SIMBA-POP: a cohort population model for long-term simulation of banana crop harvest

P. Tixier, E. Malezieux, M. Dorel

Abstract

Banana crops represent a collection of individual plants that vegetatively propagate at their own rhythm, with stabilised but unsynchronised production of inflorescences over time. Such agrosystems cannot be simulated with existing crop models due to the unsynchronised behavior of individual plants. A new simulation model (SIMBA-POP), based on the cohort population concept, was built to predict phenological patterns of the population and harvest dynamics in banana cropping systems. The model was calibrated and validated for Musa spp., AAA group, cv. Cavendish Grande Naine with field data from the French West Indies (Guadeloupe and Martinique). It can quite accurately predict temporally-varying banana harvesting dynamics (date and number of harvested bunches). The harvesting peak is predicted with a precision less than 3 weeks for the first 3 cropping cycles. The model structure is based on two linear chains of cohorts characterized by both physiological age (heat unit accumulation) and development-stage dispersion in the banana population due to flowering, harvesting and sucker selection. This model is a valuable tool for both farmers (field management) and crop scientists (to simulate and design cropping systems). This approach is a first step towards long-term simulation in non-synchronized agrosystems that cannot be simulated with existing crop models.

Keywords: Banana; Cohort population model; Harvest prediction; Simulation

1. Introduction

Crop models are now commonly used to simulate biomass and yields on a field scale for a variety of crops. They are implemented for a range of applications, e.g. research, crop management and policy support. Crop growth models of the CERES (Jones et al., 2003), APSIM (Keating et al., 2003) or STICS (Brisson et al., 1998) family are well adapted for simulating development and growth in homogeneous annual crop populations. However, they are unsuitable for the simulation of complex, multispecific or multiannual cropping systems that require consideration and simulation of plant individual asynchrony that can occur and increase with time. Tree population structure, forest stages or the variation of the number of trees in a forest can be simulated using individual based models (Philipps et al., 2003), Markov chain models (Benabdella et al., 2003) or malthus extinction models (Karev, 2003). In complex conditions, which
Fig. 1. Development stages of banana plant function of SUMT (heat unit accumulated by the crop in °C) and the six associated distributions expressed in the number of plants (np) per week (w) for two cropping cycles.

Bananas and plantains are rhizomatous herbs whose terminal bud produces the inflorescence. Each plant successively produces a series of bunches, each from a lateral shoot. The sequence can be repeated for 1–50 generations or more, which means that it can be considered as perennial (Turner, 1994). The main developmental stages of banana plants include sucker appearance, growth, flowering and harvest (Fig. 1). Banana crops represent a collection of individual plants derived from vegetative propagules. They develop at their own rhythm and do not follow a synchronous cycle. Hence, at any given time, a banana crop consists of a population of individual plants at various developmental stages.

The heterogeneity in the field population structure is due to both physiological phenomena (inter-plant variations in planting to flowering duration, in sucker emergence, death of plants and farmers’ practices (type of selected sucker, moment of selection and replacement of plants). In the literature, sucker emergence and flowering distribution in a field have been described as log-normal distributions (Fig. 1) (Gamry, 1978; Lassoudière, 1979a,b,c; 1980; Cottin, 1987). The asymmetry of the flowering distribution may be linked to different factors such as spatial heterogeneity in the field, farming practices or plant stresses (drought, root parasitism, plant nutrition, etc.). Systems under stress may have a temporally spread flowering distribution. The earliness of the “follower” (sucker of the following cycle) may vary according to the plant physiology, but the choice of follower depends on the farmer’s decision criteria. The follower is chosen among existing suckers and its growth pattern depends on whether or not other shoots have been eliminated by the farmer. Growers also often replace dead or fallen plants, due to wind and poor rooting, with new planting material. Death ratio and the strategy of replacement also determine the heterogeneity in the population structure.

At the field scale, harvest dynamics (number of bunches harvested per week over time) are highly dependent upon inter-plant asynchronism. Harvest dynamics are characterized by oscillations whose amplitude and frequency vary with time, climate, and farmers’ practices. An example of harvest dynamics (field data and simulation) is shown for one field in Martinique (Fig. 2). Farmers may want to concentrate harvests within a short timespan in the year (requires synchronous cycles), or spread harvests throughout the year (requires asynchronous cycles). The long-term behavior of this system must be understood and effectively simulated to be able to tailor field management strategies to meet farmers’ objectives. The structure of the population in a field (homogeneity versus heterogeneity, proportion of fallen plants) determines its harvest dynamics and is one of the factors that influence farmers’ decisions with respect to replanting a field (destruction of the crop, tillage). It also has a marked effect concerning on-farm labor organization. A specific representation of the system is thus needed to ensure appropriate management.
In ecology, population models are often used to simulate the evolution of plant or animal population structures over time. Systems are also often represented as a collection of stocks linked by flows (Odum and Odum, 2000). These concepts were used to build SIMBA-POP, a model aimed at describing banana population structure over time by simulating the number of bunches harvested per week in a plot. The model takes into account the main agricultural practices, such as sucker selection, that influence plant management. Banana is an ideal system to study the linkage between a population structure and plant development because of the characteristics of banana crops, e.g. half-perennial, individual plant asynchronism, and short plant cycle.

2. Model structure

2.1. The cohort population dynamics concept

A cohort can be defined as a group of individuals characterized by the same phenological stage (Deaton and Winebrake, 2000). It is an appropriate unit for analyzing demographic processes in a population. A cohort chain is a group of cohorts linked to each other by flows controlled by various processes or laws (physiological, stochastic, etc.). The cohort population dynamics concept is commonly used in ecology to simulate animal population dynamics at different stages, e.g. insects (Castanera et al., 2003; Cross and Crook, 1999; Hannon and Matthias, 1999). This concept was rarely used to represent vegetal systems (Goudriaan and van Roermund, 1989). We used it to simulate banana population dynamics. Cohort chains enable simulation of successive physiological stages of banana plant development, i.e. corm growth, inflorescence initiation, sucker emission, bunch harvest, and death of the main stem. These phenological stages can be assimilated by analogy with processes of birth, reproduction and death. Unlike existing banana models based on the mean plant concept (Mekwutanaakam, 1987), the cohort structure is well adapted for describing population dynamics in a banana field, where a cohort represents the number of individuals at a developmental stage for a given week. To be realistic, the model also has to take various environmental factors and agricultural practices that interact with the crop population and its development into account. The model presented here called SIMBA-POP, only includes the population dynamics and the main agricultural practices related to management of the population, such as sucker selection or plant replacement.

It simulates the dynamics of a banana plant population in a plot over numerous crop cycles. The main output is the number of bunches harvested per week over time. As for many plants, phenological stages are described by the accumulation of heat units that determine their durations (Bonhomme, 2000). The physiological development threshold of a banana plant was determined to be 14°C (Ganry and Meyer, 1975; Ganry, 1980; Turner and Lahav, 1983; Turner and Hunt, 1983).

2.2. Mathematical structure

SIMBA-POP was developed using the STELLA® software environment from High Performance System® (Lebanon, NH, USA). It runs with a weekly step (t) and is structured in two linked chains of cohorts that represent the plants before flowering (pre-flowering cohort chain) and plants after flowering (post-flowering cohort chain), respectively (Fig. 3). Variables used in SIMBA-POP are represented in Table 1. Variables refer to the whole population (Xt) or to the (i) cohort (Xi,t). The only input data of the model is the mean daily temperatures (Tdi) and the
Fig. 3. The cohort structure of SIMBA-POP (refer Table 1 for variable meaning).

Table 1
Variables used for SIMBA-POP simulation model

<table>
<thead>
<tr>
<th>Input data</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Td</td>
<td>Daily average temperature of day, d (°C)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Output variables</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nt</td>
<td>Total number of plants in the simulated field at step (t)</td>
</tr>
<tr>
<td>Ht</td>
<td>Total number of harvested plants at step (t)</td>
</tr>
<tr>
<td>Nht</td>
<td>Total number of harvested plants in cohort (i) at step (t)</td>
</tr>
<tr>
<td>Dht</td>
<td>Total number of dead plants in cohort (i) at step (t)</td>
</tr>
<tr>
<td>St</td>
<td>Total number of suckers that appeared in cohort (i) at step (t)</td>
</tr>
<tr>
<td>Sht</td>
<td>Total number of suckers that appeared in the simulated field at step (t)</td>
</tr>
<tr>
<td>FLt</td>
<td>Total number of plants that reached the flower stage in the simulated field at step (t)</td>
</tr>
<tr>
<td>RRt</td>
<td>Total number of plants replaced at step (t)</td>
</tr>
<tr>
<td>SUMTiti</td>
<td>Heat units accumulated by cohort (i) at step (t) (day-degrees)</td>
</tr>
<tr>
<td>SUMTi</td>
<td>Efficient temperature at step (t) (day-degrees)</td>
</tr>
<tr>
<td>st</td>
<td>Sucker selection rate in cohort (i) at step (t)</td>
</tr>
<tr>
<td>WSiti</td>
<td>Week since 1st week of sucker appearance when SUMTiti &gt; birth threshold</td>
</tr>
<tr>
<td>Filt</td>
<td>Flowering rate of cohort (i) at step (t)</td>
</tr>
<tr>
<td>WFt</td>
<td>Week since 1st week of flowering when SUMTiti &gt; flowering threshold</td>
</tr>
<tr>
<td>WHt</td>
<td>Week since 1st week of harvest when SUMTiti &gt; harvest threshold</td>
</tr>
<tr>
<td>DTTd</td>
<td>Daily thermal temperature of day, d (day-degrees)</td>
</tr>
</tbody>
</table>

i is the number of the cohort in both pre-flowering and post-flowering chains; t the running step of the model in weeks; d the day of the simulated week.
Table 2

Parameters used in SIMBA-POP

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>$a_i$, $b_i$, $c_i$</td>
<td>Parameters of the sucker appearance rate log-normal curve</td>
</tr>
<tr>
<td>$a_t$, $b_t$, $c_t$</td>
<td>Parameters of the flowering rate log-normal curve</td>
</tr>
<tr>
<td>$k_i$</td>
<td>Harvesting rate in cohort $i$ at step $t$.</td>
</tr>
<tr>
<td>$H_t$</td>
<td>Harvest threshold (day-degrees)</td>
</tr>
<tr>
<td>$D_t$</td>
<td>Death rate (falling) in cohort $i$ at step $t$.</td>
</tr>
<tr>
<td>$s_i$</td>
<td>Replacement rate at step $i$.</td>
</tr>
<tr>
<td>$v_{max}$</td>
<td>Weekly physiologically active temperature threshold of banana ($^\circ$C)</td>
</tr>
</tbody>
</table>

$i$ is the number of the cohort in both pre-flowering and post-flowering chains; $t$ is the running step of the model in weeks.

$N_{f,t} = \sum_{i}^\infty N_i(t)$ (post-flowering chain)  (4)

Flowered plants ($FL_i(t)$), harvested plants ($H_t$), and new selected suckers ($S_i$ and $S'_i$) at step $t$ are calculated in Eqs. (5)–(7) and (7'). The flowering rate ($fl_i(t)$), harvesting rate ($h_t$), and new sucker selection rate ($s_i(t)$) are calculated for each cohort in accordance with a probabilistic law whose parameters relate to plant physiology and farmers’ practices. The parameters were determined from experimental field data (see calibration).

$FL_i(t) = N_{f,i} \times fl_i(t)$ (pre-flowering chain)  (5)

$H_t = N_{f,i} \times h_t$ (post-flowering chain)  (6)

$S_i = S_i(t) \times x_i(t)$ (pre-flowering chain)  (7)

$S'_i = S'_i(t) \times x_i(t)$ (post-flowering chain)  (7')

Fallen and dead plants for both chains ($D_{i,t}$ and $D'_{i,t}$) are calculated in Eqs. (8) and (8'). Falling depends on plant mass, parasitism that affect roots and wind strength. These factors are integrated in the death rate ($d_i(t)$). In the model presented here, links with other sub-models that simulate wind and root parasitism are not taken into account.

$D_{i,t} = N_{f,i} \times d_i(t)$ (pre-flowering chain)  (8)

$D'_{i,t} = N'_{f,i} \times d_i(t)$ (post-flowering chain)  (8')

The total number of plants on the plot ($N_t$), the total number of flowered plants ($FL_t$), new selected suckers ($S_t$), the total number of harvested plants ($H_t$) and fallen and dead plants ($D_t$) are calculated for each step $t$ in Eqs. (9)–(13), respectively.

$N_t = \sum_{t}^\infty N_i(t)$ (whole population)  (9)

$FL_t = \sum_{t}^\infty FL_i(t)$ (whole population)  (10)

$S_t = \sum_{t}^\infty S_i(t)$ (whole population)  (11)

$H_t = \sum_{t}^\infty H_t(t)$ (whole population)  (12)

$D_t = \sum_{t}^\infty D_{i,t}$ (whole population)  (13)

number of harvested plants ($H_t$) for each step ($t$). Parameters relative to plant physiology are given in Table 2.
The number of plants to replace at step \( t (R_t) \) is the sum of plants to replace at step \( t - 1 \) and dead plants at step \( t \), minus the replaced ones at step \( t - 1 \) (Eq. (14)). The number of replaced plants \((R_t)\) is calculated in Eq. (15) using a replacement factor \((r_t)\) in accordance with farmers’ practices (Eq. (15)).

\[
R_t = R_{t-1} + D_t - R_{t-1} \quad \text{(whole population)} \quad (14)
\]

\[
RR_t = R_t \times r_t \quad \text{(whole population)} \quad (15)
\]

Heat units accumulated at each step by each cohort \((\text{SUMT}_{t,i}, \text{in 'degree-days') are calculated in Eq. (16). Heat units accumulated for each week \((\text{SUMT}_i)\) in (°C) is calculated in Eqs. (16) and (16)' , were daily thermal time \((\text{DTT}_d)\) is the number of heat units accumulated during one day, \(T_{\text{mean}}\) the temperature below which development is assumed to cease, and \(T_d\) the mean day temperature.

\[
\text{SUMT}_{t,i} = \sum_{i=1}^{(d=196)} \text{DTT}_d \quad \text{(whole population)} \quad (16)
\]

\[
\text{SUMT}_i = \sum_{i=1}^{(d=196')} \text{DTT}_d \quad \text{(whole population)} \quad (16)'
\]

\[
\text{DTT}_d = (T_d - T_{\text{mean}}) \quad \text{(whole population)} \quad (16)'
\]

2.3. Stochastic laws

Phenological stages were considered as being related to these heat units accumulated by each cohort. Flowering, sucker selection and harvest were assumed to follow a log-normal curve according to results reported by Guiry (1978), Lassoudière (1979c), Cottin (1987). Hence, stochastic laws were used to establish the rates of flowering \((f_{t,i})\), sucker selection \((s_{t,i})\) and harvest \((h_{t,i})\). We assumed they apply when the corresponding threshold for heat units accumulated is reached. When applied, these laws follow a log-normal curve function.

Flowering occurs in a cohort when the heat units accumulated is over the FT threshold. The flowering rate \((f_{t,i})\) of the cohort \((i)\) at step \((t)\) follows a log-normal curve function according to the number of weeks since first flowering \((WF_{t,i})\) (Eqs. (17), (17)′ and (17)′′). According to farmers’ practices, this curve is summarized by a 3-week histogram, as described in Eq. (19).

\[
f_{t,i} = a_i \times \exp \left( -0.5 \frac{\ln (WF_{t,i}/b_i)}{c_i} \right)^2 \quad (17)
\]

if \(\text{SUMT}_{t,i} < \text{FT}\) then \((WF_{t,i} = 0)\)

if \(\text{SUMT}_{t,i} \geq \text{FT}\) then \((WF_{t,i} = WF_{t-1,i-1} + 1)\)

\[(17)'
\]

Sucker selection occurs in a cohort when the heat units accumulated is above the BT threshold. The sucker selection rate \((s_{t,i})\) of the cohort \((i)\) at step \((t)\) follows a log-normal curve function according to the number of weeks since first sucker selection \((WS_{t,i})\), with \(a_s\), \(b_s\) and \(c_s\) parameters (Eqs. (18), (18)' and (18)′). We assumed they apply when the corresponding threshold for heat units accumulated is reached. When applied, these laws follow a log-normal curve function.

Harvest occurs in a cohort when the sum of accumulated heat units is above the HT threshold. The harvesting rate \((h_{t,i})\) of the cohort \((i)\) at step \((t)\) follows a log-normal curve function according to the number of weeks since first flowering \((WH_{t,i})\) (Eqs. (19), (19)' and (19)′). According to farmers’ practices, this curve is summarized by a 3-week histogram, as described in Eq. (19).

\[
h_{t,i} = \begin{cases} 0.2 & \text{if } WH_{t,i} = 1 \\ 0.625 & \text{if } WH_{t,i} = 2 \\ 1 & \text{if } WH_{t,i} = 3 \end{cases} \quad (19)
\]

if \(\text{SUMT}_{t,i} < \text{HT}\) then \((WH_{t,i} = 0)\)

if \(\text{SUMT}_{t,i} \geq \text{HT}\) then \((WH_{t,i} = WH_{t-1,i-1} + 1)\)

\[(19)'
\]

3. Parameter calibration and model validation

Calibration and validation data were collected in banana fields in Guadeloupe and Martinique (French West Indies). All data are presented in Table 3. Plants were grown in field conditions with Cavendish cv. Grande Naine (Musa spp., AAA group, cv. Cavendish Grande Naine) with no major stress (no hurricanes, drought or parasitism damage).
Table 3

<table>
<thead>
<tr>
<th>Number</th>
<th>Island</th>
<th>Field name</th>
<th>Elevation (m)</th>
<th>Observation dates</th>
<th>Number of observed weeks</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Martinique</td>
<td>HANGA</td>
<td>325</td>
<td>8 July, 1997–19 August, 2001</td>
<td>215</td>
</tr>
<tr>
<td>2</td>
<td>Martinique</td>
<td>MC07</td>
<td>350</td>
<td>18 June, 1998–3 March, 2002</td>
<td>194</td>
</tr>
<tr>
<td>3</td>
<td>Martinique</td>
<td>MIOI</td>
<td>325</td>
<td>13 May, 1998–3 March, 2002</td>
<td>199</td>
</tr>
<tr>
<td>4</td>
<td>Martinique</td>
<td>FPAIN</td>
<td>300</td>
<td>27 June, 1996–5 November, 2000</td>
<td>227</td>
</tr>
<tr>
<td>5</td>
<td>Martinique</td>
<td>LIH 2</td>
<td>315</td>
<td>20 June, 1997–3 March, 2003</td>
<td>297</td>
</tr>
<tr>
<td>7</td>
<td>Guadeloupe</td>
<td>JARDIN</td>
<td>45</td>
<td>1 October, 1996–19 December, 2001</td>
<td>272</td>
</tr>
<tr>
<td>8</td>
<td>Martinique</td>
<td>DACHI</td>
<td>260</td>
<td>16 November, 1995–17 February, 2002</td>
<td>326</td>
</tr>
<tr>
<td>10</td>
<td>Martinique</td>
<td>GOYAVE</td>
<td>200</td>
<td>10 June, 1996–16 December, 2001</td>
<td>288</td>
</tr>
<tr>
<td>12</td>
<td>Martinique</td>
<td>GCIHMI</td>
<td>340</td>
<td>18 October, 1997–3 March, 2002</td>
<td>228</td>
</tr>
<tr>
<td>13</td>
<td>Martinique</td>
<td>COMPL</td>
<td>335</td>
<td>30 October, 1996–3 December, 2000</td>
<td>214</td>
</tr>
<tr>
<td>14</td>
<td>Martinique</td>
<td>CVERT</td>
<td>295</td>
<td>24 April, 1997–21 October, 2001</td>
<td>234</td>
</tr>
</tbody>
</table>

3.1. Calibration

The flowering rate ($f_{i,t}$) was fitted to a log-normal curve using flowering data for the first cycle (fields 1–6). The parameters are: $a_f = 0.12$, $b_f = 6.35$ and $c_f = 0.47$ (Fig. 4). The FT threshold was calibrated using the sum of heat units accumulated between planting and first flowering for fields 1–7. FT is 2350 degree-days (S.D. = 223; 7 fields).

The sucker selection rate ($s_{i,t}$) was calibrated by adjusting the sucker selection parameters to minimize the error between simulation and field data for all harvesting peaks for each calibration field. The log-normal curve parameters were calibrated for fields 1–7 ($a_s = 1.00$, $b_s = 3.25$ and $c_s = 0.31$, respectively). The BT threshold was calibrated using the sum of heat units accumulated between planting and first sucker appearance. BT was 2180 degree-day (S.D. = 156; 7 fields). The harvest threshold HT was fixed to 900 degree-days according to data from the literature (Ganry, 1978).

The replacement rate ($r_t$) and death rate ($d_t$), which are, respectively related to farmers’ practices and the plant environment (wind and para-
sitism), were not considered or calibrated in this version of the model. Sub-models necessary to take falling and replacement into account are discussed below.

3.2. Validation

Banana harvest dynamics at the crop scale are characterized by oscillations over time (Fig. 2). The dynamic aspect of these outputs requires specific statistic tools for model validation. The predictive accuracy of the model depends on reproducing the harvest dynamics and magnitude of harvesting peaks through successive cycles. In this regard, the cumulated number of harvested plants and the capacity of the model to predict successive harvesting peak dates are suitable for long-term validation.

Simulations were run for seven plots (field 8–14, Table 3). Both the relation between the observed and simulated cumulated number of bunches harvested over time and the ability of the model to predict harvesting peaks (date of the maximal number of bunches harvested for each cropping cycle) were used to validate the model.

Fig. 5 shows that the model can quite accurately predict \( r^2 = 0.9858, n = 1058 \) the cumulated number of bunches harvested after many cycles for fields 8–14.

The fact that the model error is distributed equally around the median curve \( Y = X \) indicates that the model does not systematically lead to underestimation or overestimation.

Fig. 6 shows successive harvesting peaks for simulated versus observed data.

Complementary statistic methods were used to evaluate the predictive accuracy of the model to determine harvesting peak dates. The mean deviation (MD) between observed and simulated values is a measurement of the tendency of the model to over or underestimate the observed value. MD is defined as:

\[
MD = \left( \frac{1}{n} \right) \left( \sum_{i} ERR_i \right)
\]

where \( ERR_i = Y_i - X_i \) and \( Y_i \) and \( X_i \) are the \( i \)th predicted and observed value, respectively, where \( n \) is the sample size. The mean predicted error (MPE) is defined as:

\[
MPE = \left( \frac{1}{n} \right) \left( \sum_{i} |ERR_i| \right)
\]

MPE is an indicator of the accuracy of the model. The mean square error of the prediction (MSEP) is a
Table 4
Statistical results relative to the simulation of the harvesting peak date with SIMBA-POP

<table>
<thead>
<tr>
<th>Statistic method</th>
<th>All peaks</th>
<th>1st cycle peak</th>
<th>2nd cycle peak</th>
<th>3rd cycle peak</th>
</tr>
</thead>
<tbody>
<tr>
<td>MD</td>
<td>−0.38</td>
<td>0.29</td>
<td>−0.25</td>
<td>−1.08</td>
</tr>
<tr>
<td>MPE</td>
<td>1.92</td>
<td>0.94</td>
<td>2.30</td>
<td>1.88</td>
</tr>
<tr>
<td>MSEP</td>
<td>5.4</td>
<td>1.35</td>
<td>8.20</td>
<td>5.30</td>
</tr>
<tr>
<td>RMSEP</td>
<td>2.42</td>
<td>1.16</td>
<td>2.86</td>
<td>2.30</td>
</tr>
</tbody>
</table>

MD: mean deviation; MPE: mean square error; MSEP: mean square error of the prediction; RMSEP: root mean square error predicted.

4. Application of SIMBA-POP and perspectives

SIMBA-POP potentially has various applications for scientists and farmers. It may be used by scientists to evaluate different agricultural practices relative to the management of a banana population in a field. It can also be linked with other sub-models to make realistic long-term simulations of cropping system performance. SIMBA-POP can also be used as a predictive tool for farmers to optimize practices and be a powerful tool for long-term management (labour per cycle, harvesting periods, etc.).

SIMBA-POP can be linked with specific sub-models that simulate farmers’ practices and then be used to test new population management decision criteria. In banana cropping systems, main decision criteria relative to the crop population management are sucker selection and dead (fallen) plant replacement. The sucker selection criterion is defined by a set of cropping actions geared to removing unwanted suckers and to keeping only one follower (with expected characteristics that include spatial location, shape and size). Testing a new set of parameters (sucker selection parameters) is an interesting use of the model, with the aim of potentially designing new cropping systems.
be used to test new criteria to control heterogeneity in a plot.

4.2. Perspectives: linkage with other sub-models to simulate the whole cropping system

The population model SIMBA-POP is the first step of a larger model that aims at simulating the whole cropping system over the long-term. Simulation of the plant population structure in a field can provide very important information for assessing some environmental and agronomic variables of cropping systems. Long-term simulations of cropping systems requires linkage of population models with crop growth model. The development of such models involves some structural issues. In the case of SIMBA-POP, the double cohort chain structure allows easy linkage with growth sub-models to each sub-population (each cohort). In contrast with a model based on linear equations that describe the population structure, the cohort chain structure is flexible because all variables of each sub-population are accessible. First SIMBA-POP can be improved by taking into account the falling rate, linked to wind, parasitism and population management criteria, as described earlier. It also can be linked to plant growth, biomass and yield sub-models.

5. Conclusion

This study highlights several aspects of SIMBA-POP, a population model based on the cohort concept. The model was successfully calibrated and validated for banana with data from Guadeloupe and Martinique. Although there are some limits under stressed situations or high falling rates, the model can be used to predict harvesting periods over cropping cycles. It also can be used to simulate or compare new population management decision criteria. This study also shows that population models are useful for long-term simulation of agrosystems with unsynchronised plants. In this case, linkage with sub-models that simulate water balance, plant growth and soil parasitism will enable realistic long-term simulation of cropping systems in the near future. This approach could be extended to systems with asynchronous population dynamics behavior, especially for perennial or half-perennial systems based on vegetative propagation.
Acknowledgements

We are particularly grateful to the farmers of Guadeloupe and Martinique that helped us to build the plant database. We would also like to thank our colleagues from IRAD-FIfor who helped us to contact farmers and provided us with temperature data (especially André Lassoudière).

References


Dasineura tetensi


