



*Modelling the seed
dispersal of an invasive
forest tree species: how
microsatellites can help?*

SOS invasion- scientific workshop

09-03-2006

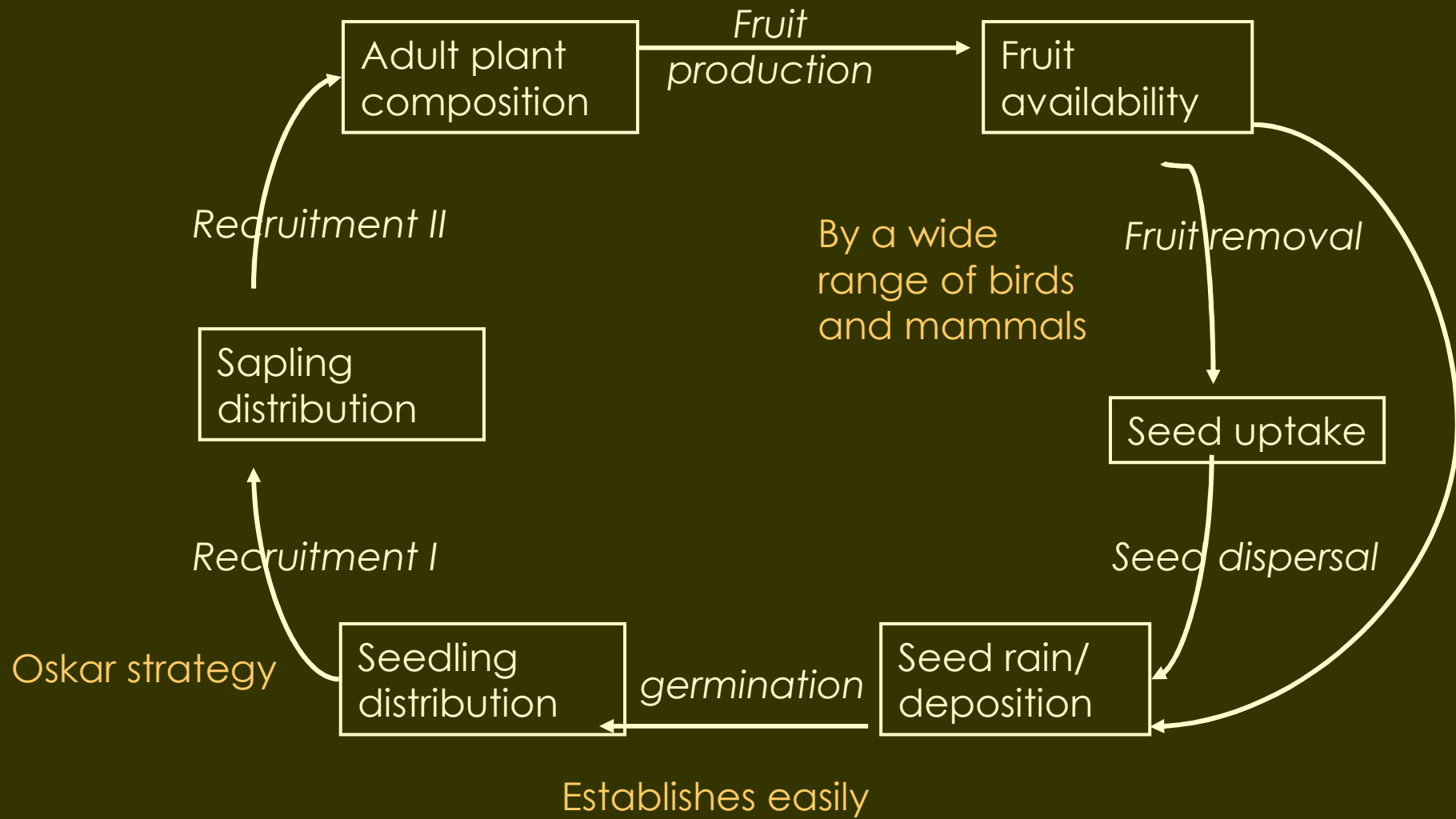
Marie Pairon, Anne-Laure Jacquemart

Introduction

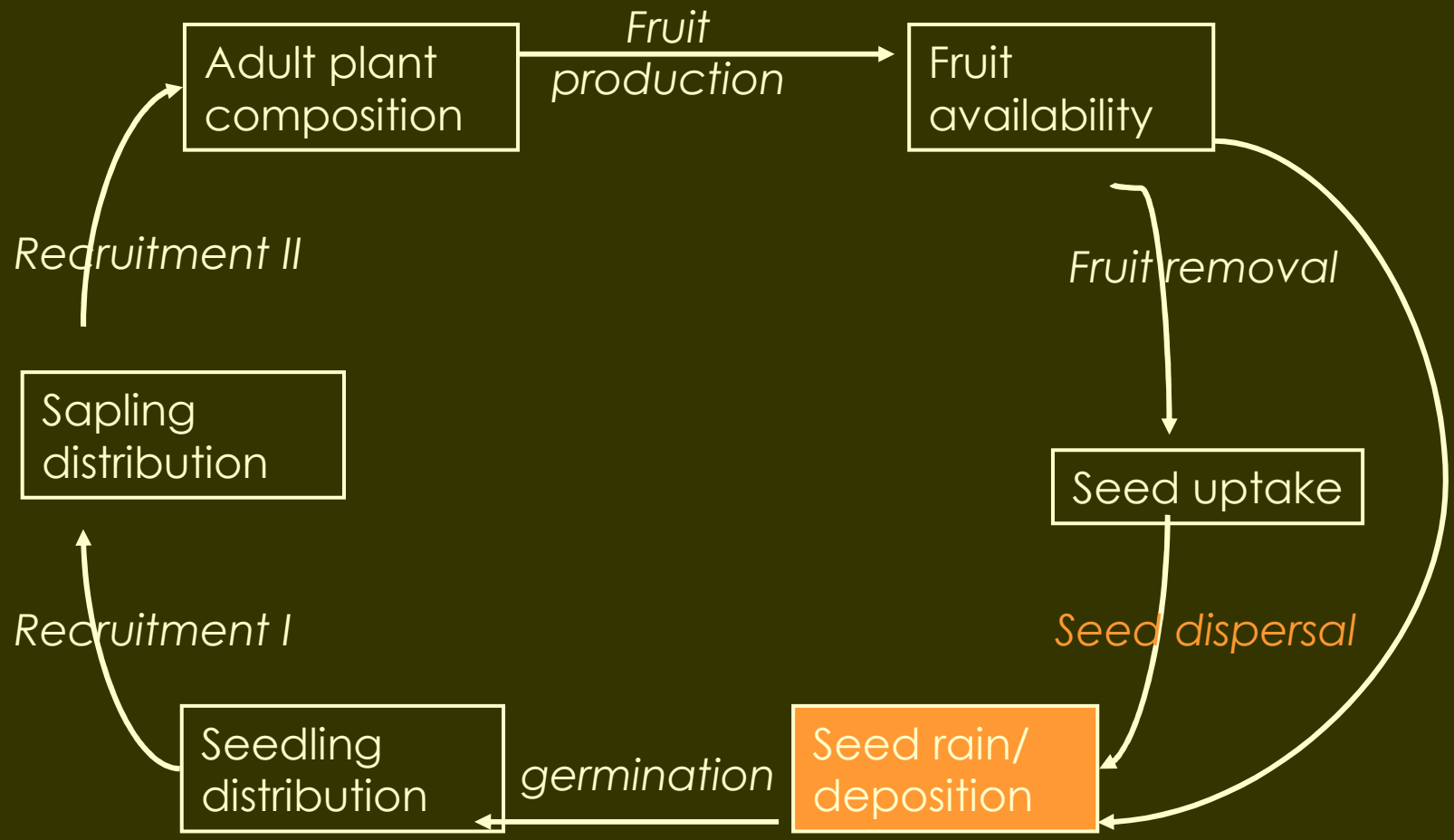
- How does the species spread and migrate?
- Process of invasion
 - Population size increase
 - Geographical range expansion
- *Prunus serotina*
 - Abundantly planted by foresters in many European countries
 - Rapidly filled the gaps between plantations
 - Highly competitive / colonizes heavily open and disturbed sites adjacent to plantation

Introduction

Abundant



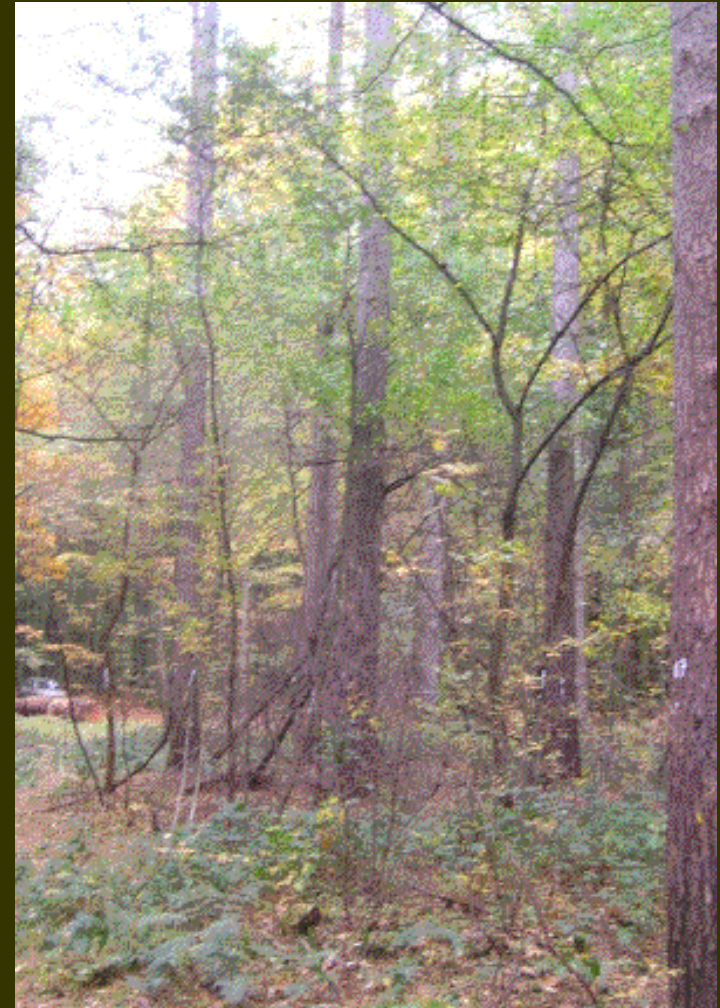
Introduction



Methods



1. Experimental plot in Meerdael
 - 0.5 hectare
 - *Pinus sylvestris* and *Pinus nigra* stand
 - 305 *Prunus serotina* in the understorey



- **62** seed traps (50 cm*50 cm)

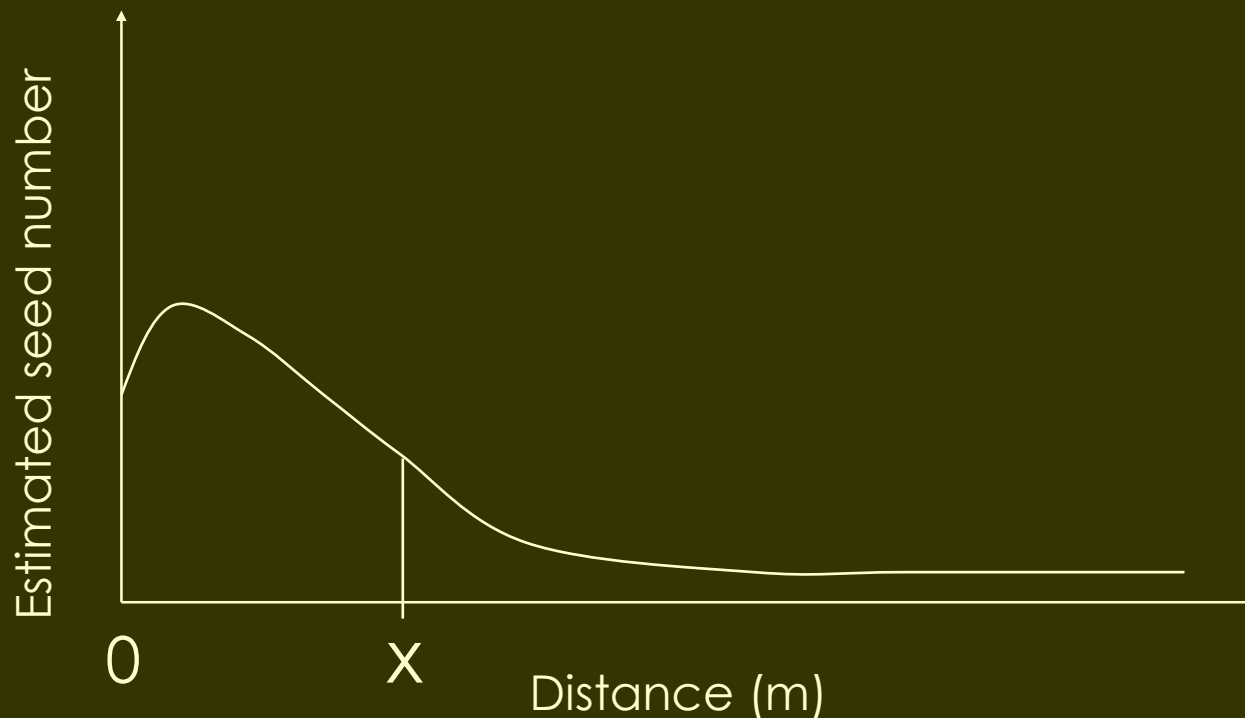


- Fruits collected **weekly** (sept-dec 2004)



2. Estimation of the seed dispersal curve

What is the estimated number of dispersed seeds **per tree** (function of the distance from the tree) ?



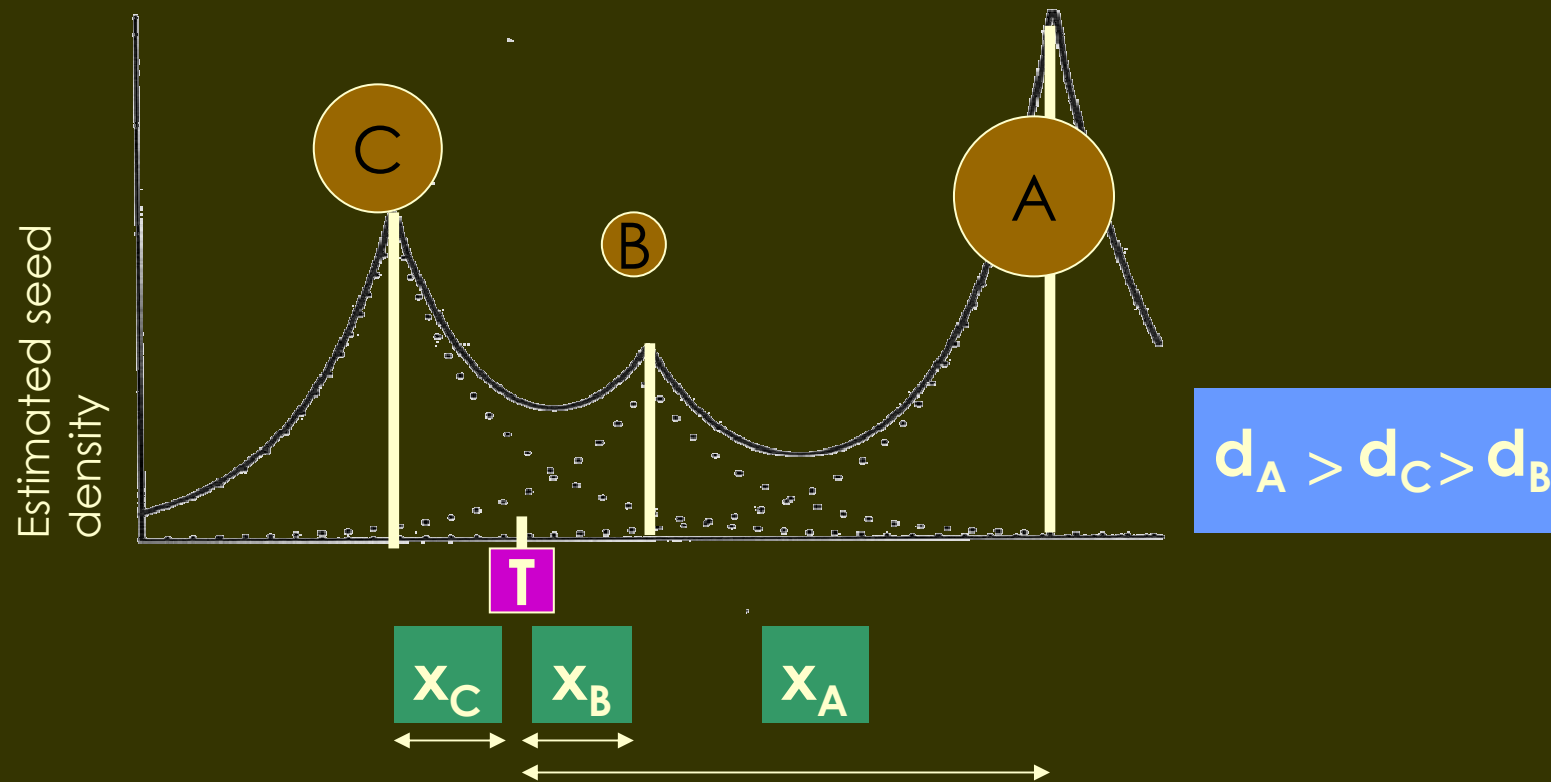
Total production * Dispersal kernel

$$Ad^\phi * \exp(-Bx^\theta) \quad (1)$$

$$* \left[\frac{1}{((2\pi)^{1.5} \theta x^2)} \right] \exp\left(-\left(\frac{(\ln(x/B))^2}{2\theta^2}\right)\right) \quad (2)$$

Where d = tree size (e.g. circumference at breast height)

x = distance from tree



Overlapping seed shadows:

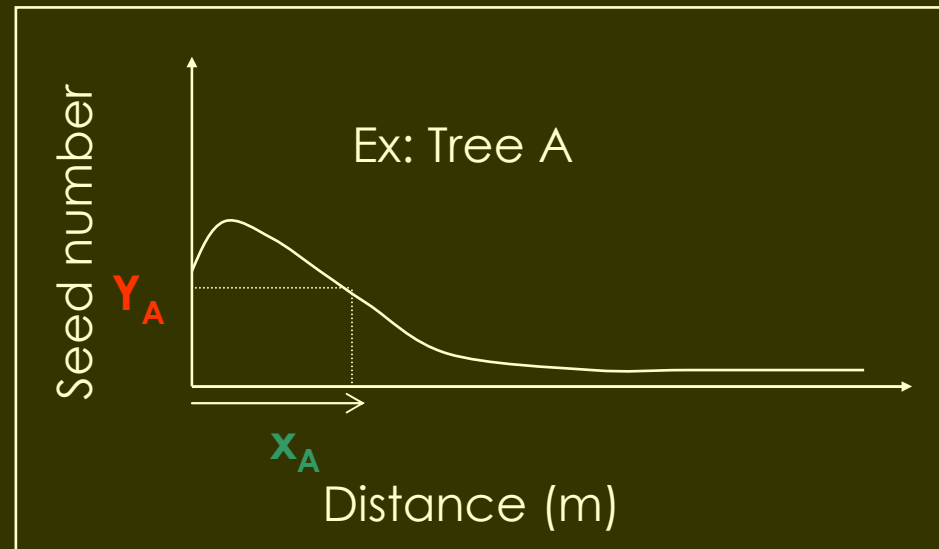
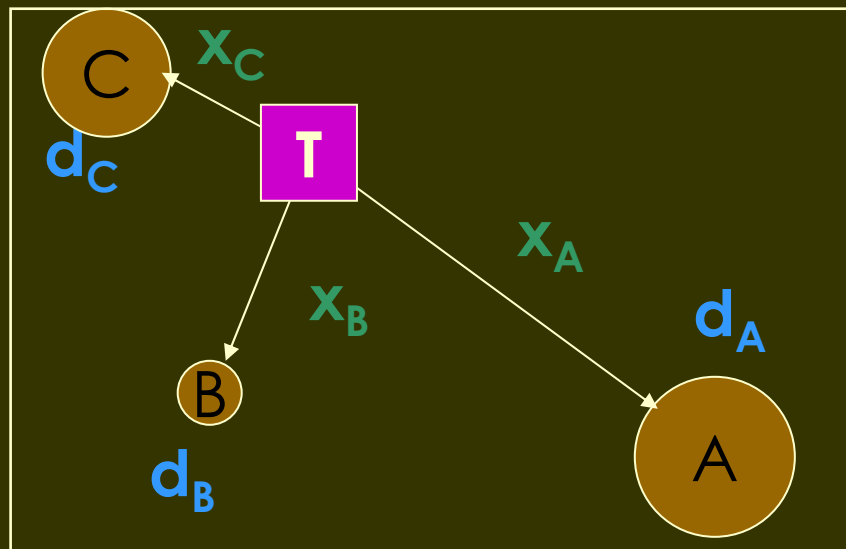
A. Inverse modelling approach

B. Highly polymorphic microsatellite markers to assign a dispersed seed to its maternal parent

2.A. Inverse modelling approach (Ribbens et al. 1997)

eq

1. Set the parameters A, B, θ, Φ to a given value
2. Calculate the contribution trees A, B, C to trap T



3. Number of predicted seeds in trap $T = Y_A + Y_B + Y_C$

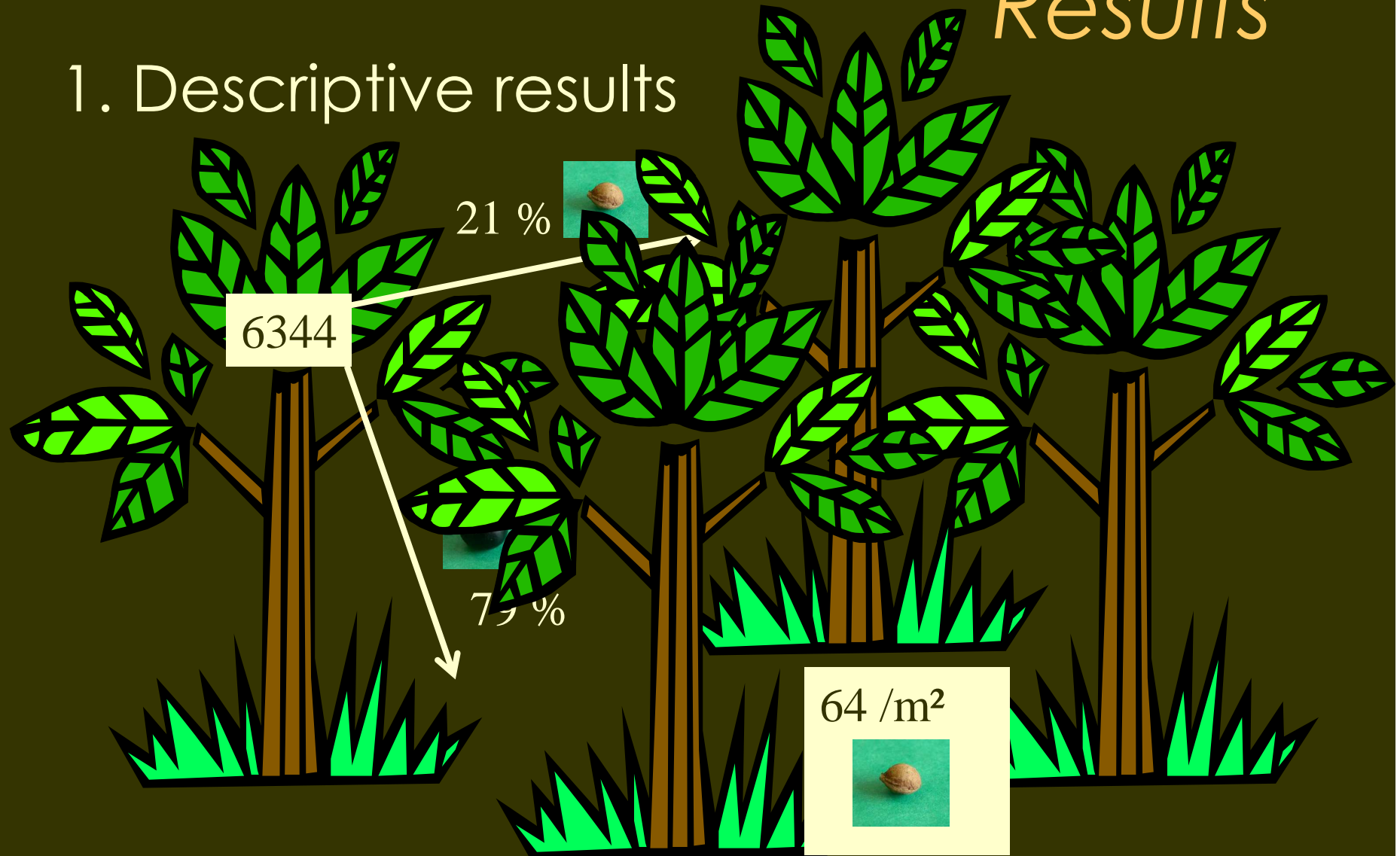
4. Compare the predicted seed number and the observed number of seeds in trap T
5. Readjust the parameters A, B, θ, Φ to better fit the observed data
6. Start again at step 2

2.B. Microsatellites

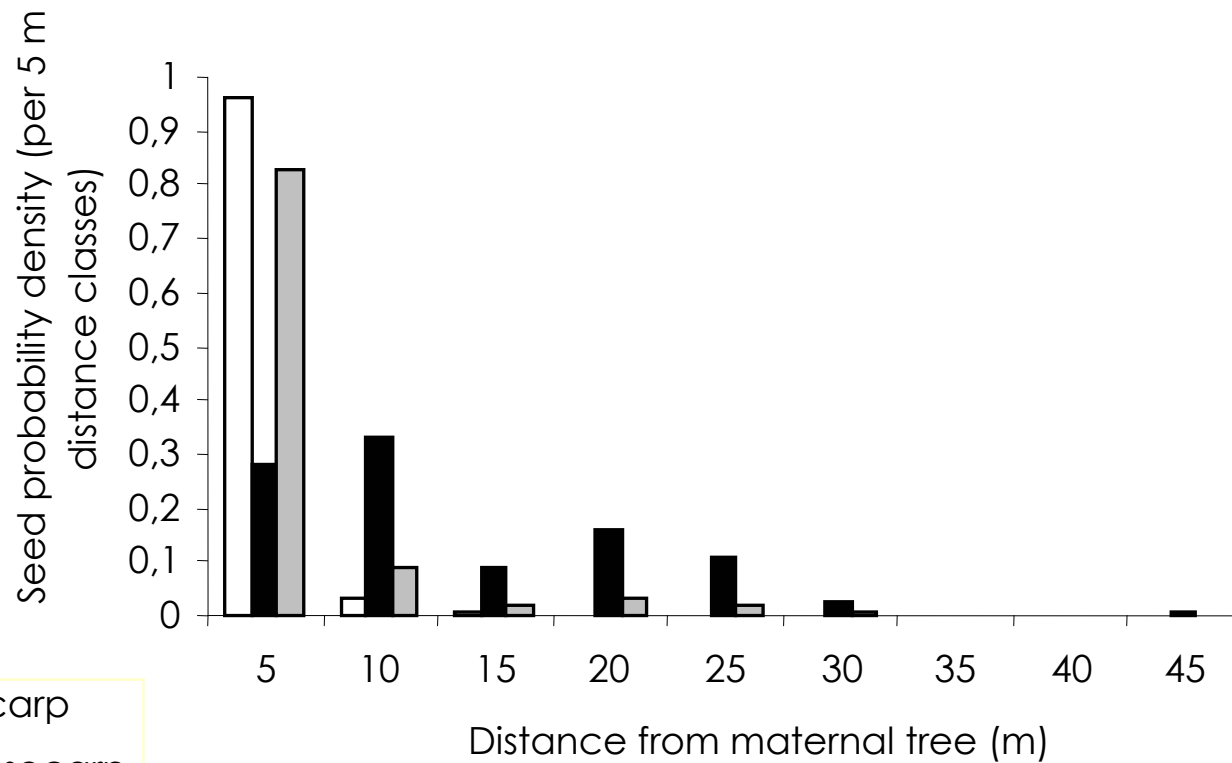
- Allow a direct assignment of the seed to its maternal parent
- How?
 - By genotyping possible parents in the stand
 - By genotyping the endocarp of the seeds (only made of maternal tissue)
 - Thanks to highly polymorphic microsatellite primer pairs (Pairen and Jacquemart 2005 JASHS), each parent has a different genotype

Results

1. Descriptive results

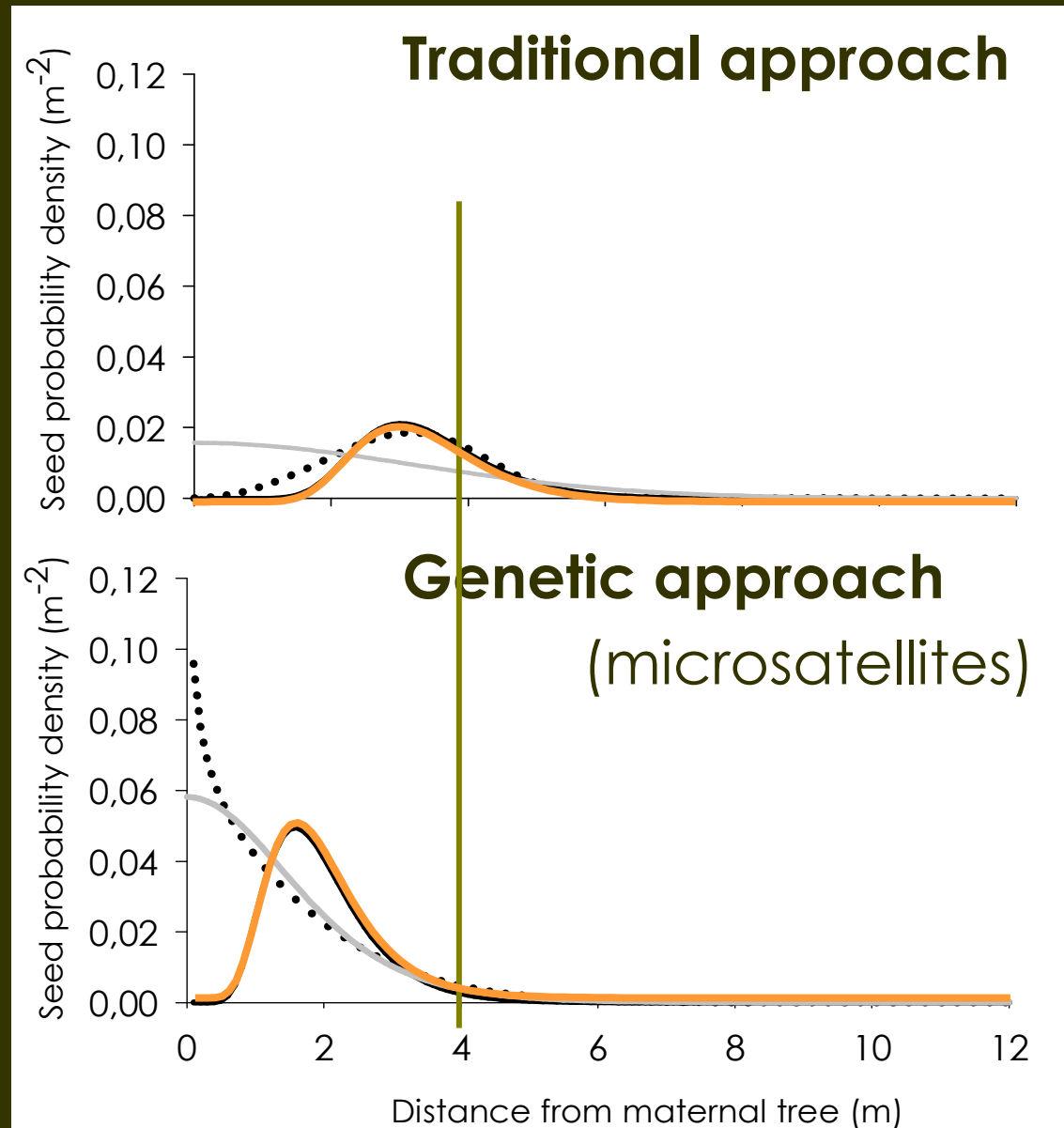


2. How far can seed disperse? Raw data from assignment thanks to microsatellites



- With mesocarp
- Without mesocarp
- Total

3. Results of the models : Fruits with mesocarp

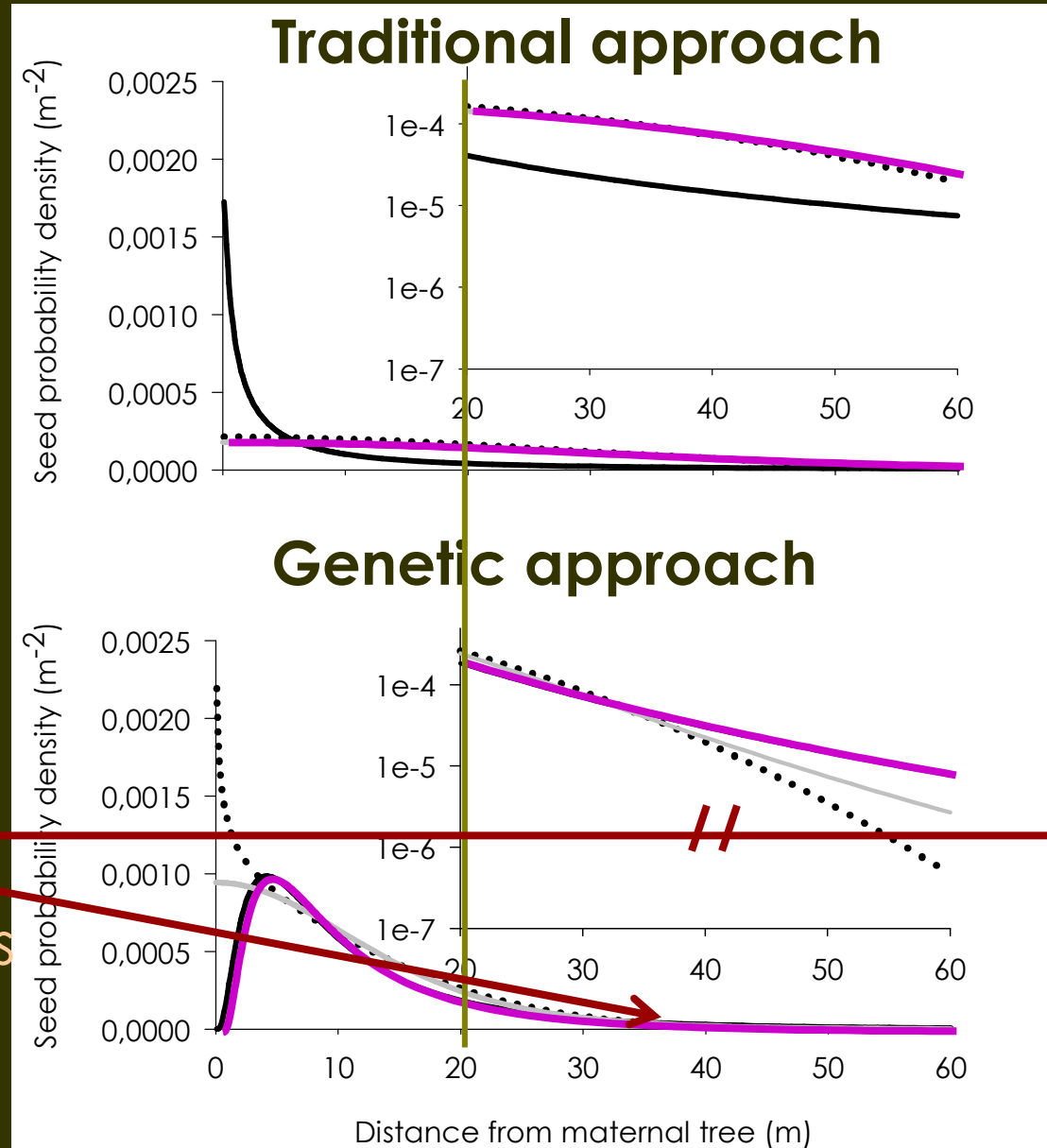


••• weibull — lognormal — 2Dt

Fruits without mesocarp







33 % of unassigned seeds
?
conspecifics



••• weibull — lognormal — 2Dt

Conclusion

- 95 % of the fruits with mesocarp  fall at distances 0 - 5 m
- 85 % of the total seed crop  +  fall at distances 0 – 5 m
- A higher proportion of fruits without mesocarp  than expected by the traditional approach falls in 0-20 m from the parent plant

Detection of LDD ?

High potential of highly polymorphic markers – provide a real estimate of the true dispersal events

Thank you for your attention

This work was financially supported by:

- the Fonds Spéciaux de Recherche (FSR) of the UCL
- the Belgian Science Policy (BelSPo) research contract InPlanBel



FNRS