Equilibrium and non-equilibrium approaches in forest genetic modelling: Population- and individually based approaches

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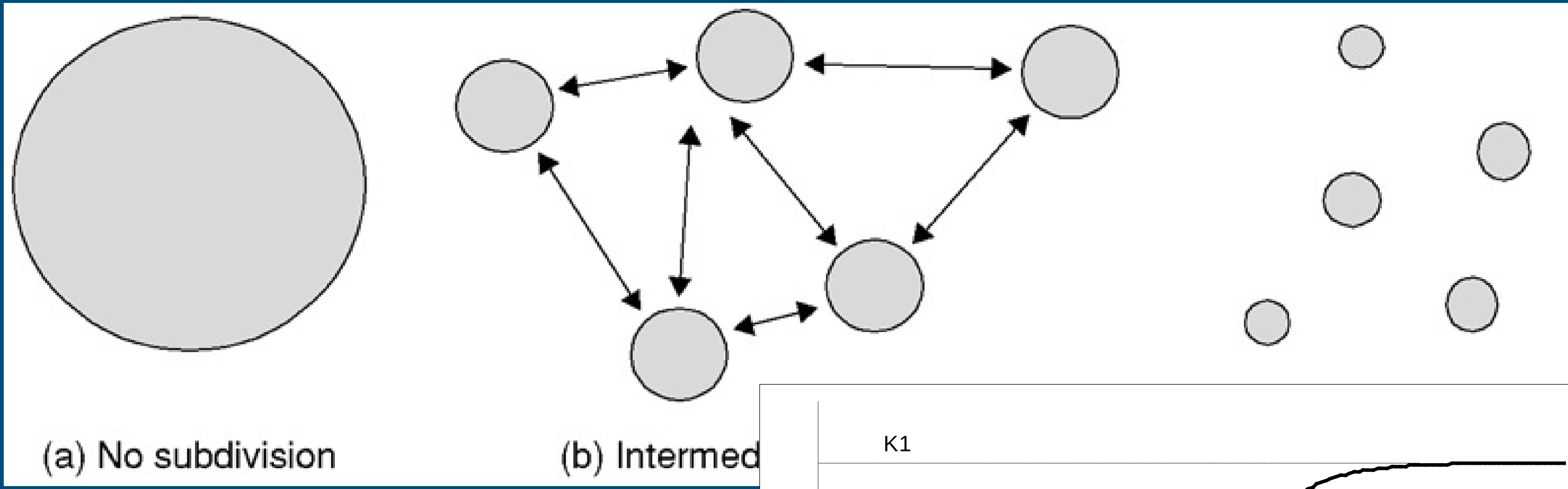
Structure of the presentation

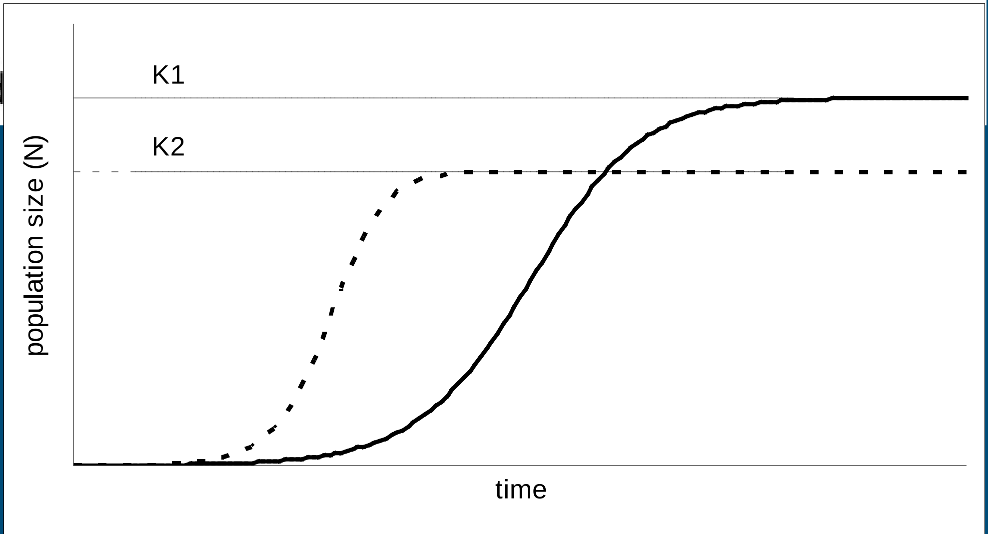
- Equilibrium approach in forest genetic modeling
  - assumptions
  - traits
  - examples of eq. modeling
- Non-equilibrium approach in forest genetic modeling
  - assumptions
  - traits
  - examples of impacts of climate change
- Discussion
  - Pros and cons of eq. and non-eq. genetic modeling
  - Future development in bridging ecophysiological and genetic of trees knowledge by process-based models

Equilibrium or demographic approach

- Assumption:
  - Environment is stationary (no trends in space nor time) relative to the rate of recovery after a perturbation
  - => following a perturbation the population returns to a previous (thus know) stable state: equilibrium
  - => we can use current knowledge on dependency of stable state to environmental factors to assess future stable states
- Traits to differentiate populations, e.g.:
  - Fecundity, survival, competition, dispersal, biomass, height, bud burst
  - i.e. usually phenotypic plastic traits (GxE interaction)
- Model parameters under study e.g:
  - Demographic: carrying capacity (K), per capita growth rate (r)
  - Genetic: optimal phenotype (Z_{opt}), selection coeficient (ω)
- Model analyses, e.g.:
  - Recovery time (# generations) to a known (future) stable state, depending on genetic structure (dominance, epistacy) and / or spatial structure of the population
- Use:
  - Provides insight in system dynamics
  - Understanding of current patterns based on historic processes

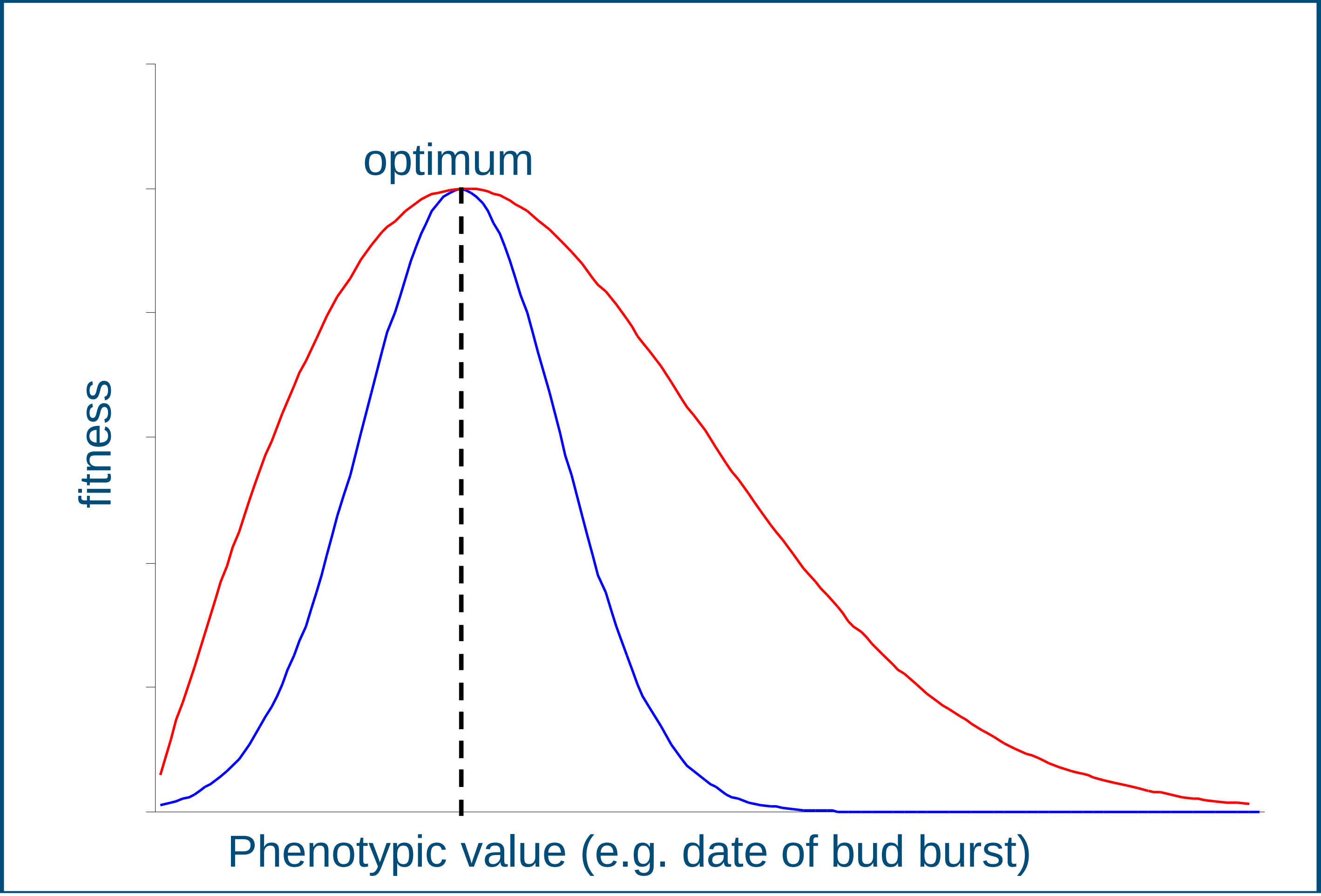
Demography in equilibrium model



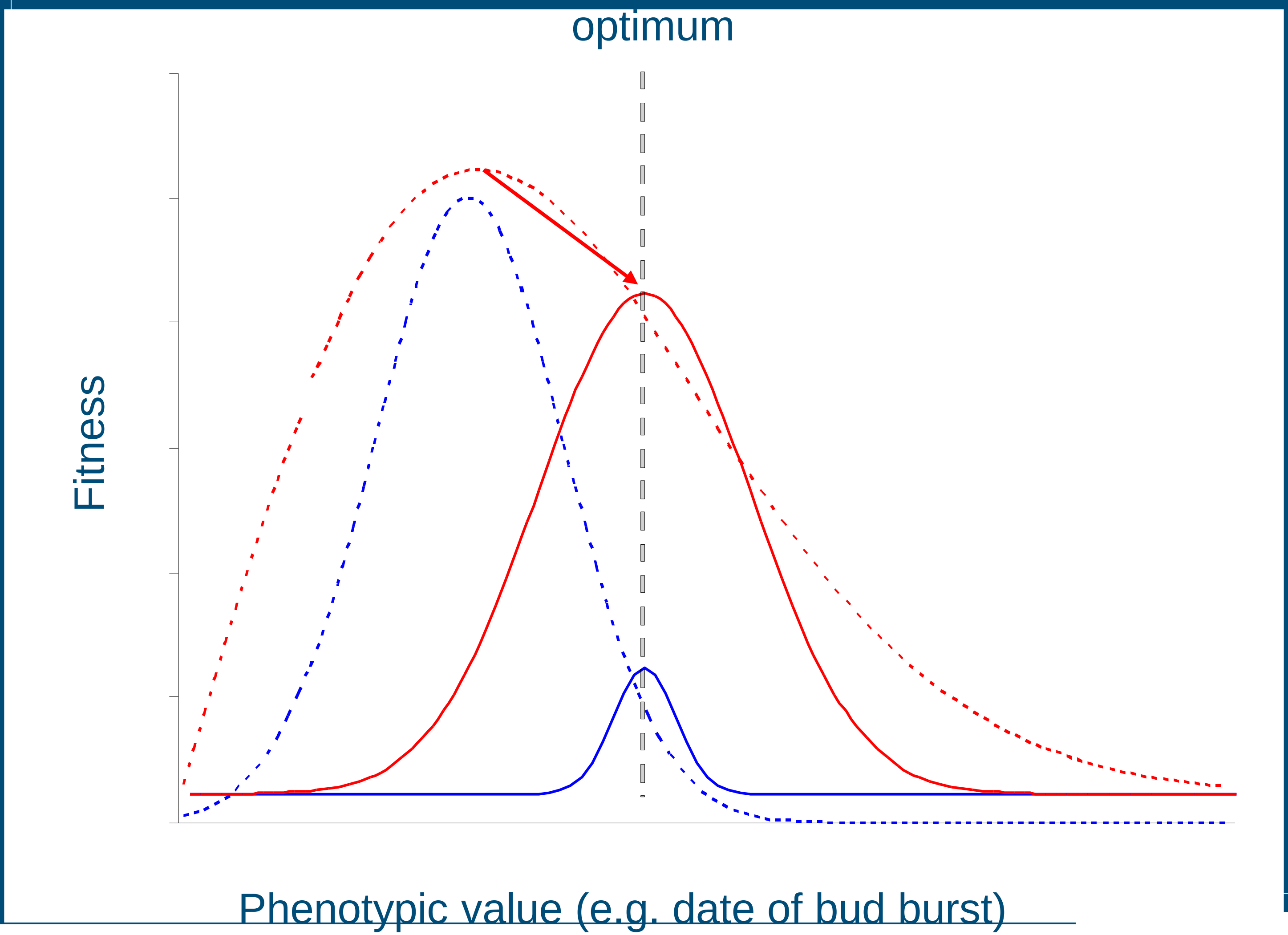


$$N_{t+1} = N_t + r \cdot N \cdot \left(\frac{K - N}{K} \right)$$

Classical population-genetic models – current situation - 2 populations



Classical population-genetic models: future situation



$$F(Z) = \exp\left(- \frac{(Z - Z_{opt})^2}{2\omega^2} \right)$$

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Non-equilibrium approach: individually-based genetic modeling

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Non-equilibrium or individualistic approach

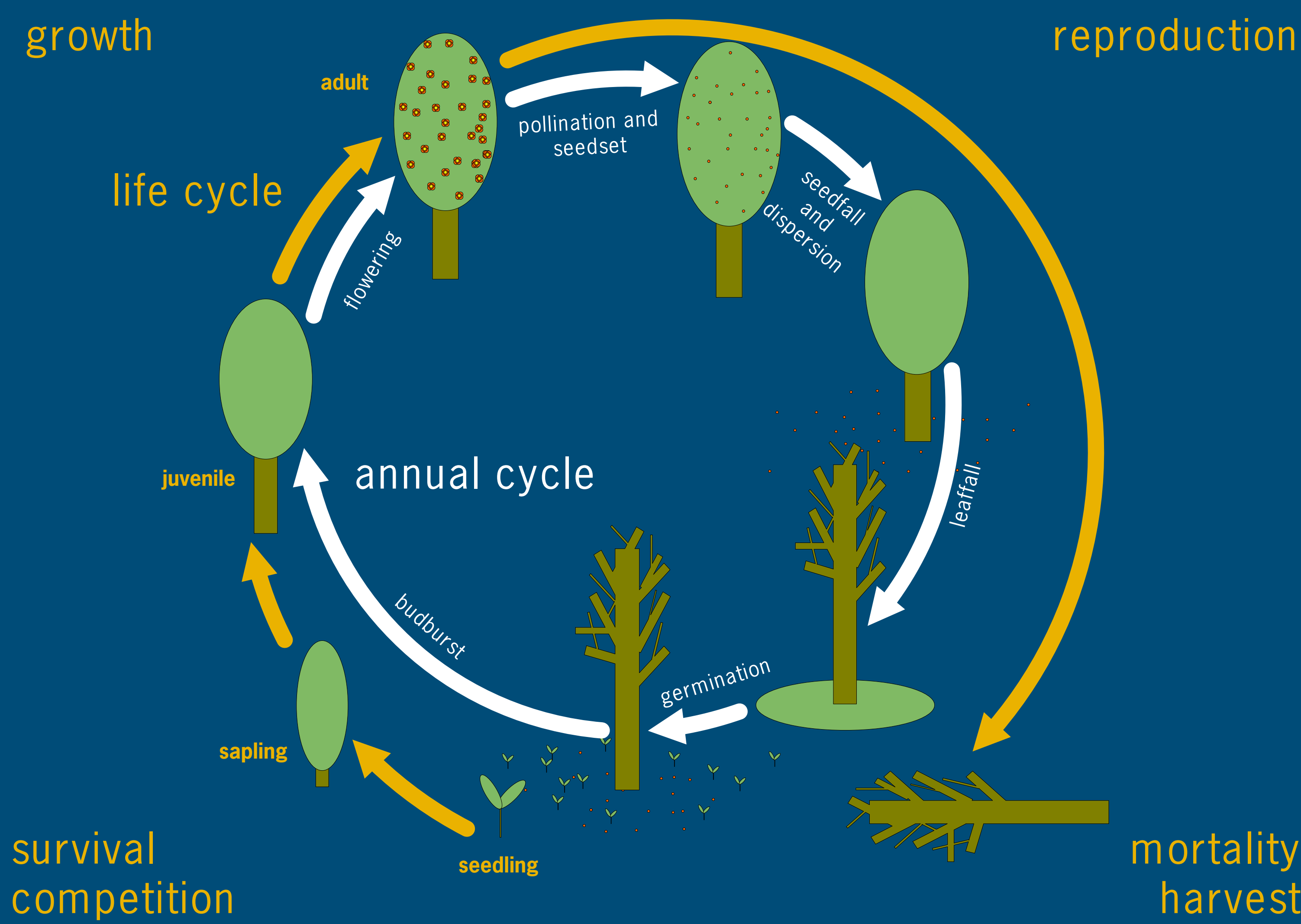
- Assumption:
  - Environment can be non-stationary in space and time relative to the rate of adaptation
  - Population is always lagging behind changing biotic and abiotic conditions – both genetic and demographic
  - => History does not provide knowledge on future “stable states”
  - => we have no information on future stable states

- Traits - broad sense, e.g.:
  - Budburst, growth, WUE, NPP, biomass, height

- Traits – narrow sense, e.g.:
  - Critical temperature thresholds, sensitivity of process to environmental driver
  - i.e. parameters that determine phenotypic plastic response but are assumed to be invariant with respect to environmental conditions

- Model analyses e.g.:
  - Determine processes and traits that are most under selection
  - Study change in phenotypic plasticity in (future) environmental conditions and assess role of spatial genetic structure, gene flow etc.

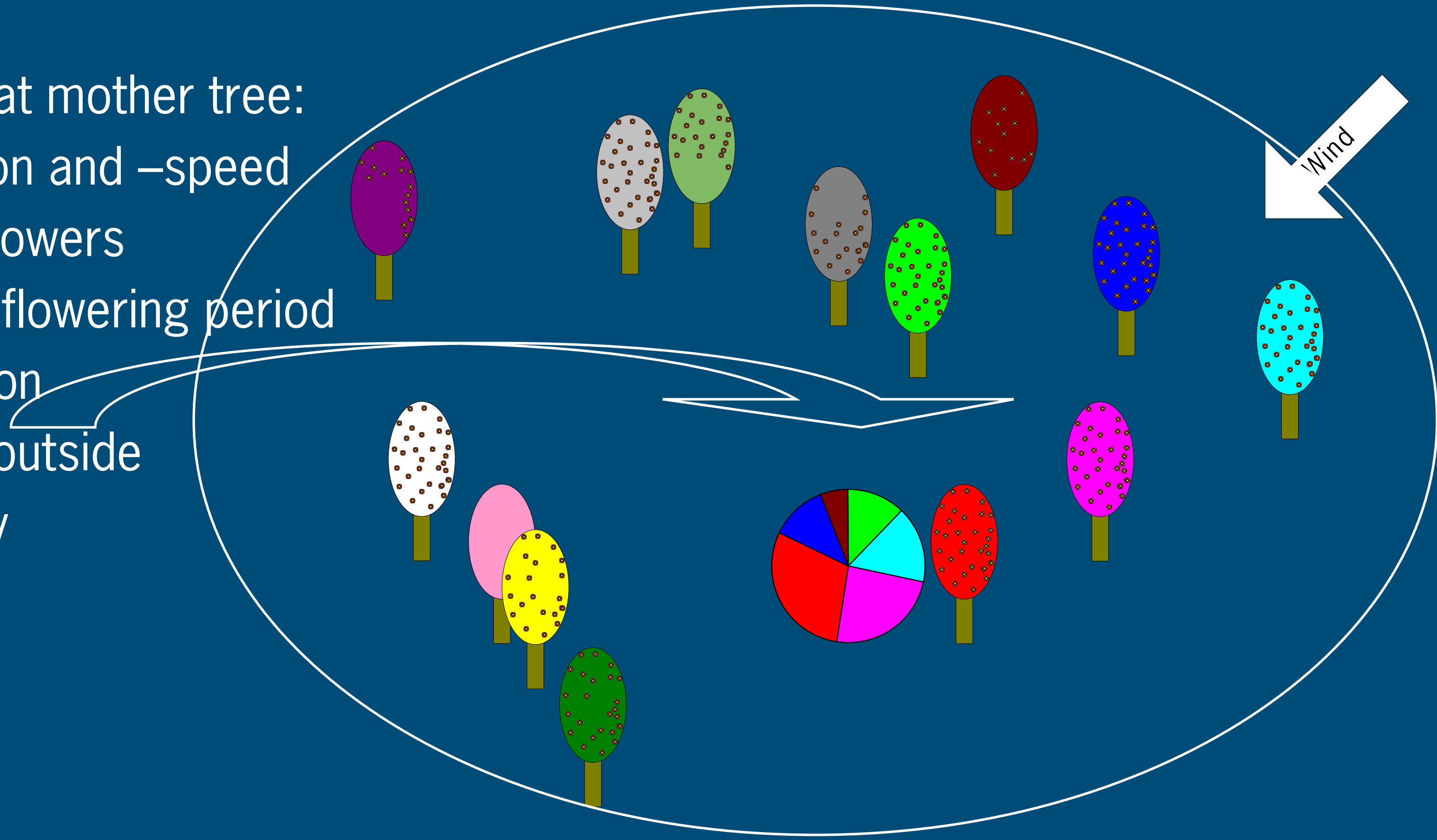
Individually-based modelling: life- and annual cycle



Gene flow by pollen dispersal

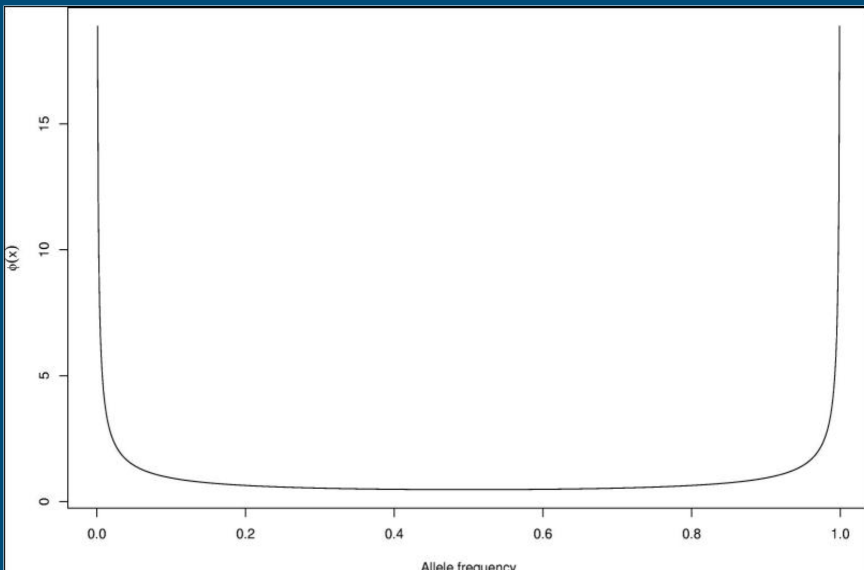
Fraction pollen at mother tree:

- Wind direction and –speed
- Number of flowers
- Overlapping flowering period
- Self pollination
- Pollen from outside
- Compatibility



Genetic component of ForGEM: Marker-trait association

Theoretical distribution of allelic frequencies (Nei)



Allele frequency

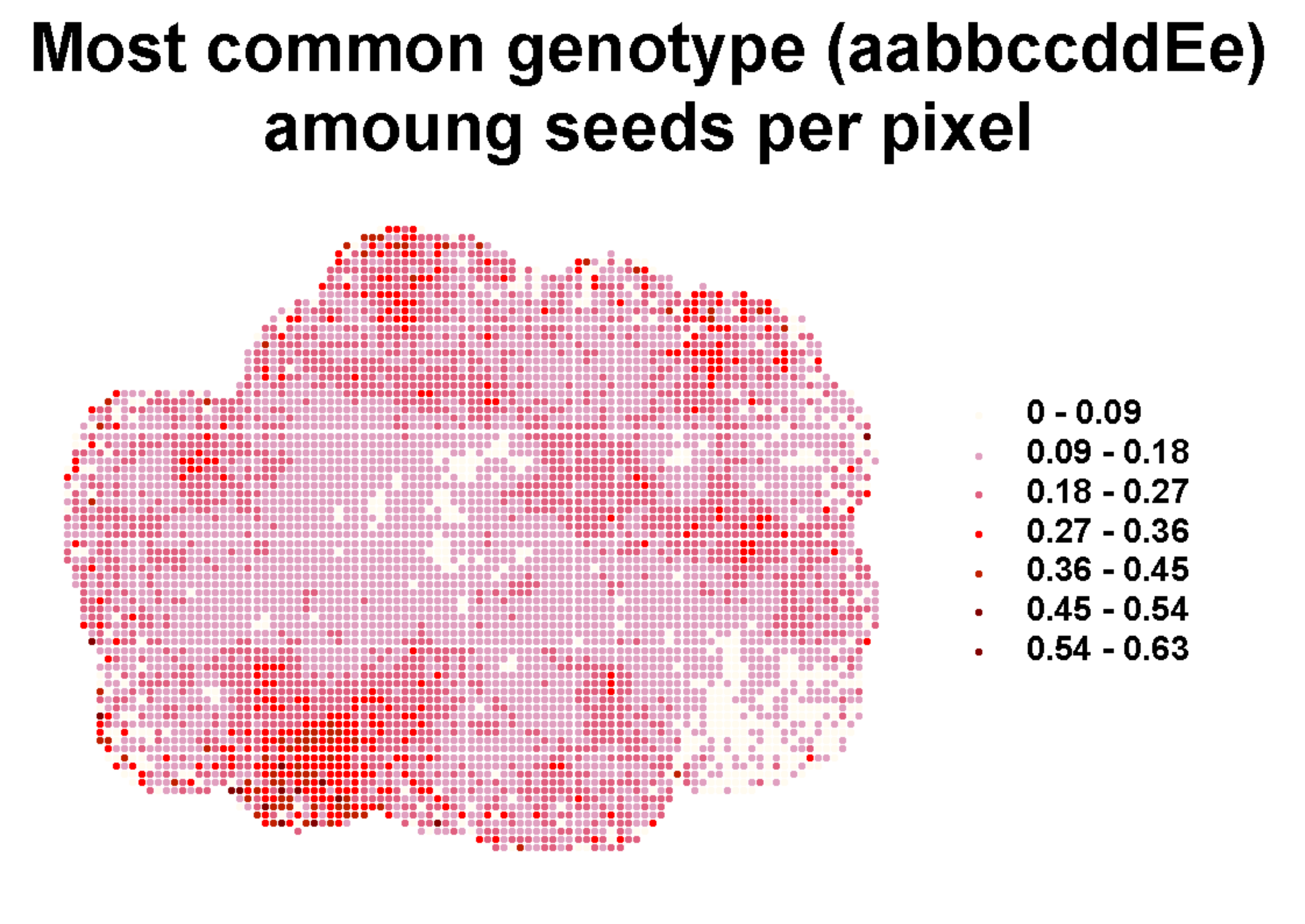
Allele	Allelic frequency *(p, q)*	*dose a*
A	0.01	+1
a	0.99	-1
B	0.05	+1
b	0.95	-1
C	0.15	+1
c	0.85	-1
D	0.30	+1
d	0.70	-1
E	0.50	+1
e	0.50	-1

$$\overline{Z} = \sum_{i=1}^{n} a_i (p_i - q_i) + 2\sum_{i=1}^{n} d_i p_i q_i$$

$$V_P = 2\sum_{i=1}^{n} p_i q_i [a_i + d_i (p_i - q_i)]^2 + 2\sum_{i=1}^{n} (d_i p_i q_i)^2 + V_E$$

- μ = 5.96; σ^2 =5.16
- transform *a* to match observed mean and variance for any model parameter / trait
- use observed h^2 to introduce initial environmental variance

spatial distribution of genotype in seeds



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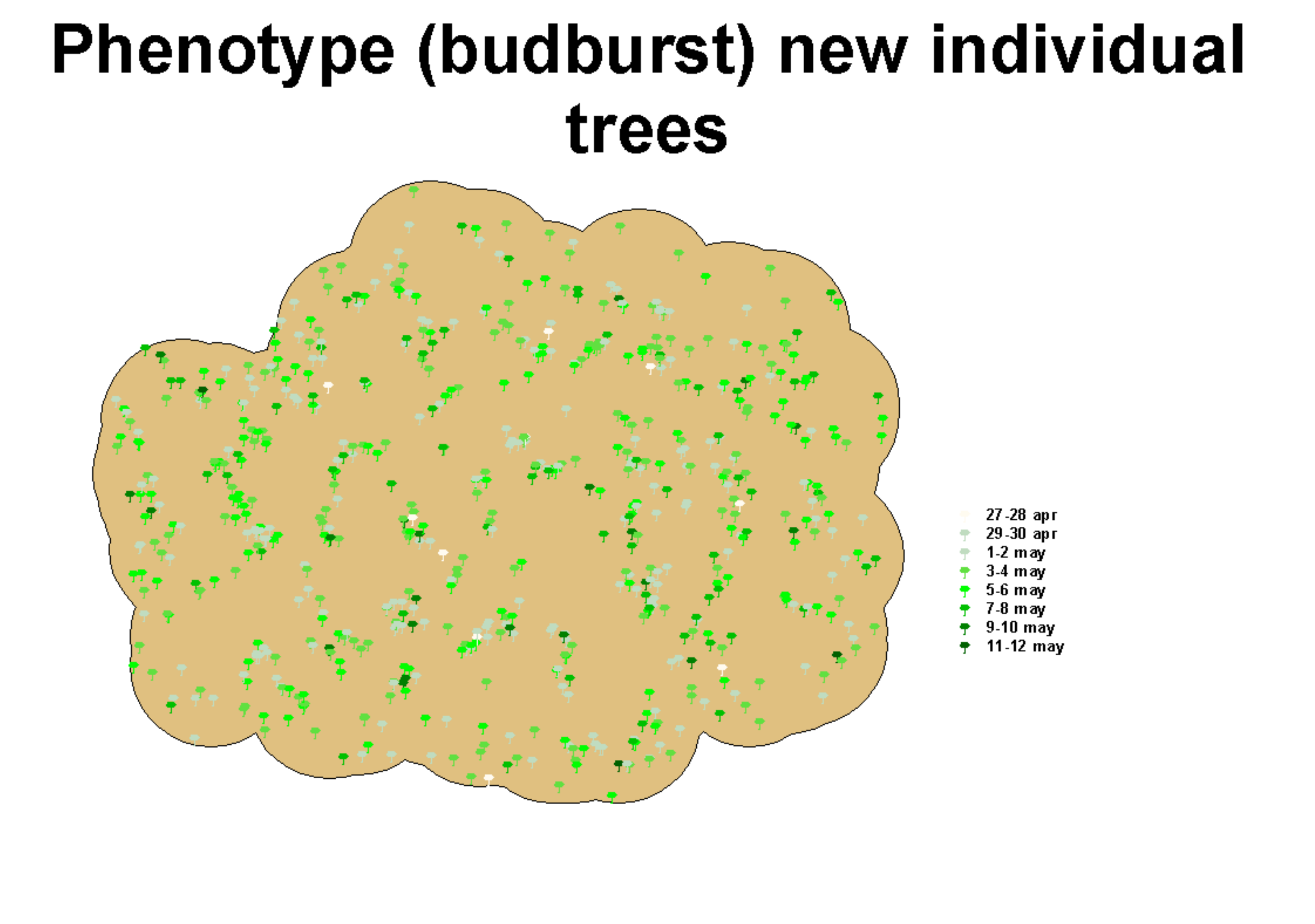
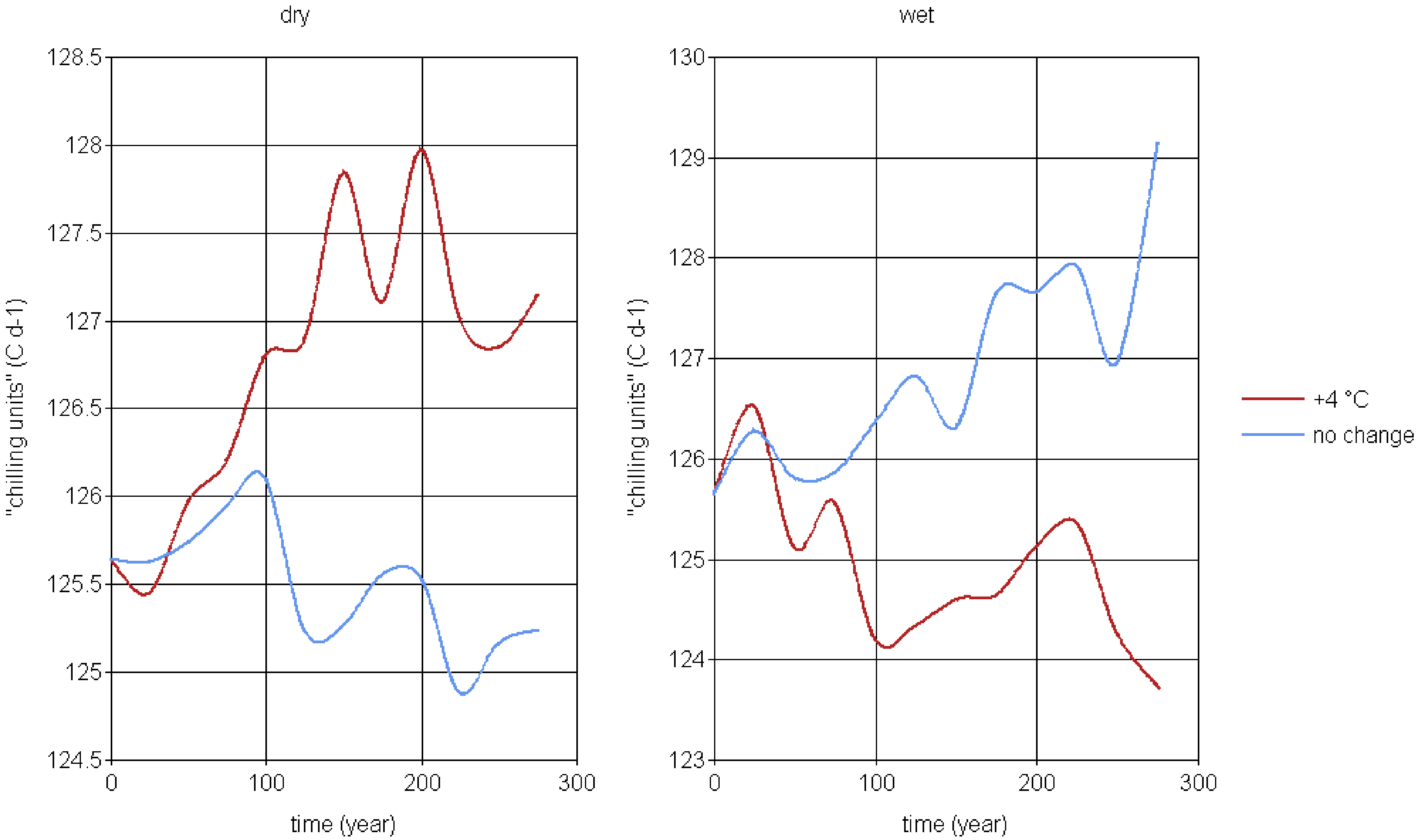
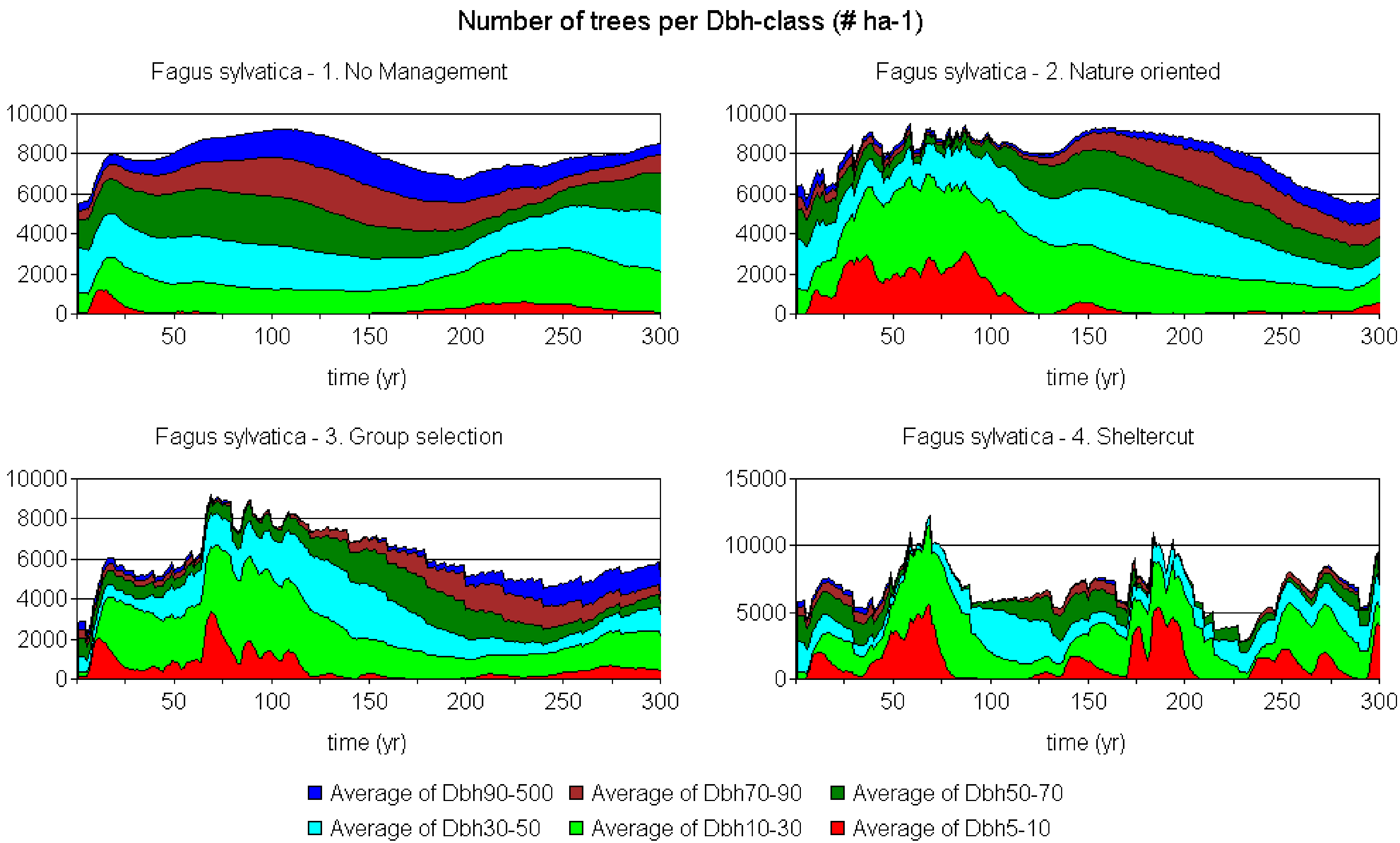
Spatial distribution phenotype in saplings



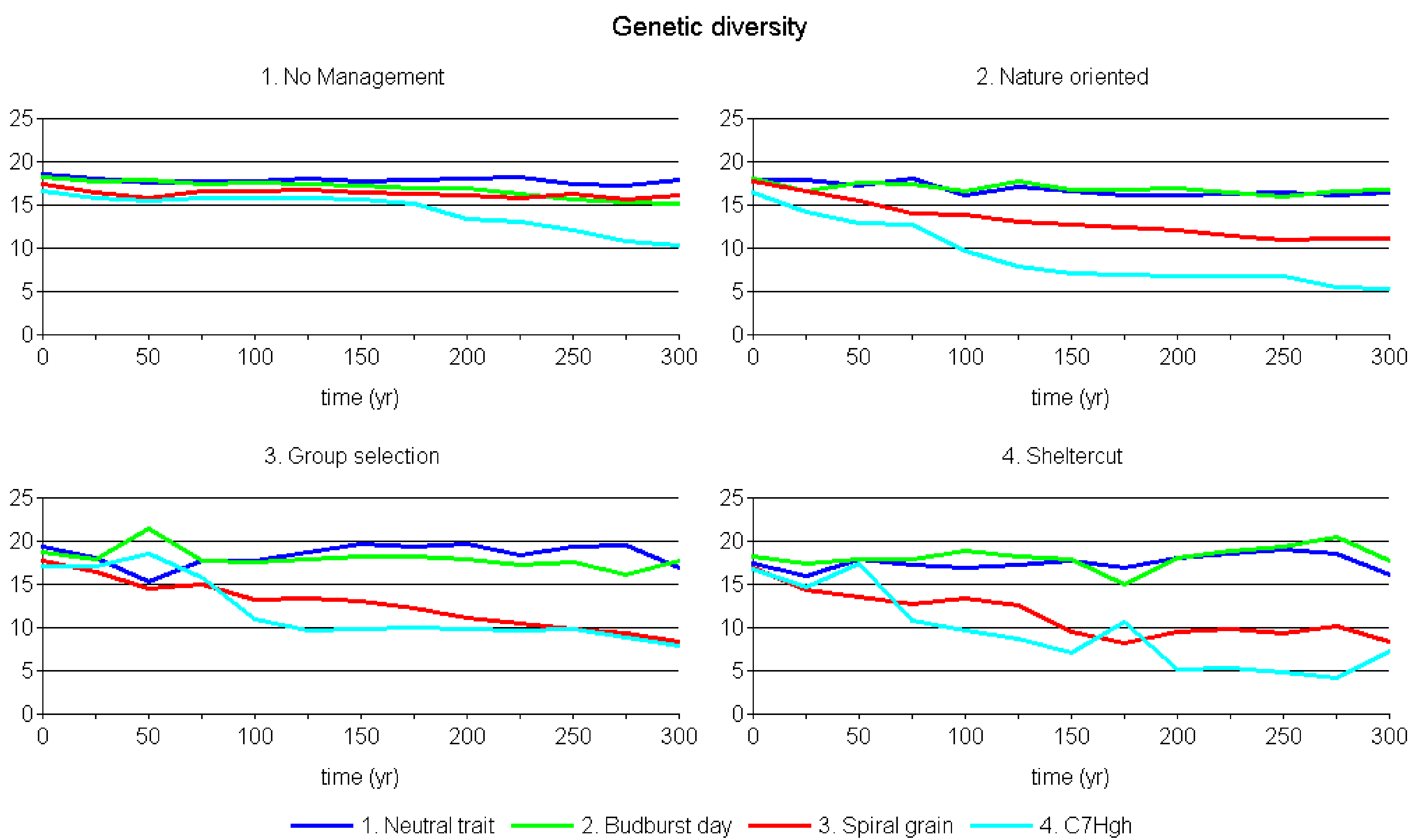
Evolution of critical state of chilling (S_{chl}^*)



Example output ForGEM: tree density



Example output ForGEM: Genetic diversity



What is the likely effect of climate change on the geographic distribution of species

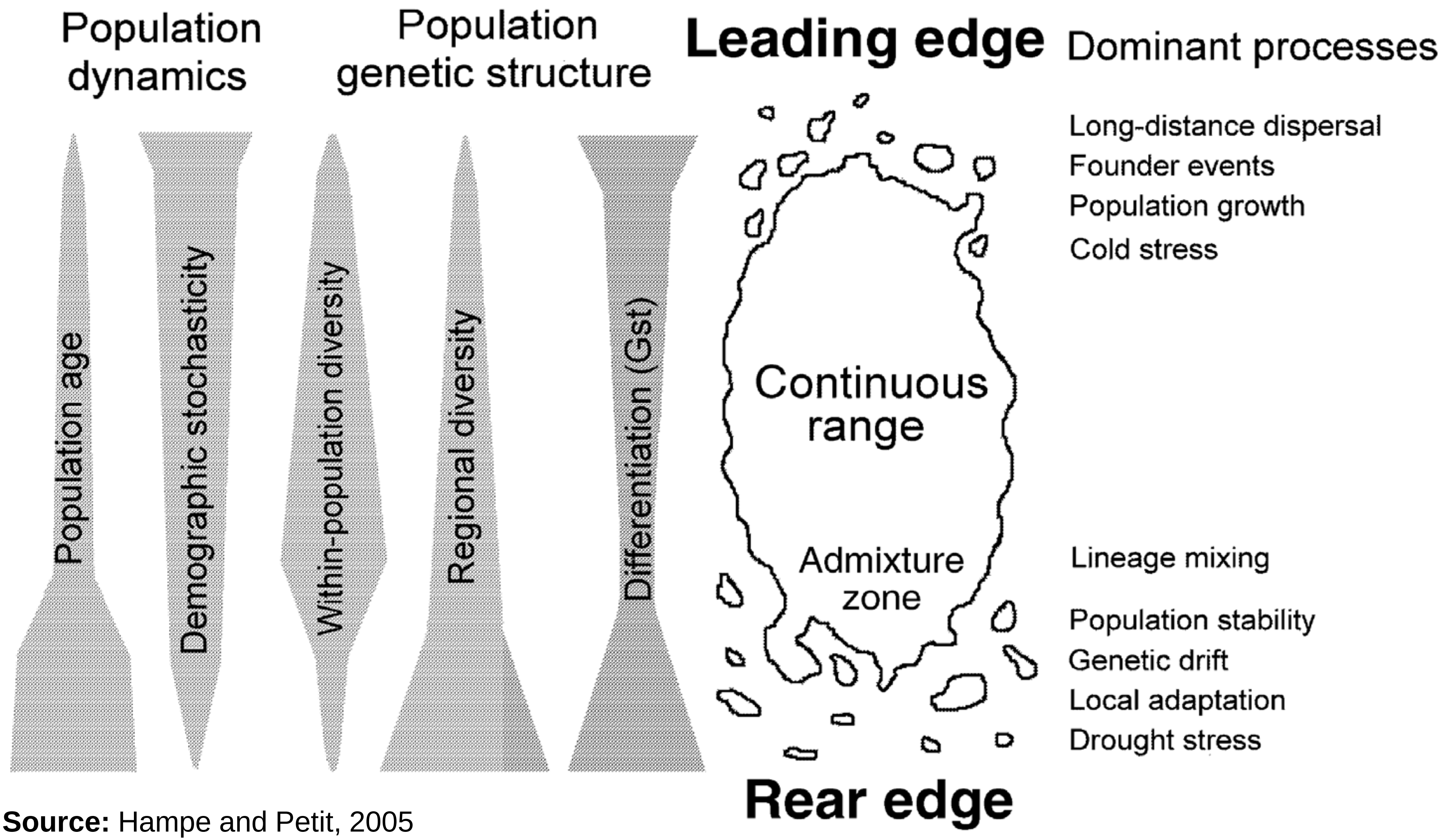
Which climatic factors are mainly responsible for this change?

What is the impact on genetic diversity?

What is the adaptive potential?

What is interaction between adaptive response to climate change and forest management?

Impacts of genetic diversity and adaptive response



Source: Hampe and Petit, 2005

Adaptive responses at limits of species' area

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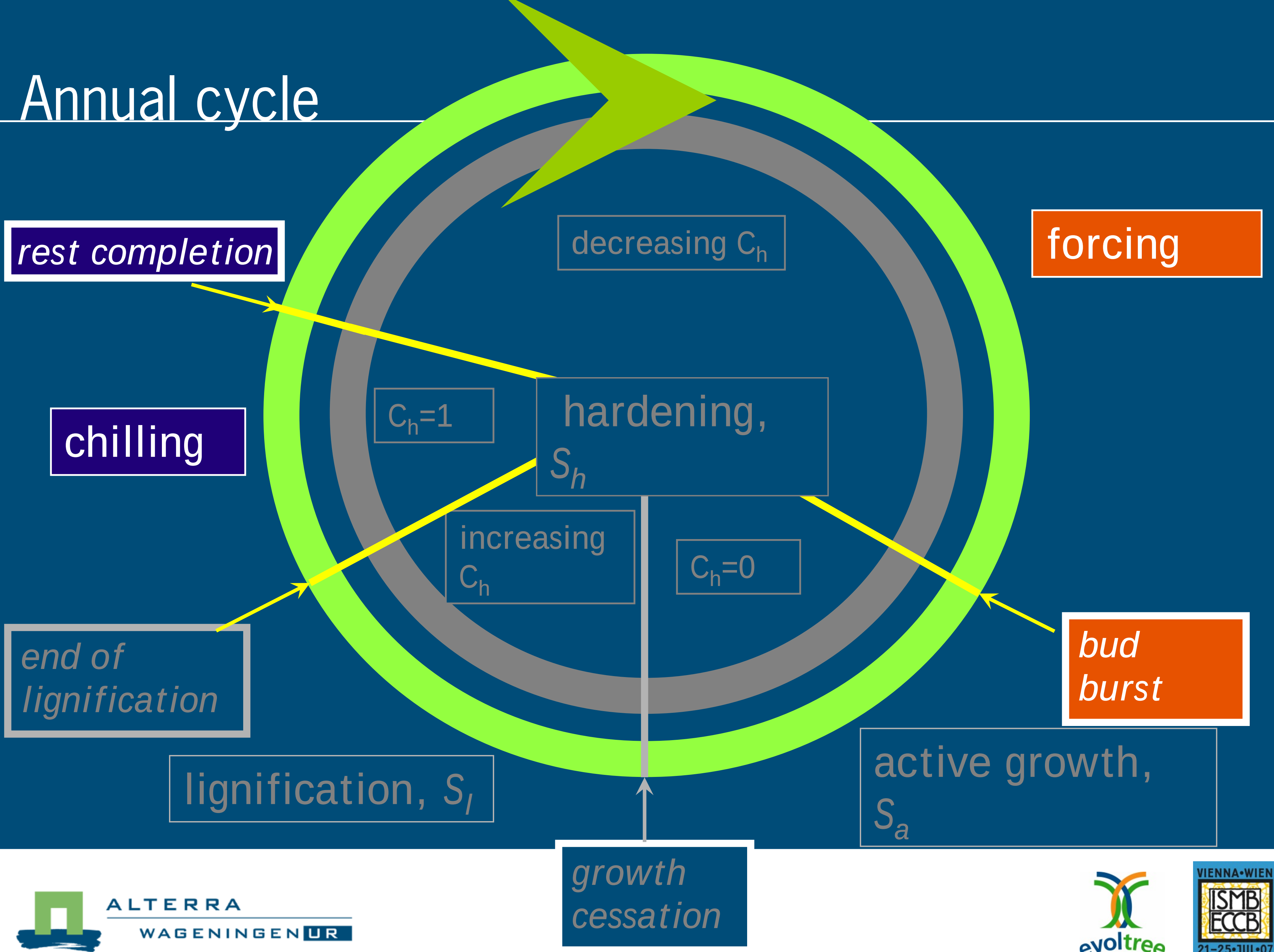
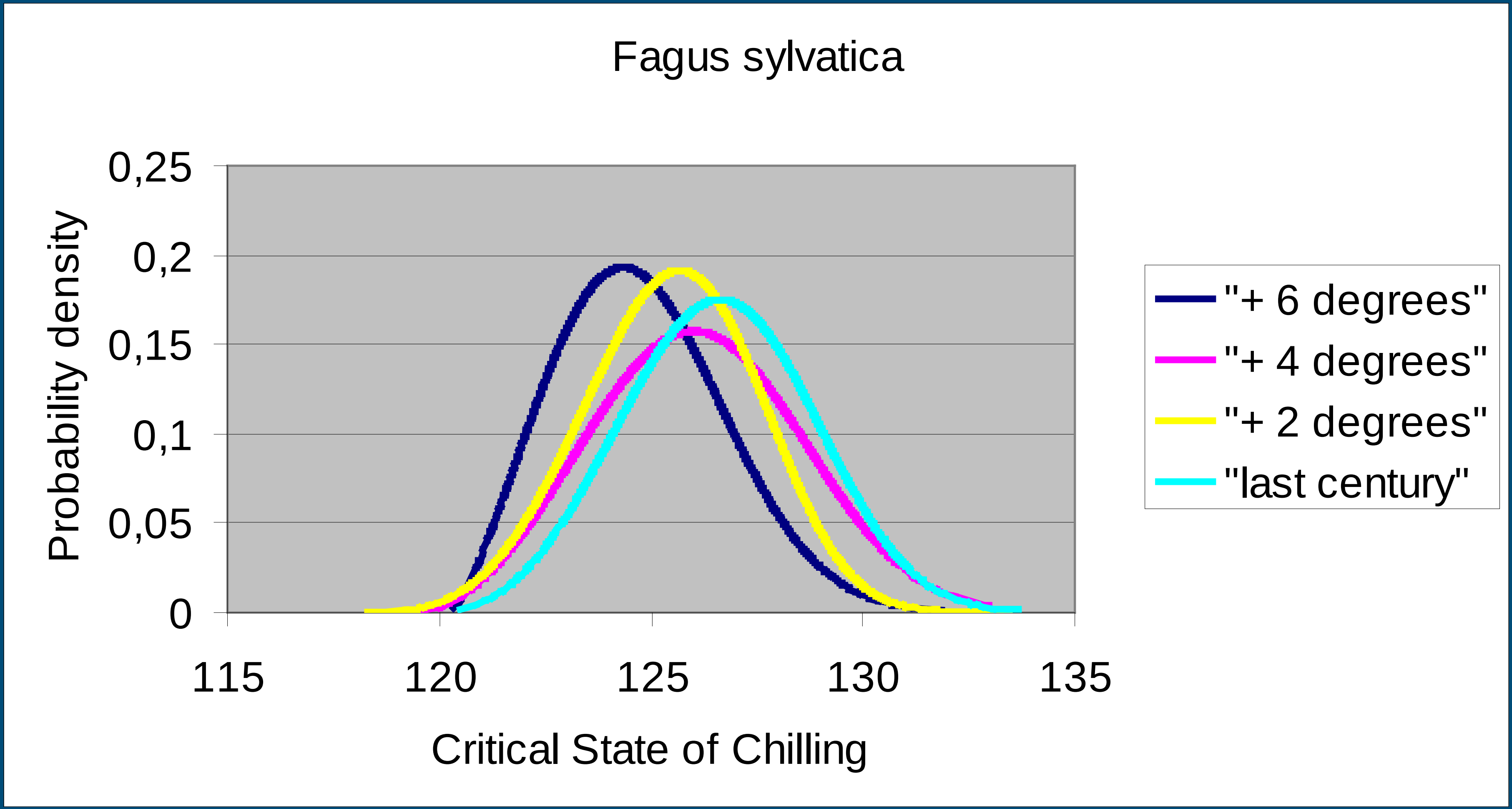
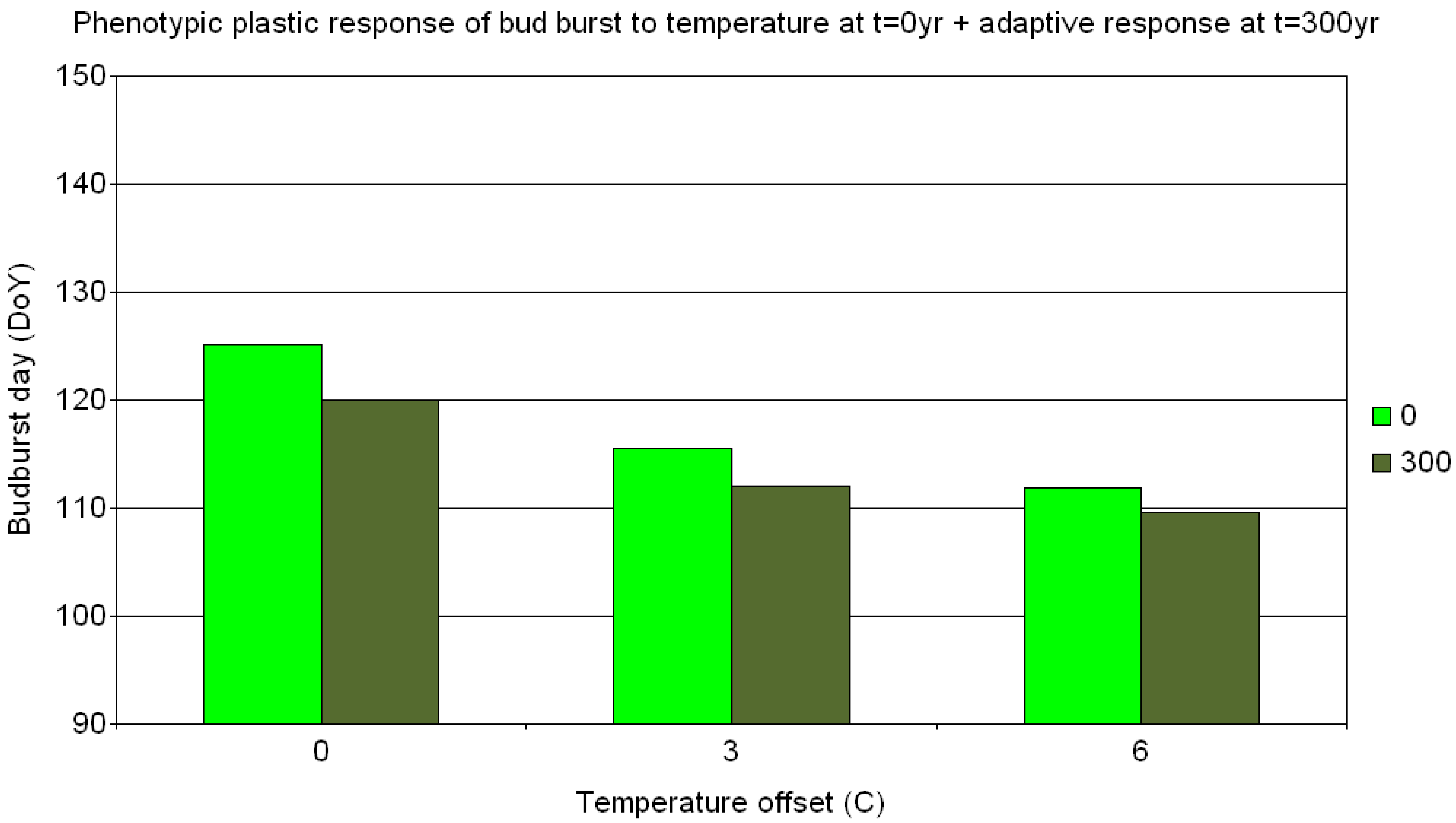
Annual cycle



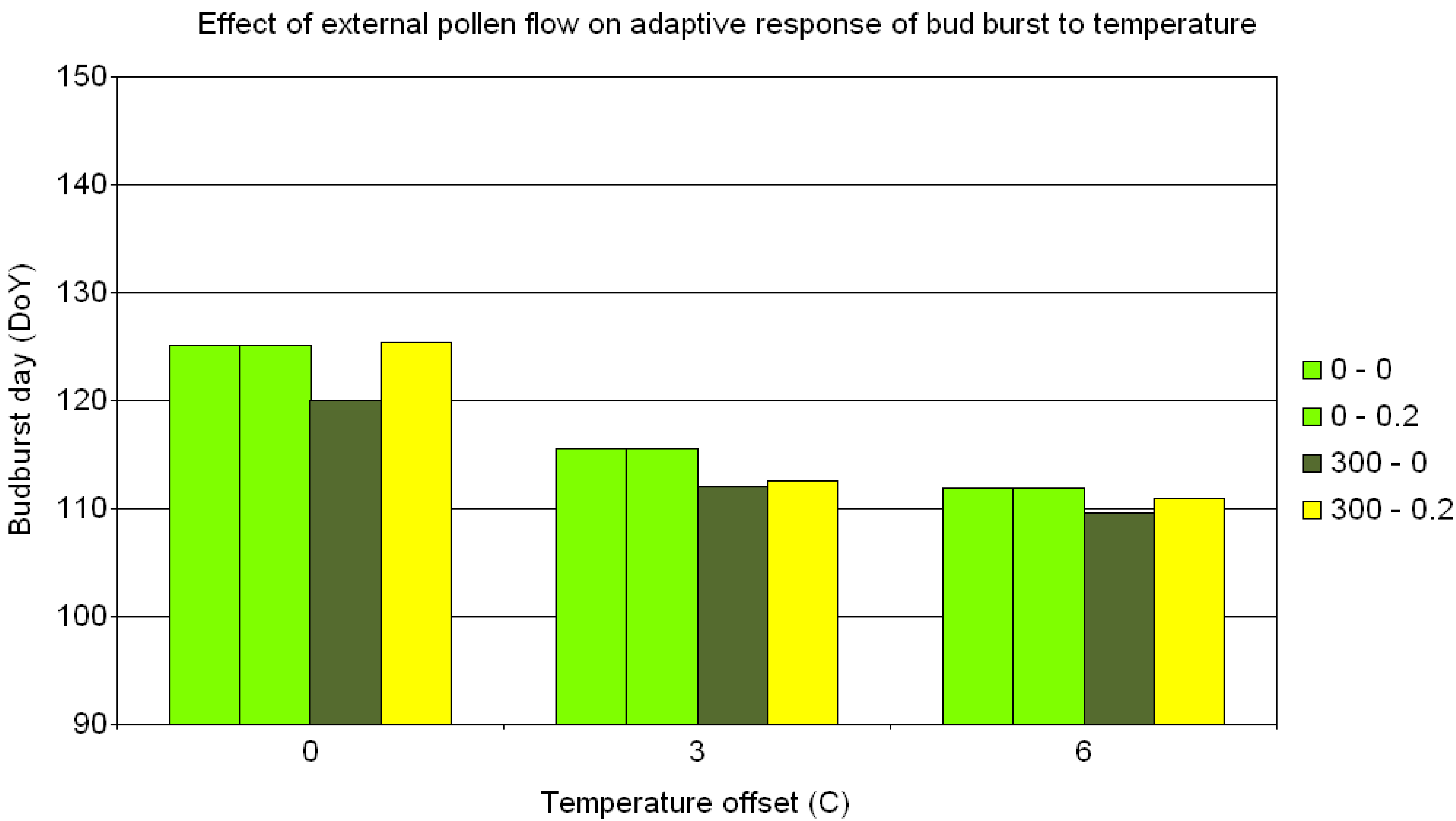
Adaptive response of chilling requirement



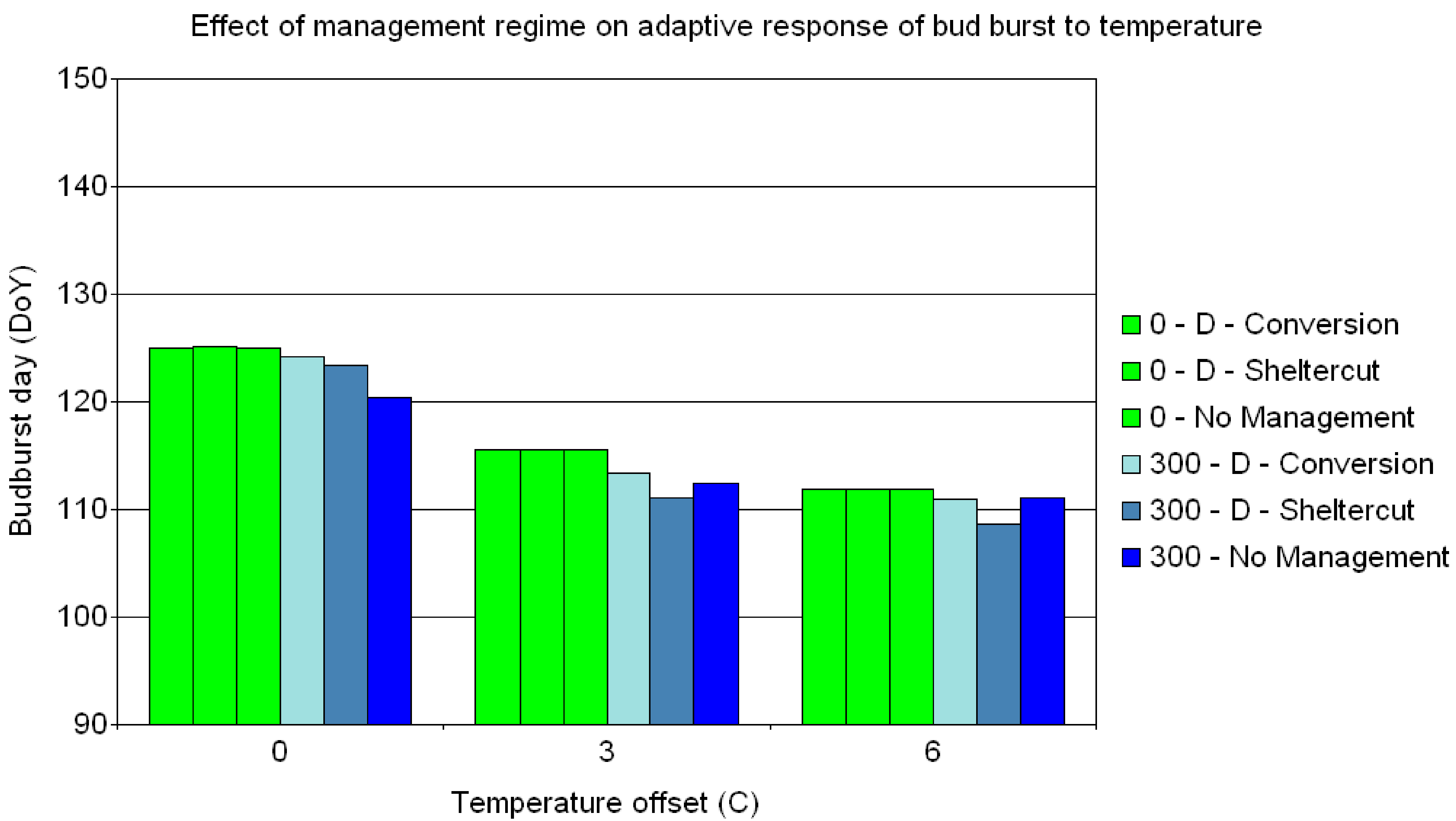
Response of bud burst to temperature



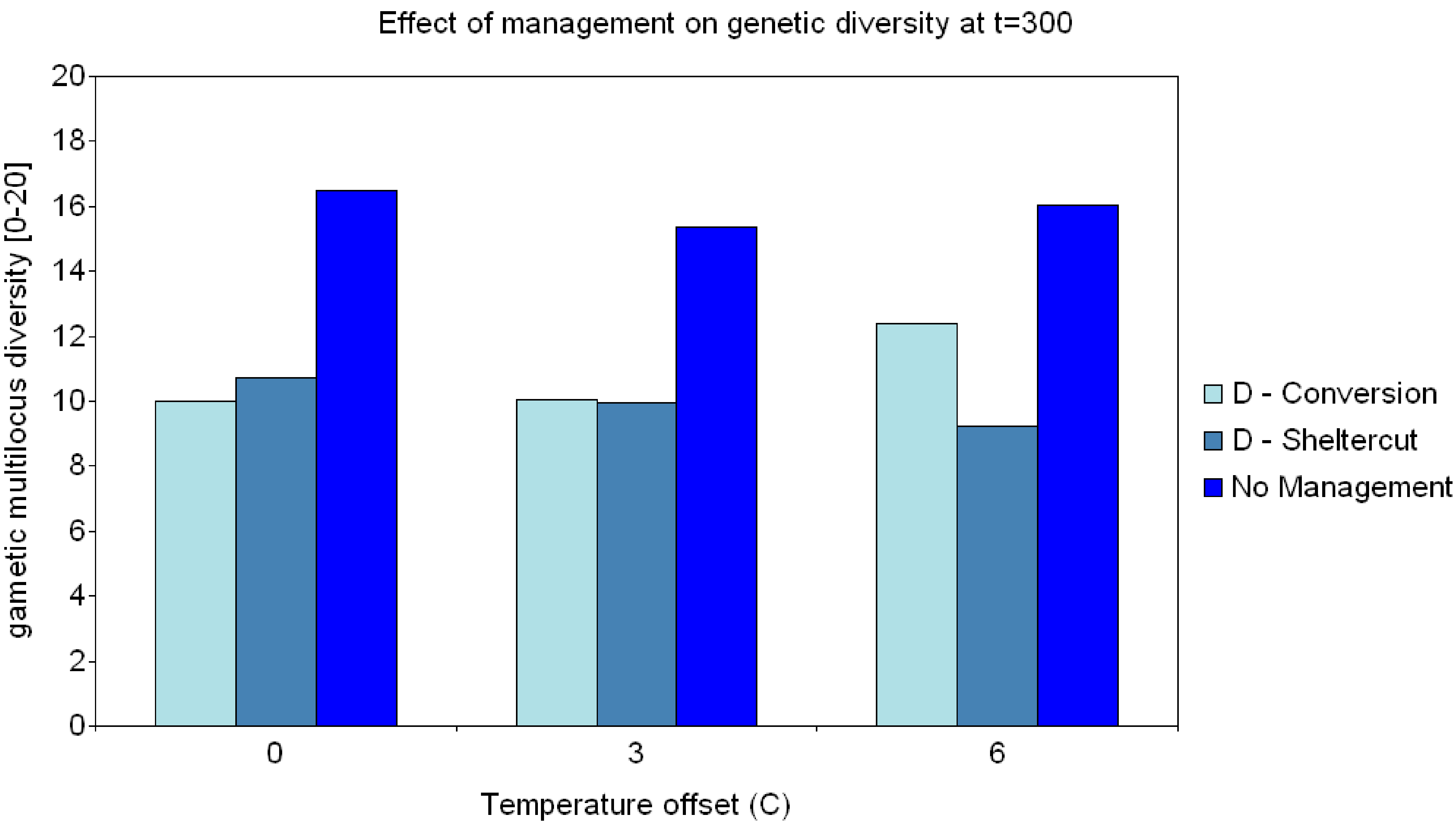
Interaction temperature - pollen flow



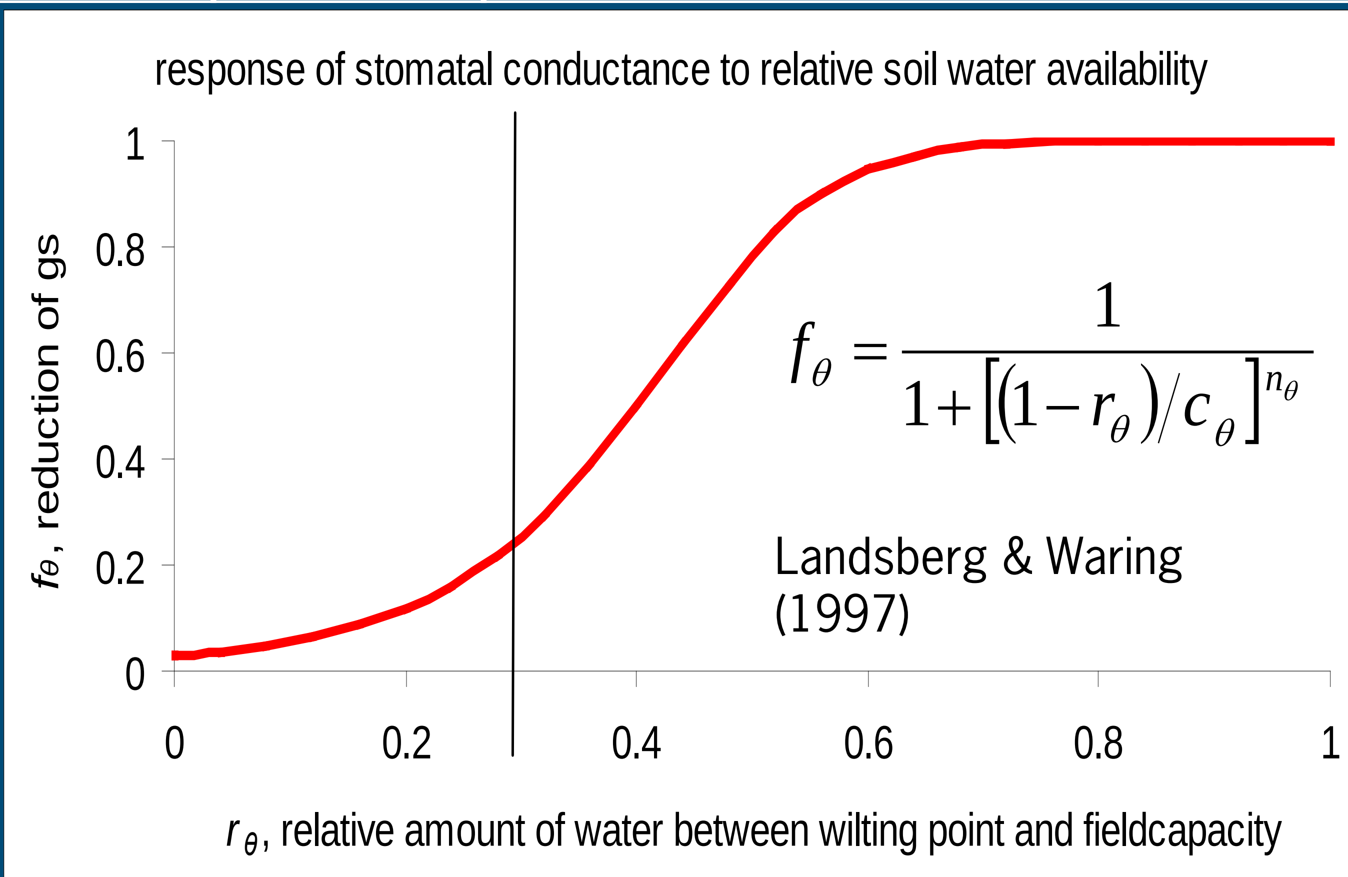
Interaction temperature-management



Management and genetic diversity



Adaptive response of stomatal conductance to drought



$$f_\theta = \frac{1}{1+\left[\left(1-r_\theta\right)/c_\theta\right]^{n_\theta}}$$

Landsberg & Waring (1997)

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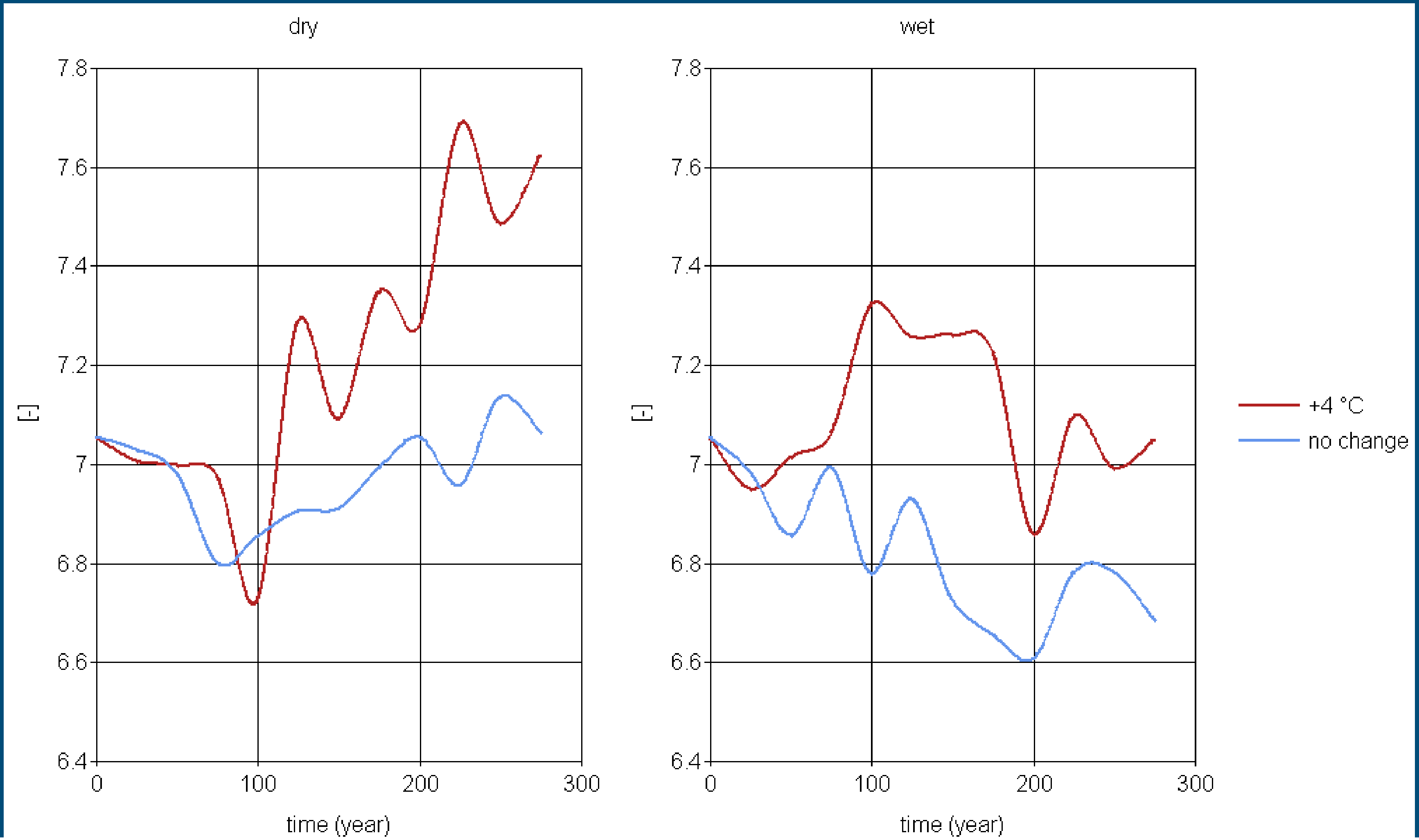
E.g. 2: Evolution of sensitivity of stomatal conductance to soil water availability



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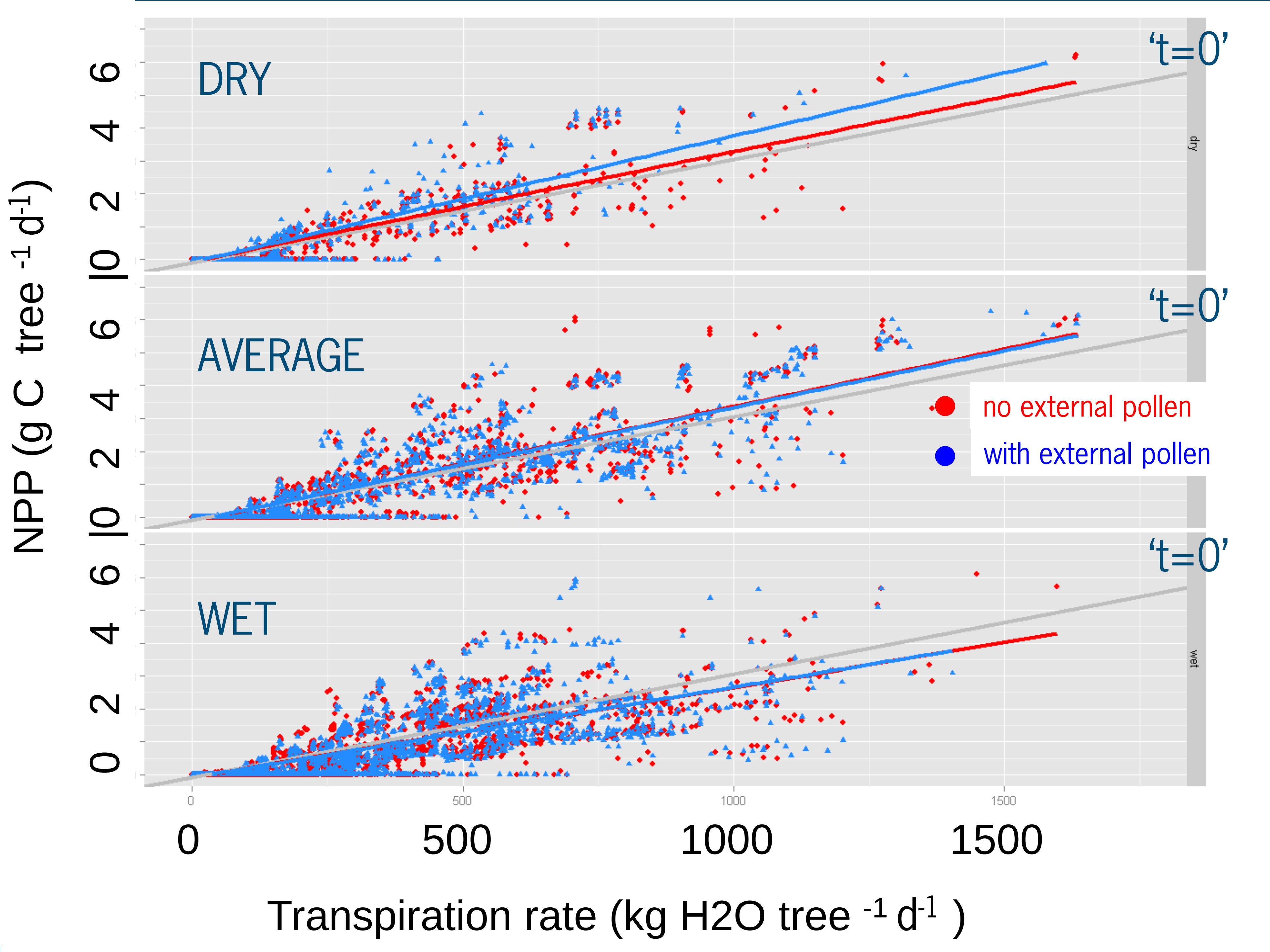

DRY
AVERAGE
WET
't=0'
't=0'
't=0'
no external pollen
with external pollen
NPP (g C tree -1 d-1)
Transpiration rate (kg H2O tree -1 d-1)
0
500
1000
1500
0
2
4
6
dry
wet

Pros and cons of eq. and non-eq. genetic modeling

- Eq.:
  - Generic, suitable for analysis of past, long-term evolutionary processes
  - Abstract traits related to whole tree fitness function
  - Not suitable for short-term future assessment because equilibrium states and selection pressure are input to the model

- Non-eq.:
  - Realistic, suitable for prediction at short-term, also for future equilibriums
  - Traits that have trade-off in resource use and fitness, that results in phenotypic plastic responses (morphological / physiological)
  - Not operational for long-term (>100s of generations) evolutionary processes
  - Future developments: include observed genetic information of adaptive traits in non-eq. models & apply at the whole species' area