and few small

Table 2 − Above-ground dry woody biomass production from the 2 first biennial rotations, assessed via 3 approaches. Total production refers to the production of the total of 14.5 ha planted, converted to 'Yield' expressed in Mg ha^{-1} y^{-1}. Approach 1 involves the quantification via a detailed diameter inventory, combined with allometric equations; Approach 2 is the weighing of the harvested biomass on a weighing bridge at the chipping stage; Approach 3 (*only applied at the second rotation) involves weighing of the harvested stems on the harvester Stemster MKIII during harvesting. See text for a more detailed description of the three approaches.

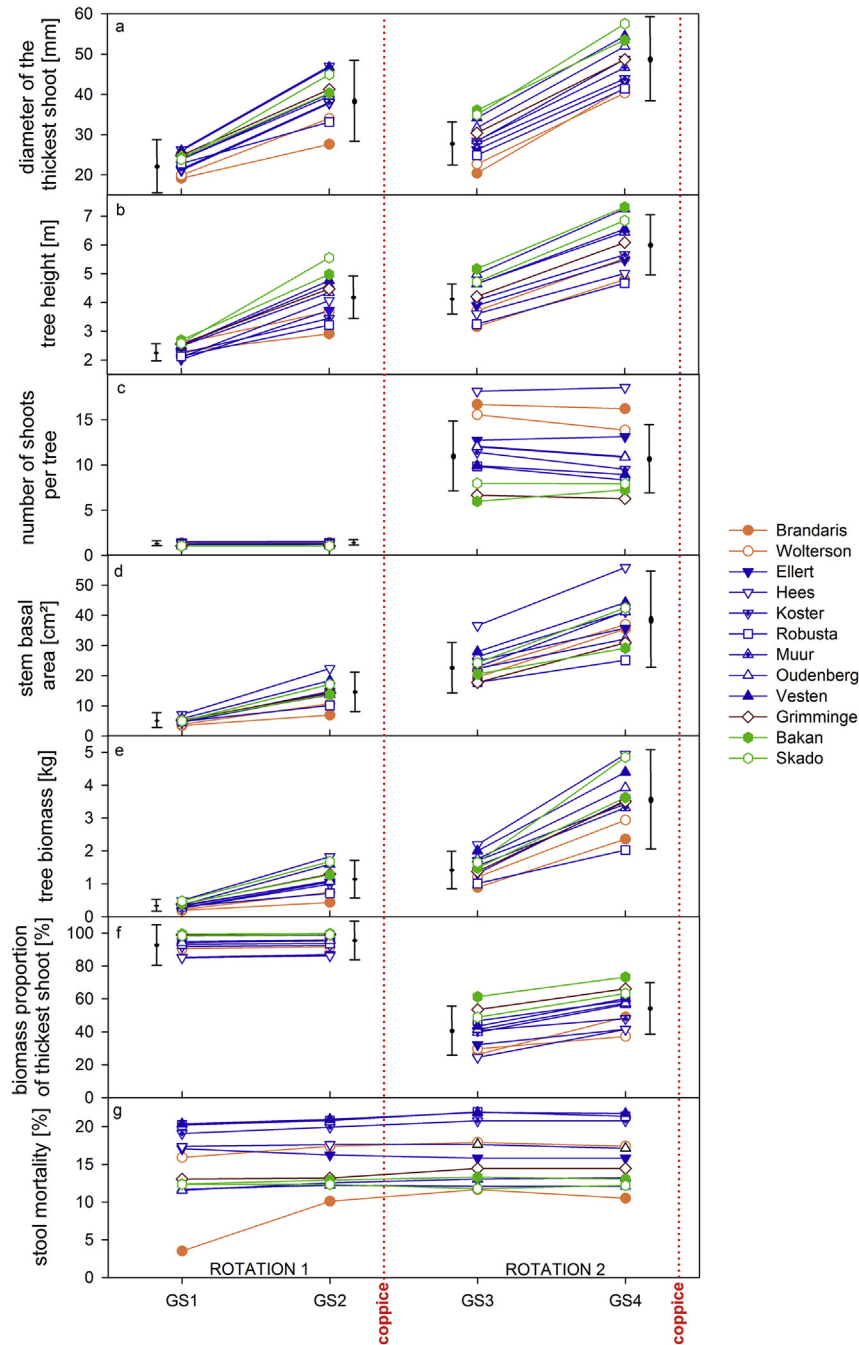|			Approach 1 diameter inventory	Approach 2 chipping stage	Approach 3 harvesting machine*
Rotation 1	Total production	Mg	117	103	−
	Yield	Mg ha^{-1} y^{-1}	4.0	3.6	−
	Relative to Approach 1	%	100	88	−
Rotation 2	Total production	Mg	355	357	346
	Yield	Mg ha^{-1} y^{-1}	12.2	12.3	11.9
	Relative to Approach 1	%	100	101	97

Fig. 2 − Different above-ground biomass productivity and yield characteristics − at the individual tree level − for 12 poplar genotypes over two biennial rotations. Symbols indicate genotypic means measured at the end of each growing season (GS); connecting lines indicate the continuation of a characteristic to the next GS; black dots with error bars represent the overall mean value and mean standard deviation; 'coppice' indicates the two harvests of the total above-ground biomass. Different symbols indicate different genotypes; colors indicate the parentage (orange: *P. nigra*; blue: *P. deltoides* × *P. nigra*; dark red: *P. deltoides* × (*P. trichocarpa* × *P. deltoides*); green: *P. trichocarpa* × *P. maximowiczii*). Panels show: (a) shoot diameter at 22 cm height of the thickest shoot within a tree; (b): height of the thickest shoot within a tree; (c): number of shoots within a tree; (d): cumulated stem basal area at 22 cm height of all shoots within a tree; (e): cumulated aboveground dry woody biomass of all shoots within a tree; (f): ratio of the dry biomass of the thickest shoot to the sum of dry biomass of all shoots within a tree; (g): ratio of the number of dead or missing trees to the number of originally planted cuttings.
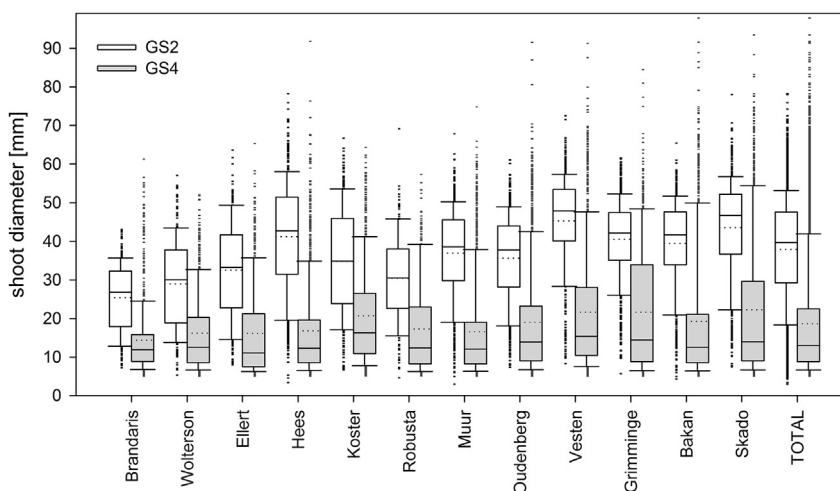
Fig. 3 – Boxplots showing the distribution of individual shoot diameters (at 22 cm height) of all shoots (multiple shoots per tree) measured at the end of the second growing season (GS) of the two biennial rotations, i.e. just before coppicing. Dotted lines on the boxplots represent the mean values, solid lines represent median values. Data for 12 poplar genotypes are shown, as well as the total for all measured shoots.

additional shoots, not showing a strong apical growth. Genotype Grimminge (D × (T × D)) showed a similar growth strategy. The D × N and especially the N genotypes on the other hand, resprouted in a large amount of straight erecting shoots. After coppicing the single-stem trees, the trees thus resprouted in multiple, different numbers of shoots, but no specific trend in the change of this number (viz. self-thinning) was observed towards the second growth year (GS4). With a mean of 18.6 shoots per tree genotype Hees had the highest number of shoots after resprouting. Following, both *P. nigra* genotypes Brandaris and Wolterson resprouted with 16.2 respectively 13.8 shoots. The T × M genotypes Bakan and Skado resprouted with the lowest number of shoots (means of 7.3 and 7.8 shoots, respectively). Skado and Hees were the top producers achieving a biomass production of respectively 11.0 and 11.9 Mg ha^{-1} of DM during R1, and 31.9 and 32.4 Mg ha^{-1} during R2 (Fig. 1). With a productivity of 2.7 and 14.8 Mg ha^{-1} of DM after R1 and R2 respectively, Brandaris showed the lowest productivity among the 12 genotypes.

4. Discussion

The overall biomass production of 8.14 Mg ha^{-1} y^{-1} of DM falls within the range of 5–10 Mg ha^{-1} y^{-1} of reported yields of poplar for biomass (see references in Ref. [5]). Studies often report large variations – ranging from less than 1 to over 25 Mg ha^{-1} y^{-1} – among different genotypes within the same culture (e.g. Refs. [11,27,28]). Depending on the climate and abiotic environment, higher yields are generally achieved when fertilization and/or irrigation is applied [29–31], or when the plantation is intensively managed (incl. careful or complete weed control). To our knowledge, our results are among the highest yield values achieved in our climate in a less intensively managed plantation (i.e. without irrigation or fertilization) (M. Steenackers 2014, personal communication). Given the fact that small plot yields generally perform better

than (operational) field scale yields [4,5], the mean yield of 12 Mg ha^{-1} y^{-1} of DM during the second rotation of our SRC large-scale plantation is a promising result.

There was high genotypic variation in biomass productivity and among other yield related characteristics, as a.o. number of shoots and shoot diameters. Next to genotype Hees (D × N), T × M genotype Skado performed best in terms of biomass yield. This last mentioned observation confirmed the high productivity of hybrids of *P. trichocarpa* and *P. maximowiczii* among a variety of genotypes shown before [28,32,33]. In a study comparing biomass production of 36 poplar genotypes, the substantial differences between parentages contrasted with the minor differences between genotypes within parental groups [28]. In our study, however, we observed similar productivity results for the two genotypes within the T × M group as also for the two genotypes in the N group, but the results of the seven D × N genotypes showed a larger variation. Obviously, these findings are difficult to compare given the limited and different numbers of genotypes within parental groups as the plantation was established with the readily available commercial genotypes. The wider range of biomass values for the D × N genotypes was previously partly attributed to the different breeding institutions: the three genotypes bred by INBO as well as the three bred by "De Dorschkamp" (Table 1) showed more similarities among each other [32]. As an exception the poorly performing D × N genotype Robusta, the 'oldest bred/selected' genotype (Table 1), is known for its poor rust resistance [34] and its slow growth [35,36]. During R1, the rust infection of Robusta led to advanced leaf fall [12,32]. In R2 this led to a reduced wood biomass production with Robusta showing the lowest biomass increment rate among the 12 genotypes. On the other hand, the two highly productive T × M genotypes were the most recently commercialized genotypes of the ones used in our study. Nevertheless, the use of a sufficiently broad genetic diversity among genotypes in a plantation remains essential to limit cultivation risks as diseases and pests. However, in the scope of these infestation risks, older

Table 3 – Statistics results from the paired T-Test for different biomass productivity and yield traits of 12 poplar genotypes and parentages. Values represent the magnitude of the difference and indicate a significant difference with P-value <0.05. 'NS' indicates that there is no significant difference. Values give difference between consecutive years (growing season) or rotations. R = rotation; GS = growing season;* = bridging (the first) coppice.

			All	Bakan	Skado	Muur	Oudenberg	Vesten	Ellert	Hees	Koster	Robusta	Grimminge	Brandaris	Wolterson	T × M	D × N	D× (T × D)	N
n-range			257–4907	25–668	22–613	68–653	22–529	22–513	14–201	9–326	5–307	8–137	24–610	21–230	17–178	47–1281	148–2637	24–610	38–399
Basal area increment	ΔR2-R1*	$cm^2\,m^{-2}\,y^{-1}$	11.9	13.9	25.0	7.1	12.4	12.4	7.6	12.6	NS	7.3	9.5	15.3	14.8	19.1	9.1	9.5	15.1
Tree biomass increment	ΔR2-R1*	$kg\,m^{-2}\,y^{-1}$	1.453	1.941	3.300	1.104	1.361	1.389	1.046	1.274	NS	0.704	1.252	1.134	1.498	2.577	1.169	1.252	1.297
Diameter at 22 cm height of the thickest shoot	ΔGS2-GS1	mm	17.0	14.6	20.6	15.4	14.6	18.9	16.9	20.0	17.0	22.0	17.0	13.3	15.4	17.5	17.1	17.0	14.2
	ΔGS3-GS2*	mm	−10.1	−2.9	−10.0	−11.1	−6.4	−9.3	−19.2	−17.8	−11.6	−19.9	−9.3	−10.4	−16.5	−6.5	−11.7	−9.3	−13.1
	ΔGS4-GS3	mm	19.9	21.2	26.6	18.3	20.3	22.8	15.3	20.8	14.9	15.7	19.0	20.8	18.0	23.8	18.8	19.0	19.5
Number of shoots per tree	ΔGS2-GS1	–	0.01	NS	NS	0.02	0.03	NS	0.03	0.03	NS	NS	NS	NS	0.02	NS	0.02	NS	0.02
	ΔGS3-GS2*	–	9.34	4.98	6.99	10.86	10.78	8.86	10.80	16.7	10.15	8.61	5.62	15.54	14.22	5.94	10.98	5.62	14.98
	ΔGS4-GS3	–	−0.42	1.31	NS	−1.15	−1.18	−0.96	0.40	0.51	−1.88	−1.44	0.39	−0.47	−1.62	0.67	−0.89	0.39	−0.84
Stem basal area at 22 cm height	ΔGS2-GS1	cm^2	9.73	8.59	12.16	9.05	8.48	12.62	1.02	15.32	9.53	5.33	9.05	3.52	6.91	10.28	10.35	9.05	4.93
	ΔGS3-GS2*	cm^2	8.38	7.61	9.17	7.18	12.27	9.49	9.73	12.43	5.77	5.32	3.58	10.70	8.81	8.38	9.24	3.58	9.87
	ΔGS4-GS3	cm^2	21.22	22.47	37.60	17.28	21.46	25.03	19.47	24.78	NS	11.19	18.26	19.09	21.37	29.72	19.25	18.26	20.11
Tree biomass	ΔGS2-GS1	kg	0.838	0.875	1.187	0.714	0.675	1.219	0.623	1.035	0.641	0.373	0.902	0.218	0.473	1.023	0.812	0.902	0.324
	ΔGS3-GS2*	kg	0.348	0.201	NS	0.450	0.678	0.353	0.858	0.661	0.268	0.187	0.093	0.473	0.414	0.123	0.500	0.093	0.447
	ΔGS4-GS3	kg	2.293	2.823	4.513	1.984	2.151	2.610	1.951	2.306	2.220	1.008	2.150	1.394	1.994	3.633	2.046	2.150	1.662
Biomass proportion of the thickest shoot	ΔGS2-GS1	%	0.8	0.2	0.6	1.0	1.3	0.5	2.0	1.2	0.6	NS	NS	1.1	1.2	0.4	1.0	NS	1.1
	ΔGS3-GS2*	%	−52.3	−38.8	−50.9	−56.0	−54.3	−55.9	−55.2	−60.6	−52.4	−47.5	−45.6	−68.4	−64.0	−44.8	−55.4	−45.6	−66.5
	ΔGS4-GS3	%	15.1	12.4	13.4	16.5	16.5	16.6	8.2	16.3	NS	17.9	11.9	20.5	14.3	12.9	15.7	11.9	17.7
Stool mortality	ΔGS2-GS1	%	0.8	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	ΔGS3-GS2*	%	0.5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	ΔGS4-GS3	%	NS	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–

Table 4 – Results of the Kruskal–Wallis test for various biomass productivity and yield traits quantified for 12 poplar genotypes and different parentages. Letters indicate homogeneous subsets of the post-hoc, pairwise comparison Mann-Withney U test. GS = growing season.

Genotype	Diameter at 22 cm height of the thickest shoot				Number of shoots per tree				Basal stem area at 22 cm height				Tree dry biomass				Biomass proportion of thickest shoot			
	GS1	GS2	GS3	GS4	GS1	GS2	GS3	GS4	GS1	GS2	GS3	GS4	GS1	GS2	GS3	GS4	GS1	GS2	GS3	GS4
Bakan	cde	b	g	def	a	a	a	b	d	c	bcd	abc	f	d	cd	c	c	d	f	f
Skado	cde	de	g	f	a	a	b	b	cd	d	e	e	g	e	de	d	c	d	de	de
Muur	bcd	b	cd	b	bc	b	d	d	d	c	bcd	ab	d	c	cd	c	b	b	bc	bcd
Oudenberg	bc	b	ef	cde	bc	b	d	d	d	c	de	cde	de	c	de	c	b	b	c	cde
Vesten	cde	de	fg	ef	a	a	c	c	e	d	ef	de	def	e	e	c	c	d	cd	de
Ellert	e	cd	bcd	ab	d	c	d	e	bcd	c	cde	bcde	bc	bc	cde	c	a	a	ab	a
Hees	de	de	cd	bcd	d	c	f	f	f	e	f	e	h	e	e	c	a	a	a	a
Koster	b	bc	cd	ab	c	b	cd	c	bc	c	abcd	abcd	bc	c	abc	bc	b	b	bc	ab
Robusta	de	e	abc	ab	bc	b	c	bc	cd	b	a	a	cd	b	a	ab	b	b	cde	bcde
Grimminge	cde	c	de	bc	a	a	a	a	d	c	a	a	ef	d	bc	bc	c	d	ef	ef
Brandaris	a	a	a	ab	ab	b	e	e	a	a	ab	ab	a	a	a	a	b	b	a	abc
Wolterson	b	a	ab	a	c	b	ef	e	ab	b	abc	abcde	ab	b	ab	abc	b	b	a	a
Parentage																				
T × M	b	b	c	c	a	a	a	b	b	c	b	b	d	d	c	c	b	b	b	c
D × N	b	b	b	b	b	b	b	c	c	c	b	b	c	c	c	b	a	a	b	b
D × (T × D)	b	b	b	b	a	a	a	a	bc	b	a	ab	b	b	b	b	b	b	c	c
N	a	a	a	a	b	b	c	d	a	a	a	a	a	a	a	a	a	a	a	a

genotypes should generally be avoided because of their increased vulnerability.

The high initial tree mortality after GS1 was primarily caused by weed pressure and by minor accidents during weed management (see details in Ref. [12]). The differences between genotypes were rather linked to the spatially heterogeneous weed control. Weeds caused minor effects in terms of mortality during the following years. The limited influence of coppicing on tree mortality, indicated good coppice-ability up to R2. These observations re-emphasize the importance of weed management and careful weed monitoring during the establishment phase. Once established additional mortality was very low or insignificant. The insignificant change in mortality during the third rotation could partly be attributed to the nutrient-rich soil [12,37], stemming from the year-long fertilization during the former agricultural activities on the land before plantation establishment. The sufficient precipitation in the region also eliminated competition for water (Table S1, supplementary information), and thus drought-induced mortality. The low mortality also illustrated that coppicing had no negative effects on the performance of the stumps. A study showed that shorter rotations result in lower mortality rates as compared to longer rotations [38]. Successive coppicing might, however, have a negative effect on stump mortality as demonstrated for different SRC woody species [39]. In another experimental SRC poplar plantation in Boom (Belgium), the successive harvesting resulted after 16 years in high mortality (up to 95%) rates for some genotypes, but for other genotypes mortality remained very low (only 5%) and the highest annual production was reached after 16 years [40].

During R2, being the first 'coppice' rotation, the within-tree mortality – i.e. shoot mortality – was close to zero. In the above mentioned field site in Boom (Belgium) with 17 poplar genotypes, a decrease in the number of shoots per stool was observed already in the second year after coppice [40,41]. An increase in the number of shoots with an increasing number of rotations was observed at this site in Boom, but within each rotation the number of shoots decreased year by year [42]. One of the factors contributing to the difference with the present study is the higher planting density: 10000 trees ha^{-1} in Boom versus 8000 trees ha^{-1} in the present plantation. As in the Boom SRC plantation the N genotypes showed the largest number of shoots [42], which was attributed to the weak inter-shoot competition in *P. nigra*, as also *P. trichocarpa* × *Populus balsamifera* parentages, leading to many shoots per stool (cfr. [43]). Whereas the N genotypes Brandaris and Wolterson performed weakly in the first (and second) rotation in our study, N genotypes showed the highest productivity and survival rate on the long term (16 years) in the SRC plantation in Boom (Belgium) [27,40]. Possibly the N genotypes perform better after multiple rotations as they seem to sustain the frequent coppicing more than most of the other hybrid genotypes. Up to R2 our present results do not clearly show which growth strategy is best for a high productivity: genotypes Hees and Skado showed a similarly high productivity, with Skado sprouting in few but thick and high shoots, while Hees produced many smaller shoots.

The wide range of shoot diameters has important consequences for the harvesting operation. The maximum harvestable D of the harvesting machines currently available for Belgium, ranges between 6 and 20 cm [23]. Opting for longer rotations implies higher D, and eventually different harvesting machines. On the other hand, prolonging the rotation length often generates higher-quality wood and higher annual yields [38,44–46] and also improves the energy balance of the overall SRC system [47]. In that case the SRC is moving more from an agricultural toward a forestry-type operation.

There was a very good agreement among the three assessment approaches used to quantify the total biomass yield of the plantation. Because of the extensive and very detailed character of the diameter inventory (>5000 trees were measured annually) and the reliable upscaling procedure, we consider the quantification according to the inventory based method as the most accurate and reliable. We expected that the yield quantified on the field and at the time of chipping would have been lower than as assessed via the diameter inventory, mainly because of harvest losses [23]. Other sources of error may include a.o. the resolution of the weighing scales, the assessment of the wood moisture content and the experimenter's bias of the different persons involved. In two methodological papers on the SRC harvesters used in the present plantation [23,24] the error of the Stemster harvester was estimated as 5–10%. The precision of the biomass determination at chipping stage was mainly determined by the precision of the weighbridge (weighing accuracy 20 kg; capacity 60 Mg) and losses during processing at the company, which however were estimated very low at max. 0.5% (SME Groep Mouton, personal communication).

To conclude, we quantified and confirmed the high genotypic variation in biomass production (yield) and productivity-related characteristics. Genotypes Hees (D × N) and Skado (T × M, selected in 2005) reached the highest productivity among genotypes, i.e. 16 Mg ha^{-1} y^{-1} of DM in the R2 which was more than double than the poorest performing genotype Brandaris. After two rotations no meaningful changes in the ranking of genotypes according to their yield-related characteristics was observed. Productivity was very high after the coppice: the biomass increment rate increased and a much higher production was achieved. As the result of coppicing the plantation average dry biomass productivity of 4.04 Mg ha^{-1} y^{-1} of DM in R1 increased to 12.24 Mg ha^{-1} y^{-1} of DM in R2. The influence of coppicing on tree mortality was negligible. However, the single coppice event does not allow to generalize coppicing effects. Monitoring subsequent rotations over the plantations' lifetime – which counts for SRC bioenergy cultures in general – is inevitable to evaluate productivity in the long term.

Acknowledgments

Appendix A. Supplementary information

Supplementary information associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.biombioe.2014.12.012.

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