Incorporating genetic gain into stand level modeling: a forest genetics perspective

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Overview: a forest genetics perspective

- Deployment policy/guidelines of selected material must consider:
  - future unknown risk (e.g., exotic pests)
  - known risks / pests (e.g., weevils, MPB)
  - growth potential, yield & stability
- Breeding Values (BV) > Genetic Worth (GW) > stand level projections
- Future research issues

Loblolly pine in the southern US

Full or half sib forestry

- nursery advantages real
- silviculture handling, also 'real'
- growth and yield advantages?
- no 'value added' as of yet?

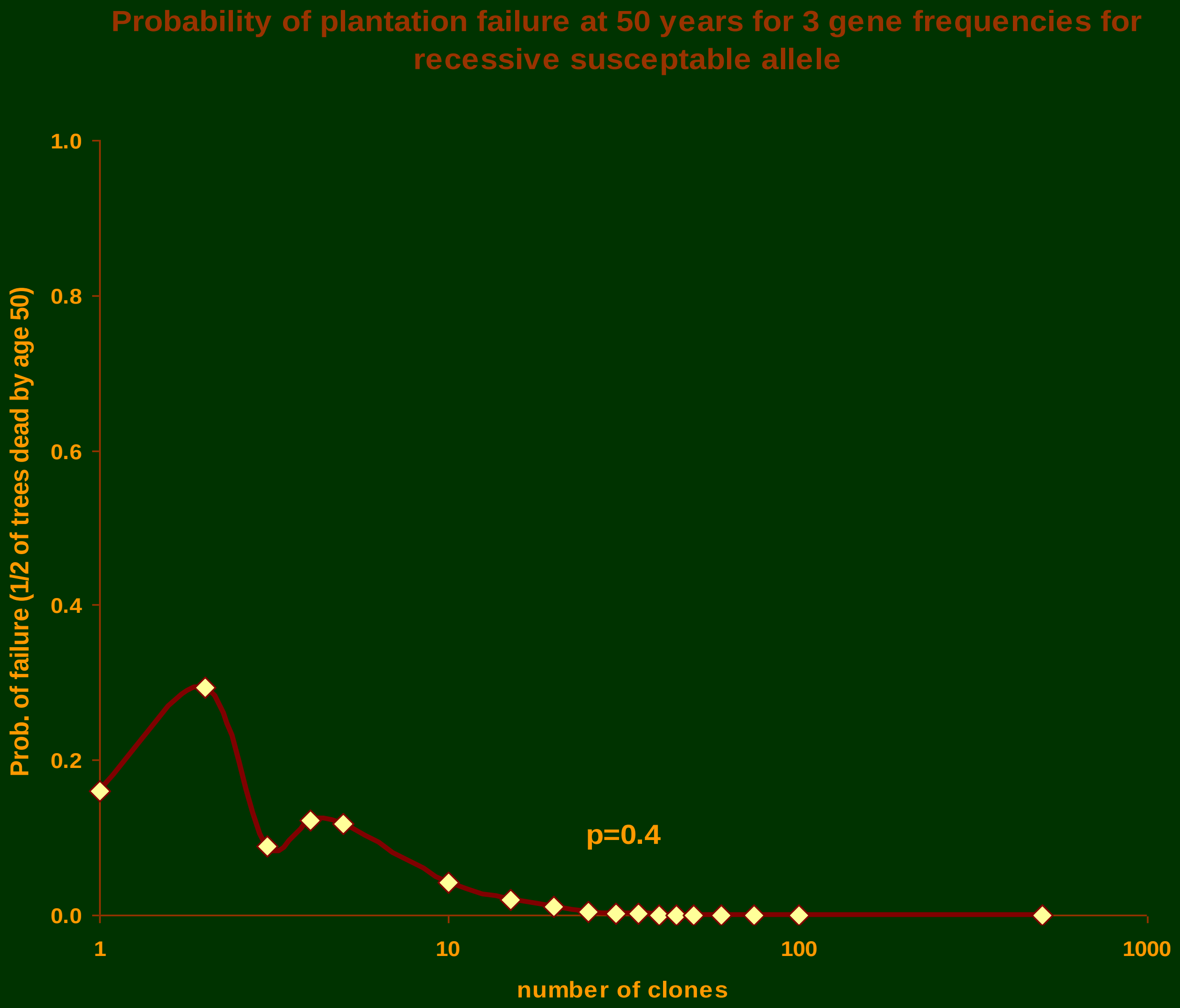
Eucalyptus in Brazil

All clones still mixed at the mill!

Reforestation ‘Landscapes’ in B.C.

Deployment for Unknown Risks

- Past models of deployment, e.g., Libby (1982), Roberds et al (1990), etc.
  - Largely ‘single gene-for-gene’ models,
  - Plantation ‘failure’ at an arbitrary value (e.g., 50% mortality), show;
    - more than 30 clones does not provide any advantages
    - sometimes 1 is best
    - Incredibly sensitive to gene frequencies of resistant genes in natural populations



Probability of plantation failure at 50 years for 3 gene frequencies for recessive susceptable allele

Adapted from Bishir and Roberds (1997)

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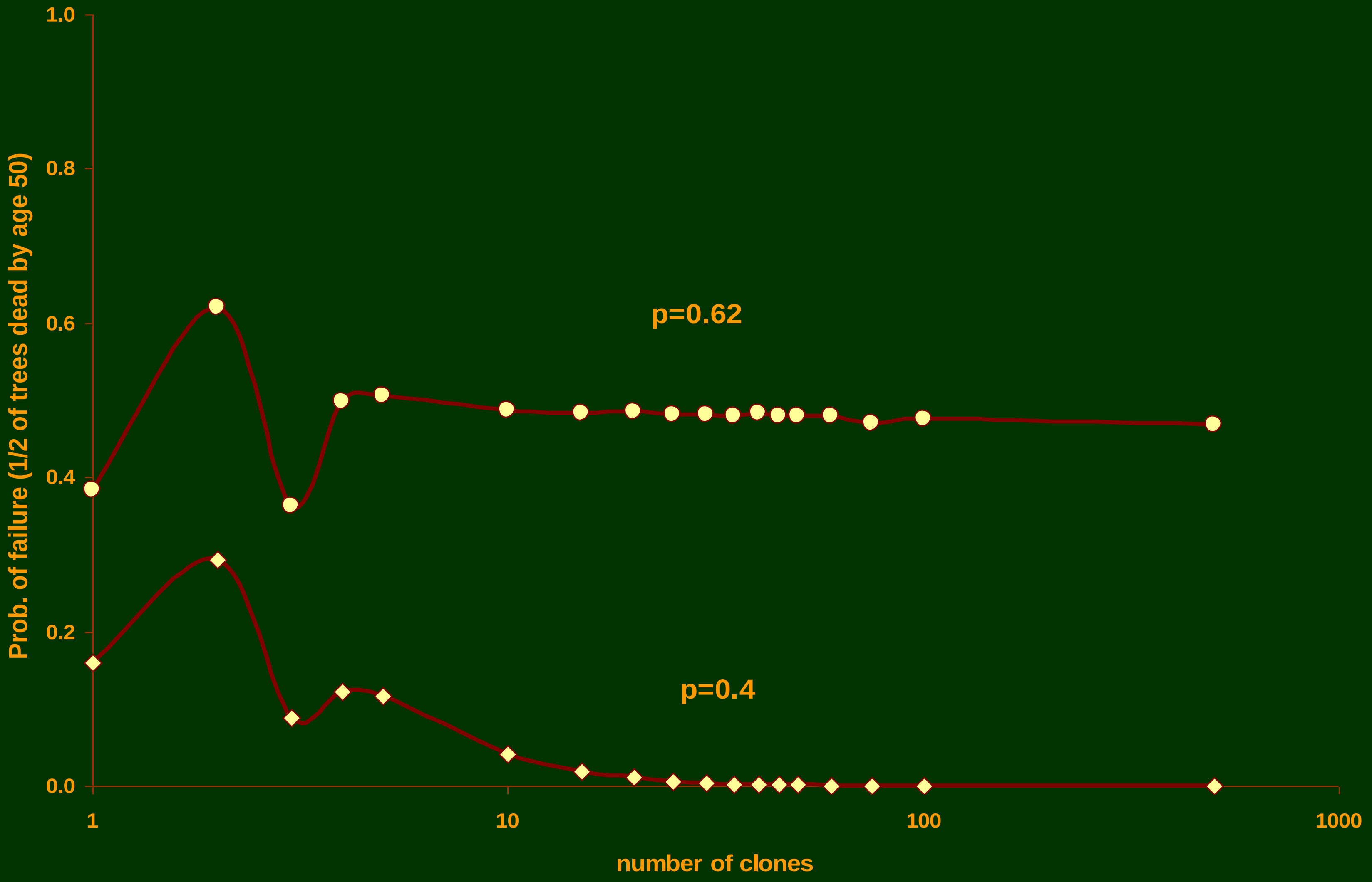

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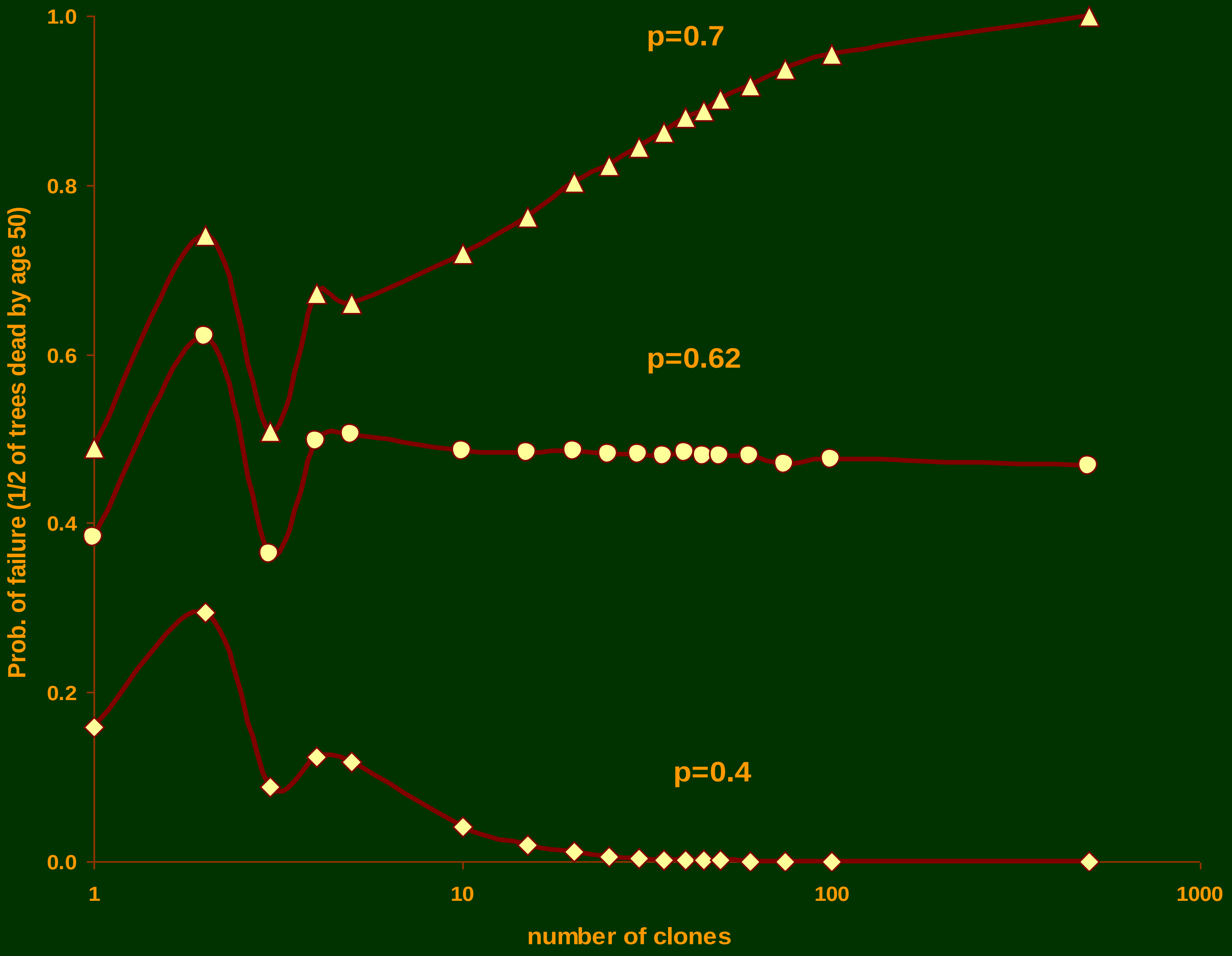


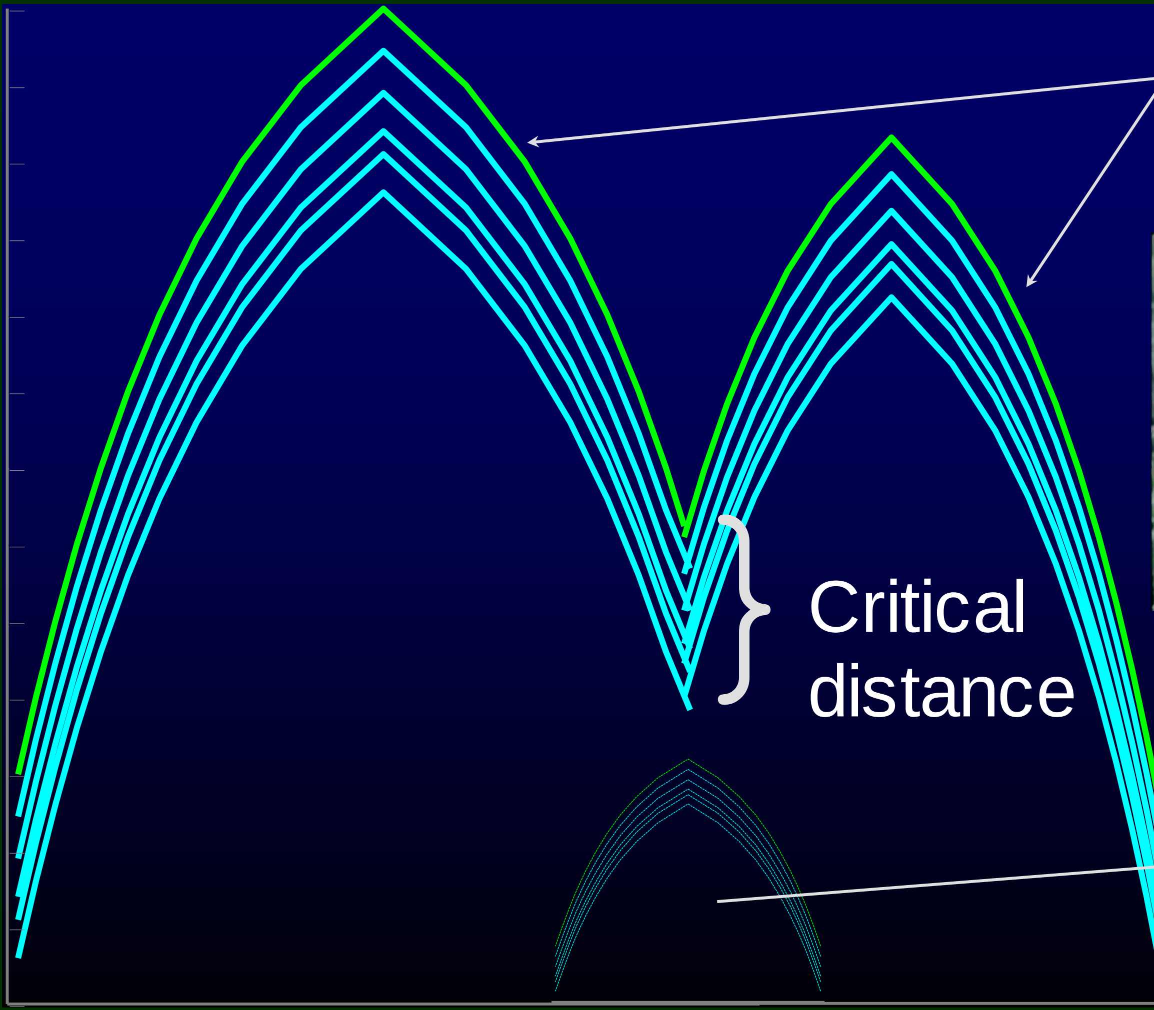
Adapted from Bishir and Roberds (1997)

Deployment for Unknown Risks…cont.

Recent work:

- Spruce Growth & Yield with an insect population dynamics model
  - Spruce terminal weevil model
- Tree and Stand Simulator (TASS - B.C. For.Ser.)
  - individual trees, competition-driven model

Key elements of the Tree and Stand Simulator (TASS)(*Mitchell, 1975*)

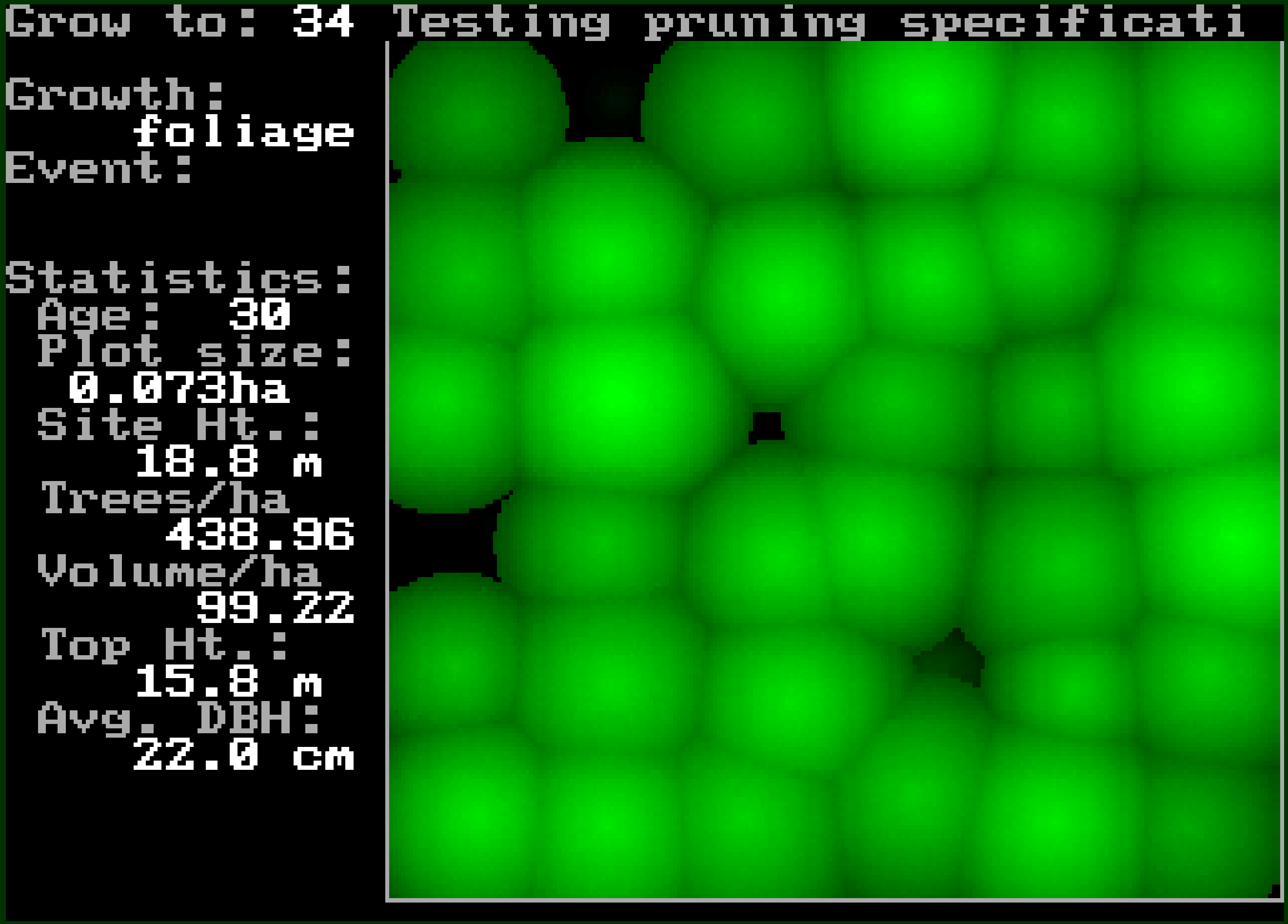


Live trees,

Critical distance

Dead tree

Key elements of the Tree and Stand Simulator (TASS)…cont.



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Grow to: 34 Testing pruning specificati

Growth:
    foliage
Event:


Statistics:
 Age:   30
 Plot size:
  0.073ha
 Site Ht.:
    18.8 m
 Trees/ha
     438.96
 Volume/ha
      99.22
 Top Ht.:
    15.8 m
 Avg. DBH:
    22.0 cm
```

BC TASS / Pest Dynamics Model

Spruce weevil resistance mechanisms

- ATR - attractiveness (volatiles)
- RES - rate of resin flow rate
- TOX - toxicity of resin
- GRW - tree ‘vigour’

- h^2<‘1.0’ for ATR, RES, TOX
- $h^2=0.5$ for GRW
- GRW correlated with RES ($r_g=0.5$)

BC TASS / Pest Dynamics Model

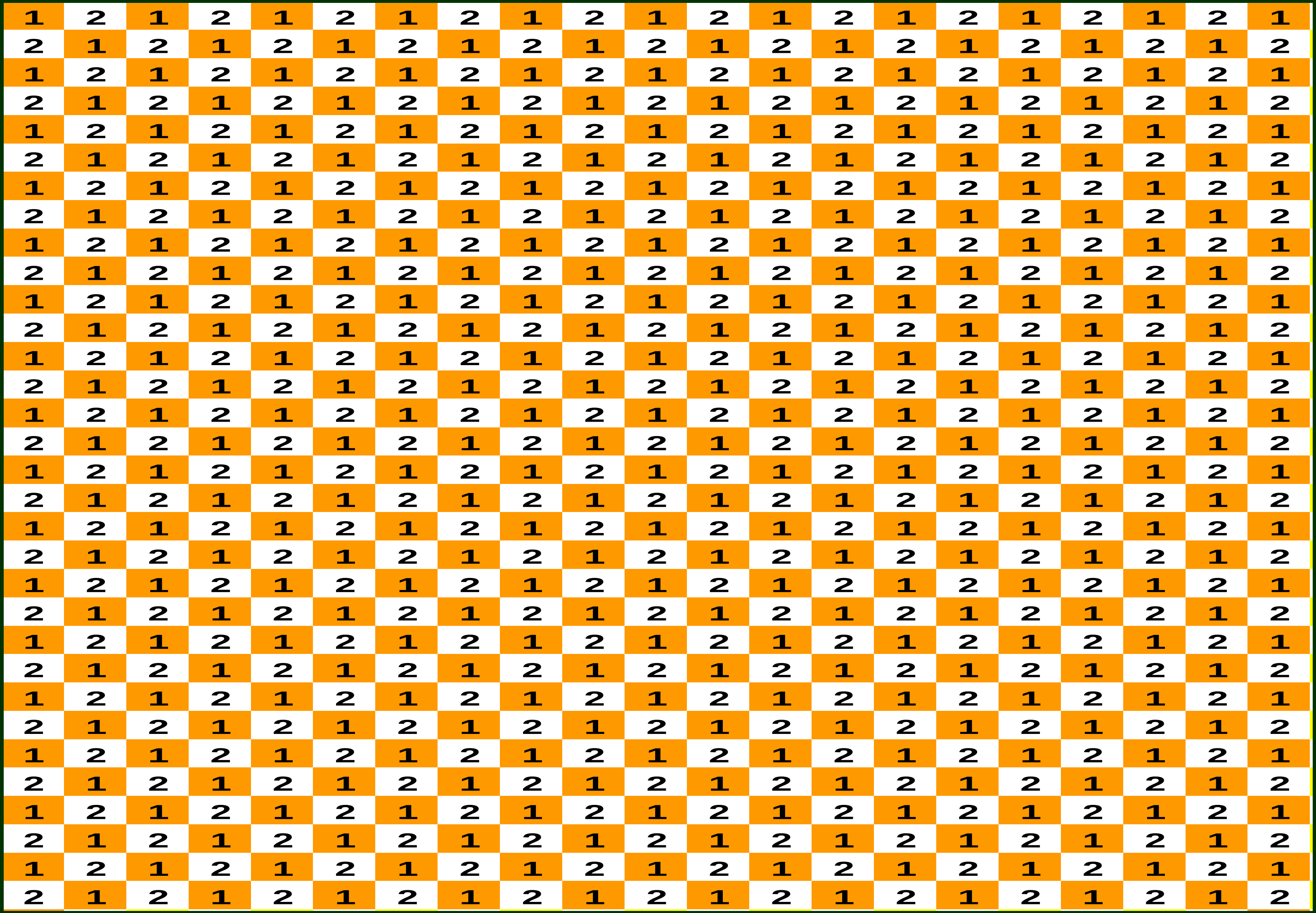
- **Spruce weevil movements and site characteristics**
    - **temperature**
    - **plantation size**
    - **weevil distribution**
    - **site index**

BC TASS/Pest Dynamics Model

- Numbers of clones
  - 2
  - 6
  - 18
  - 30

- Deployment strategies
  - Random Mix (RM)
  - Single Clonal Blocks (SCB)
  - Mosaic of Clonal Blocks (MCB)

‘Random’ Mixes – 2 clones



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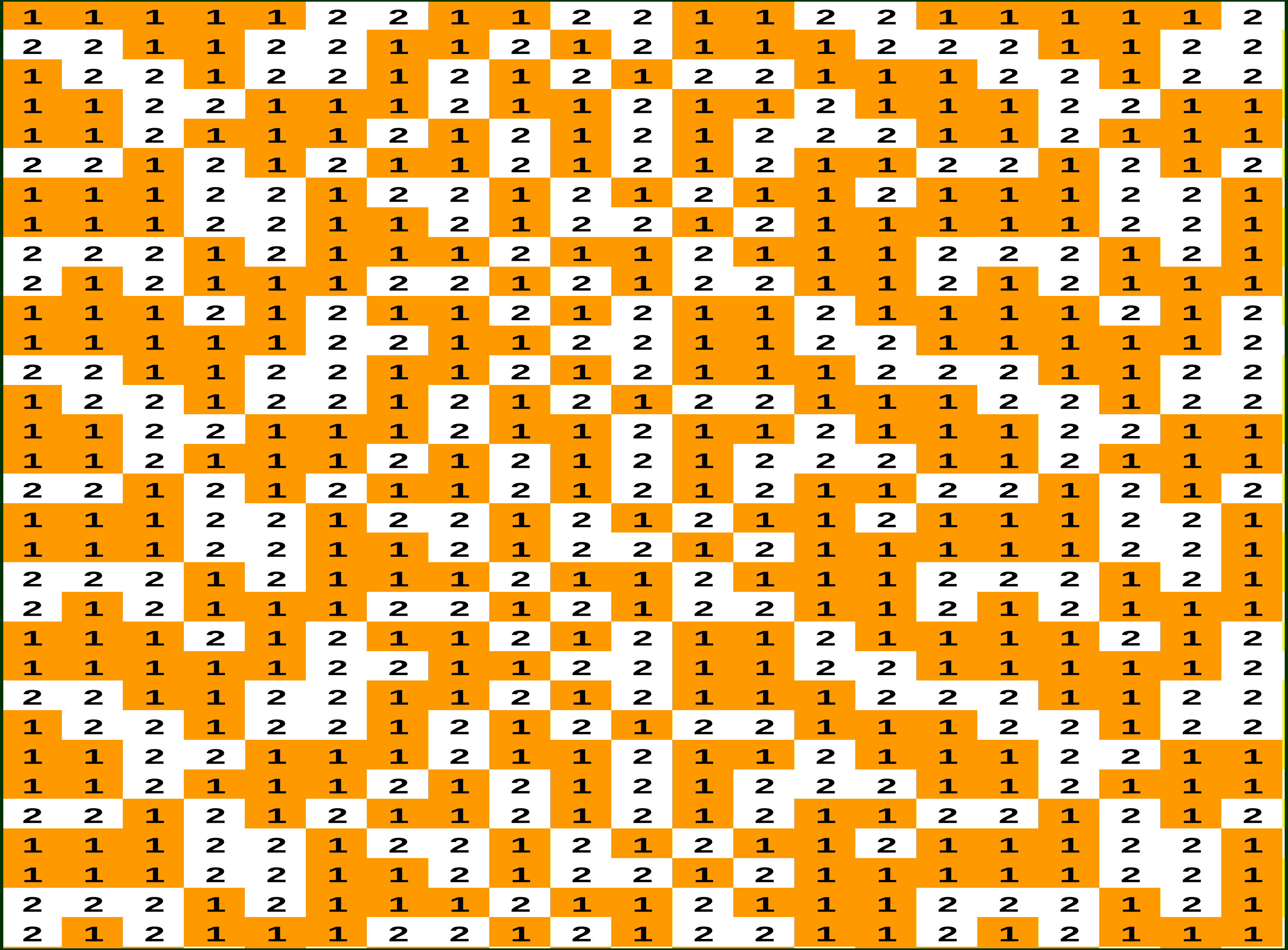
Random Mixes – 2 clones



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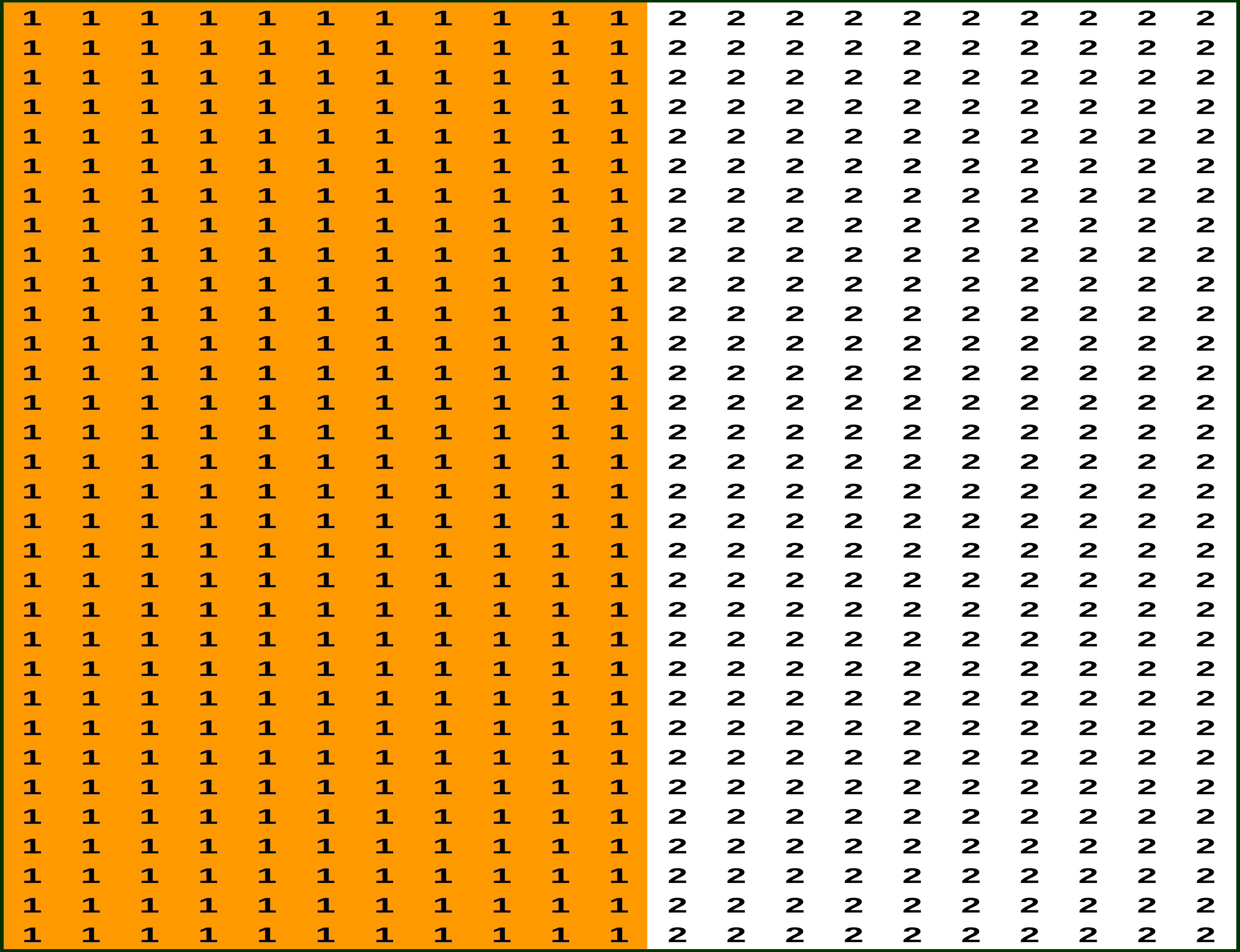
Single Clone Blocks – 2 clones



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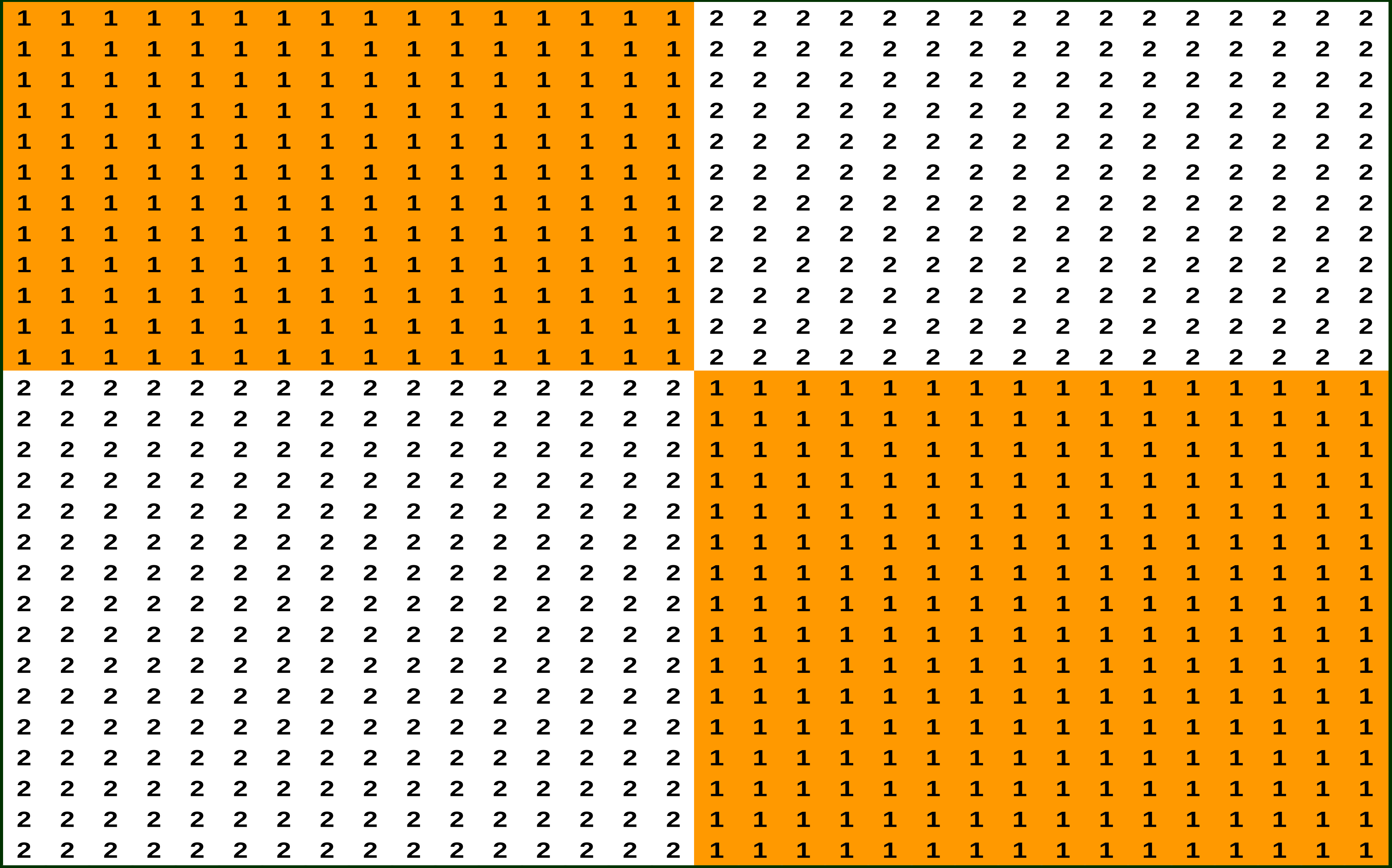
Mosaic of Clonal Blocks - 2 clones



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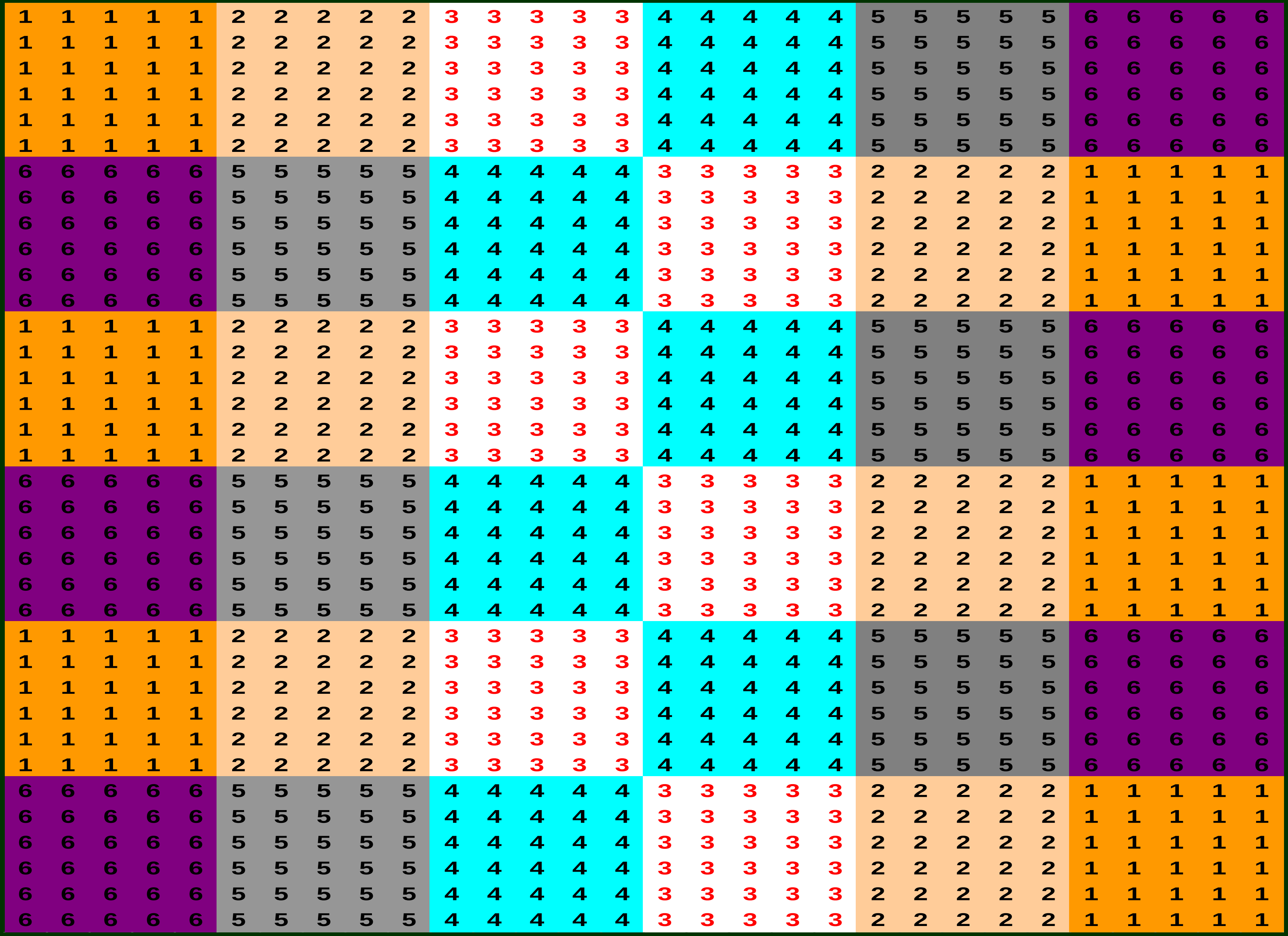
Mosaic of Clonal Blocks - 6 clones



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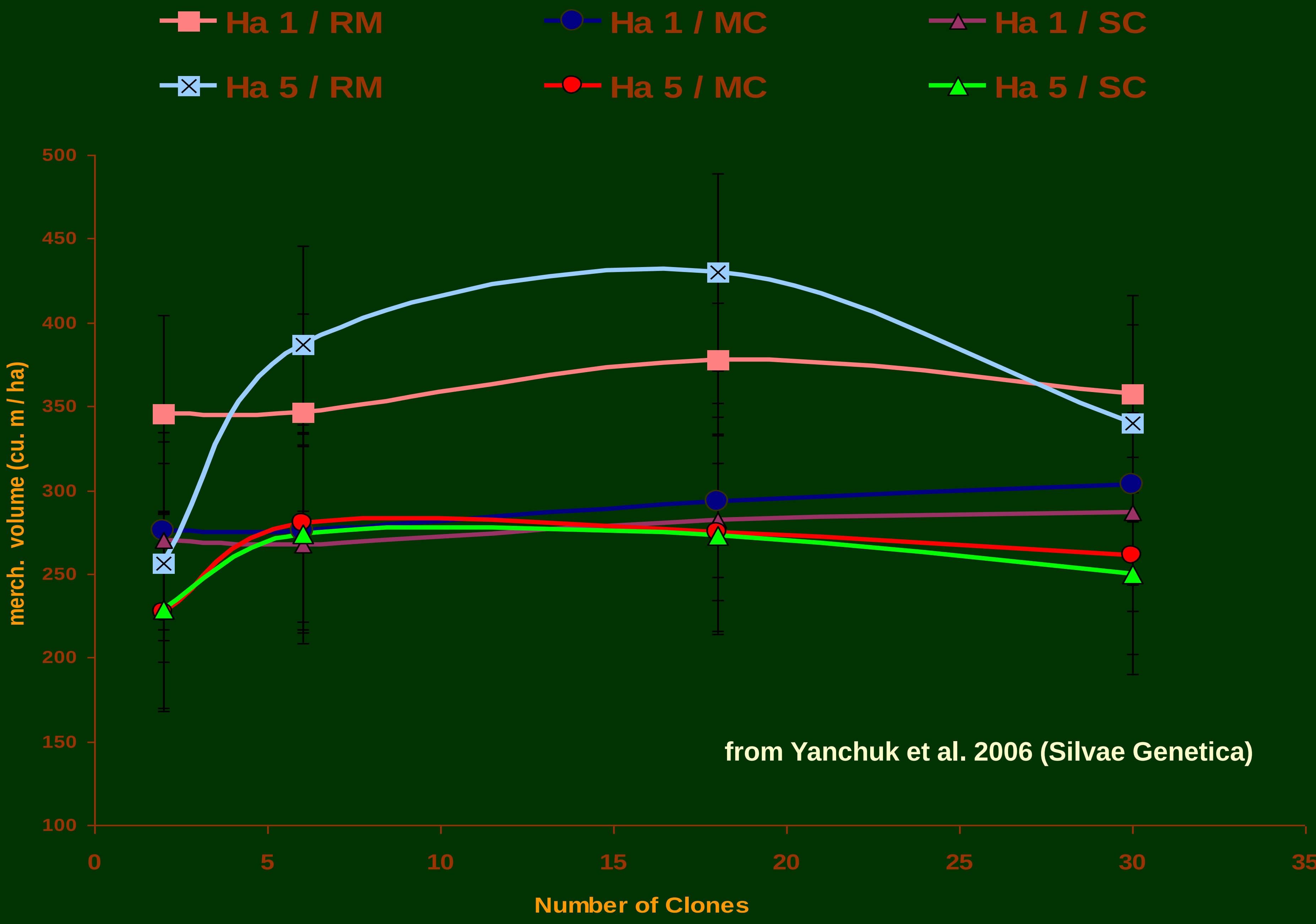
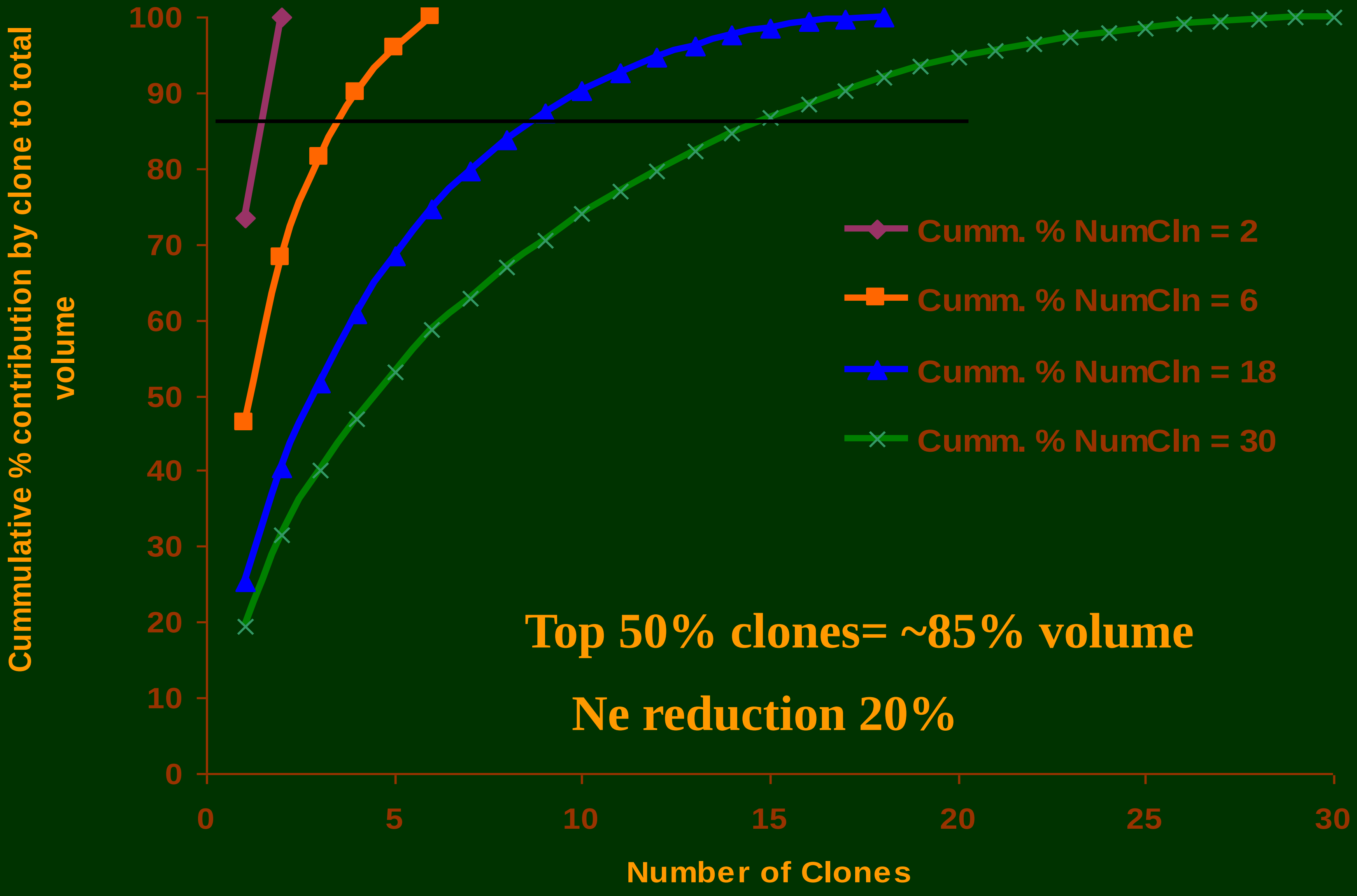
6	6	6	6	6	5	5	5	5	5	4	4	4	4	4	3	3	3	3	3	2	2	2	2	2	1	1	1	1	1

Random Clones (WD=1, TMP=11, SI=30)



from Yanchuk et al. 2006 (Silvae Genetica)

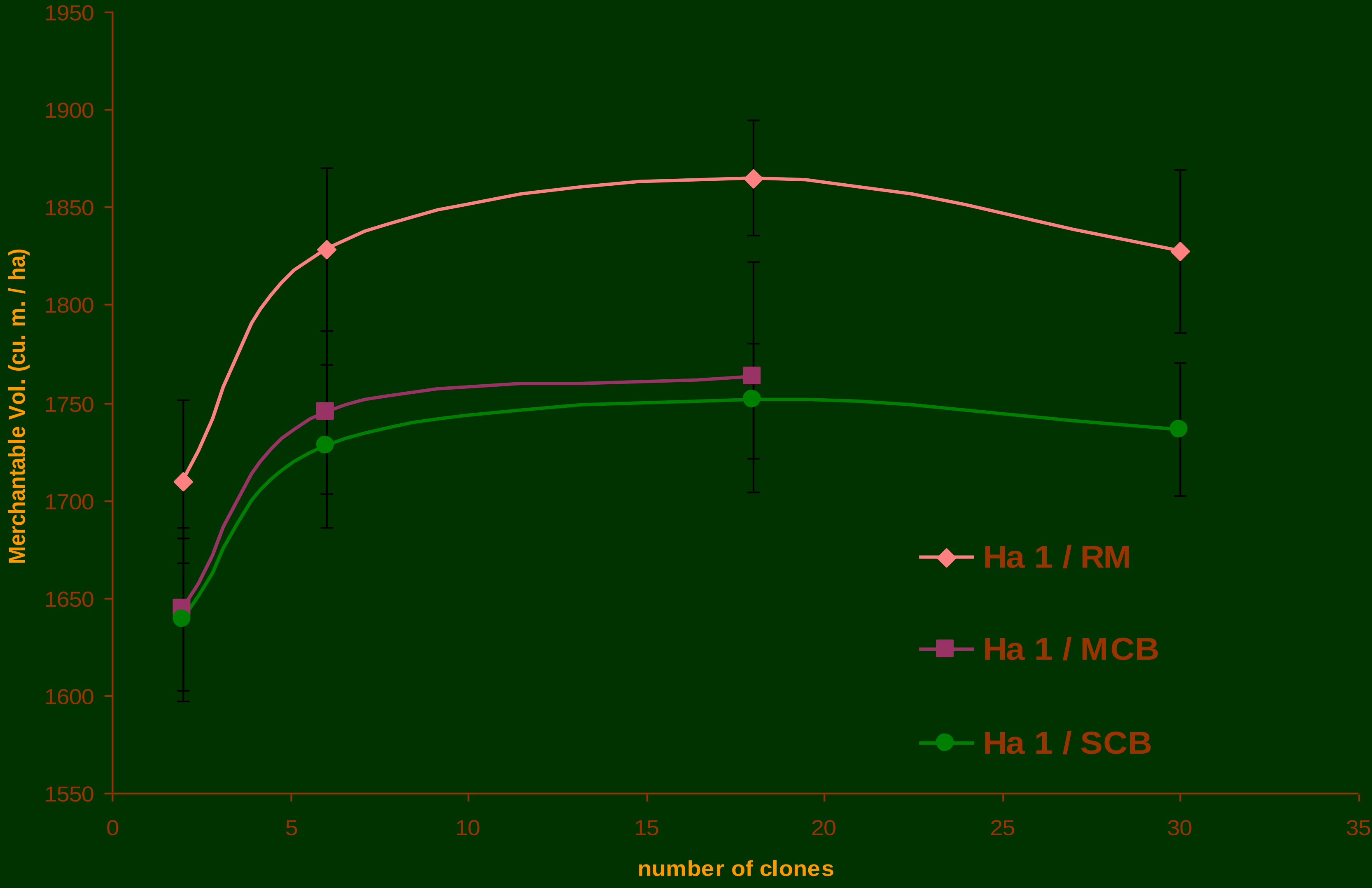
RANDOM CLONES (WD=1, SI=30, Ha = 1)



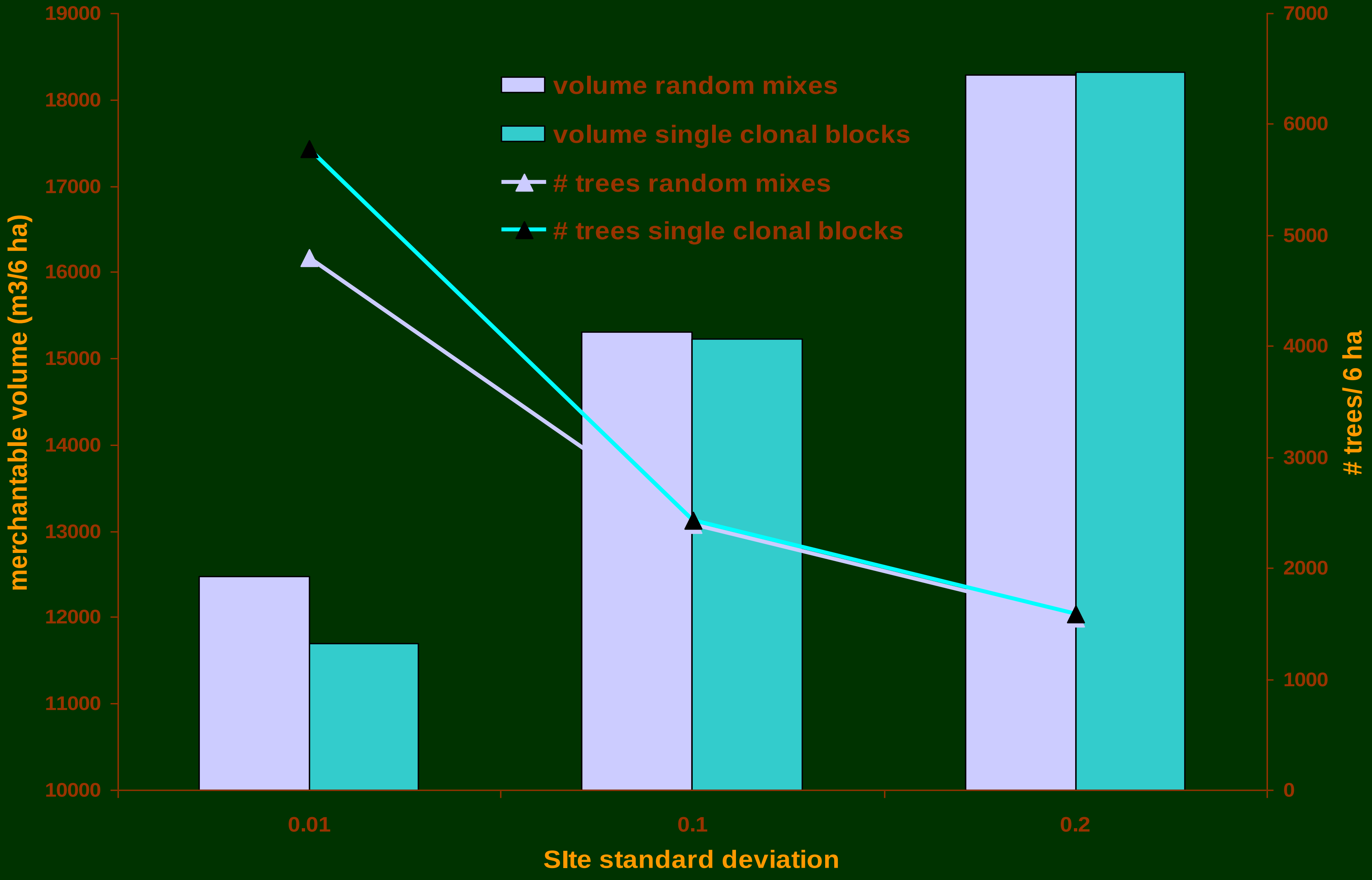
Top 50% clones= ~85% volume

Ne reduction 20%

SI 30, no weevils, Temp 11, C



Random mixes versus single clonal blocks for 6 fixed clones: Western redcedar at 100 years



Conclusions from Modelling

For a well-characterized pest behaviour and polygenic resistance model:

- **for unknown risks,**
  - ‘acceptable’ numbers of clones is around 5-25
- **for both unknown risks and known pest behaviour,**
  - random mix was always the best
  - G&Y predictions can be highly variable and driven by site variations
  - the best genotype(s) do most of the work
  - effective pop. size change only by ~20%

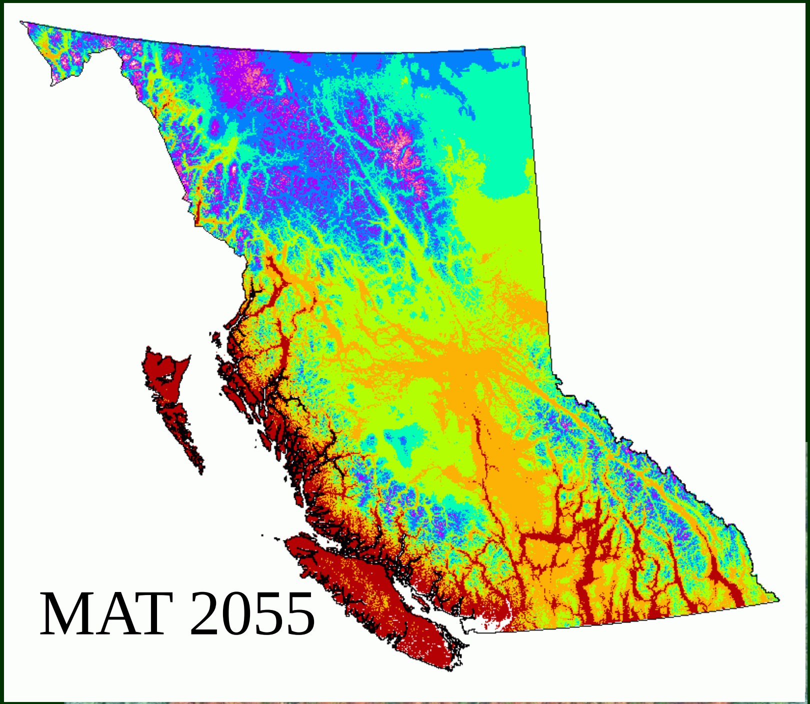
    (however, surviving #’s of stems is misleading)
  - still need to factor in pest/disease ‘evolution’ potential

Policy for B.C.

- **Vast, variable landscapes**
- **still addressing extensive management; long rotation ages**
- **Current research was policy-driven**
  - supports our minimum Ne of 10
  - most ‘responsible’ approach is random mixes
  - first ‘bullet proof’ stands genetically
  - landscape diversity accomplished at seed zone level

Additional Research

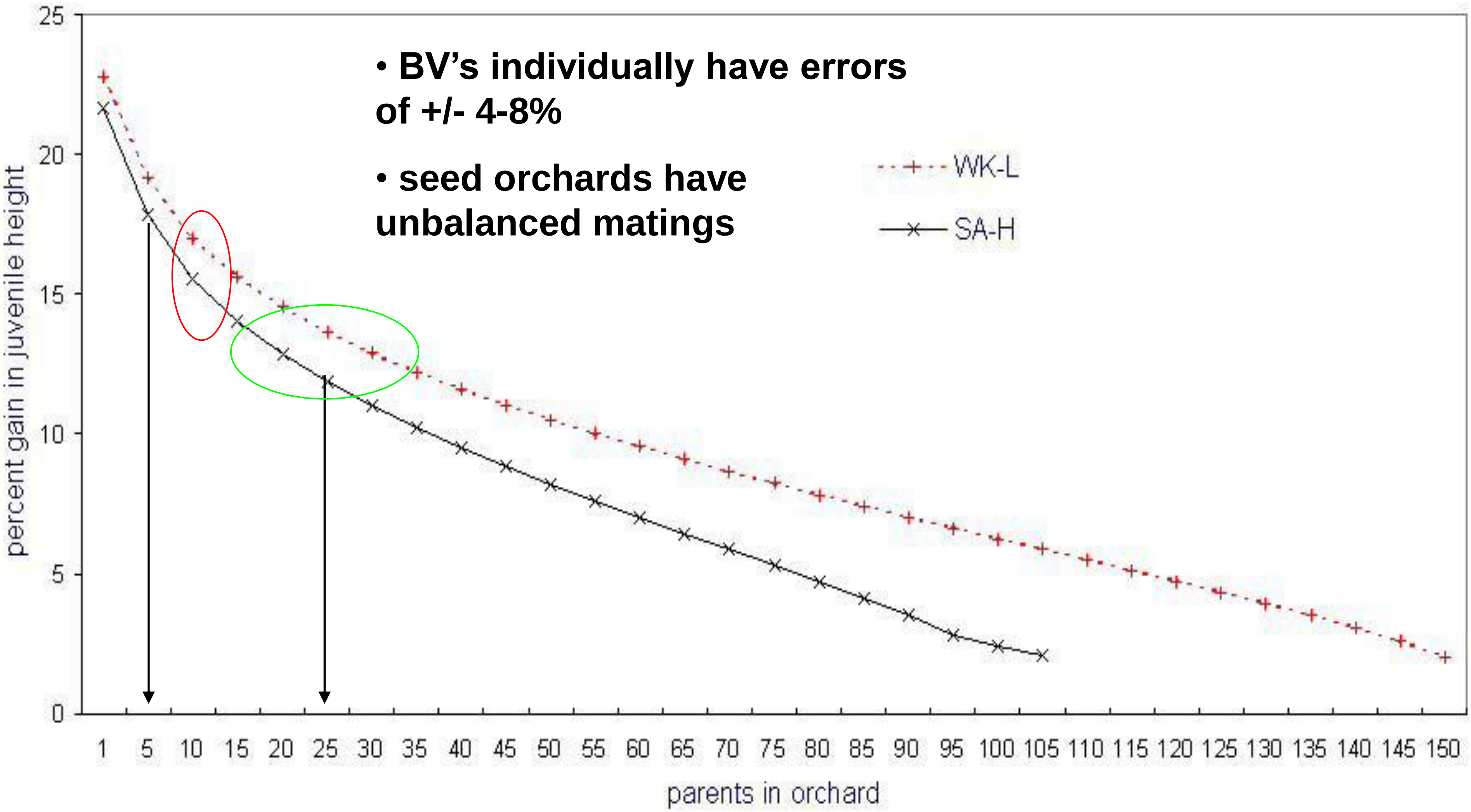
- **single gene effects**
- **blister rust / MPB >> mortality**
- **orchard families vs clones?**
- **variable genotypic representation in stands?**
- **climate change**
  - moving and modelling population growth functions in space and time?
  - seed planning units?
- **build in empirical results into our ‘theoretical’ models**



Breeding Values and Genetic Worth

- **breeding value (BV) – predicted genetic ‘value’ of a parent**
- **BV – measured as the mean of a parents offspring relative to the mean of wild stand progenies (e.g., %)**
- **after competition sets in, progeny tests cannot predict unit area yields!**

Genetic worth = average BV of parents making up a seed orchard seedlot, adjusted for gain at rotation age



Two examples of the relationship between numbers of parents in an orchard and genetic gain for spruce and WK-low and SA-high

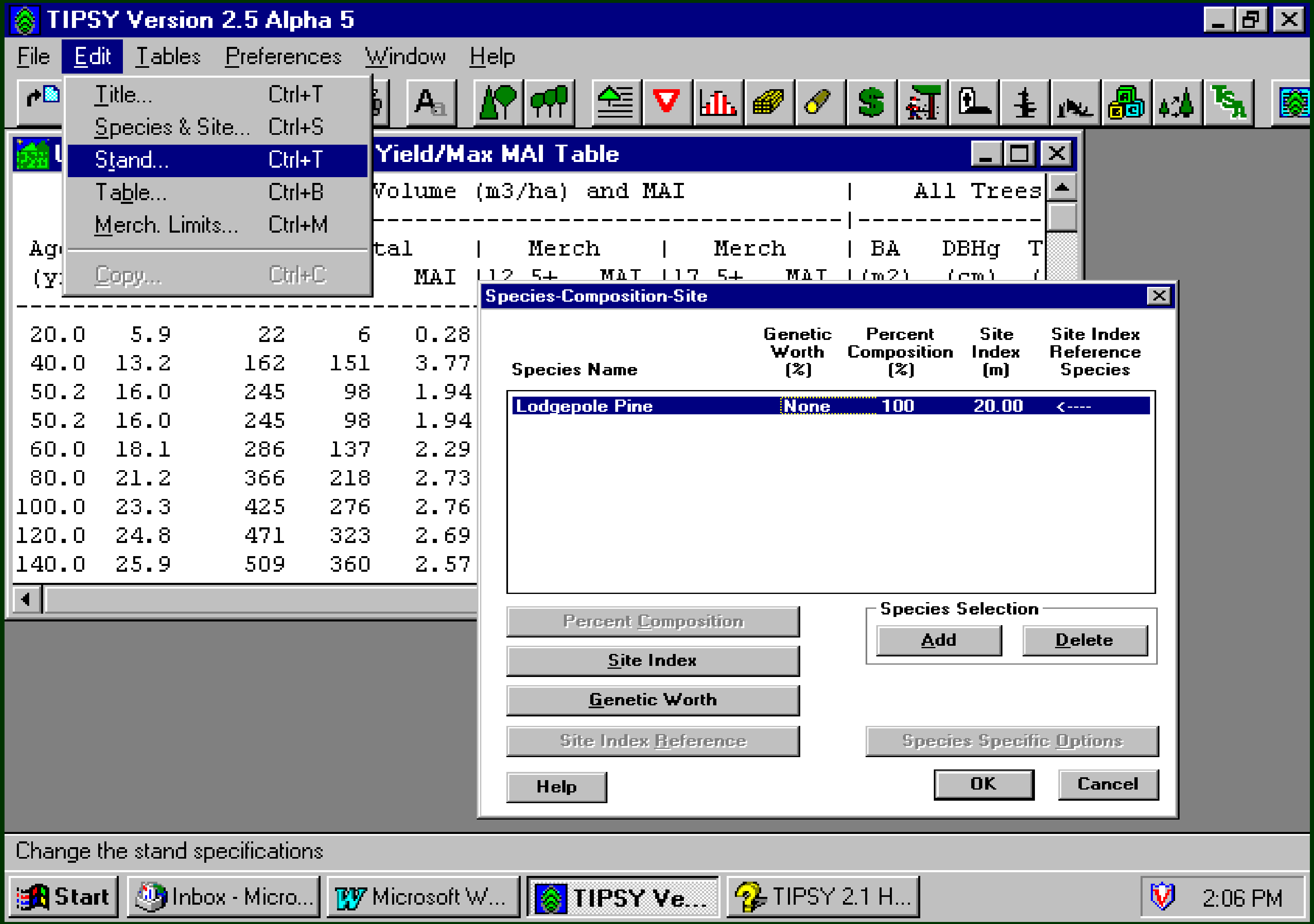
- **BV’s individually have errors of +/- 4-8%**
- **seed orchards have unbalanced matings**

Estimating the effects of genetics on stand-level yields in B.C.

- Historical approach was a direct lift to site index (e.g., 5, 10, 15%, etc) by orchard 'category'
- Mid-90's changed to have Genetic Worth (GW) of a seed orchard lot (%) lift site index (SI)
  - GW is a volume estimate at 'rotation/ index age' at max MAI
  - so we adjusted SI at an index age, by GW / 2 (a general rule of thumb)
  - however, there are problems with magnitudes of gain before and after 'index age'
- New approach
  - users input GW of seedlots directly into TIPSY
  - now adjusts for GW from 'age of selection' to anticipated 'harvest age' (Xie and Yanchuk, 2003)

‘TIPSY’

Table Interpolation Program for Stand Yield

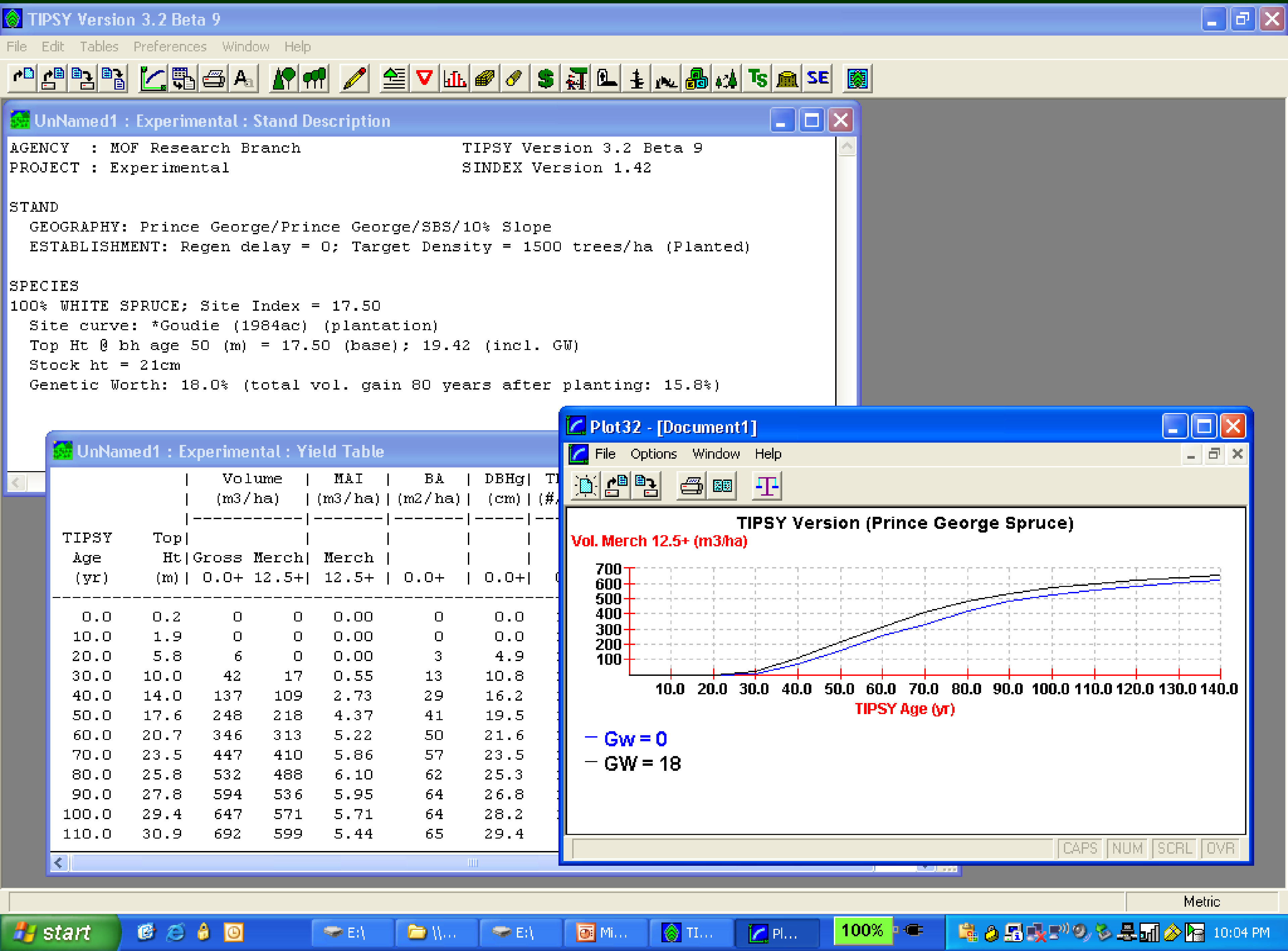


```
                  Volume (m3/ha) and MAI              |    All Trees
                 -------------------------------------|-------------
Ag               tal    |    Merch      |    Merch    | BA    DBHg   T
(Y:                 MAI |12 5+     MAI  |17 5+    MAI |(m2)   (cm)   (
-------------------------------------------
 20.0    5.9      22      6    0.28
 40.0   13.2     162    151    3.77
 50.2   16.0     245     98    1.94
 50.2   16.0     245     98    1.94
 60.0   18.1     286    137    2.29
 80.0   21.2     366    218    2.73
100.0   23.3     425    276    2.76
120.0   24.8     471    323    2.69
140.0   25.9     509    360    2.57
```

Species-Composition-Site

Species Name	Genetic Worth (%)	Percent Composition (%)	Site Index (m)	Site Index Reference Species
Lodgepole Pine	None	100	20.00	<----

Change the stand specifications



```
AGENCY  : MOF Research Branch                TIPSY Version 3.2 Beta 9
PROJECT : Experimental                       SINDEX Version 1.42

STAND
  GEOGRAPHY: Prince George/Prince George/SBS/10% Slope
  ESTABLISHMENT: Regen delay = 0; Target Density = 1500 trees/ha (Planted)

SPECIES
100% WHITE SPRUCE; Site Index = 17.50
  Site curve: *Goudie (1984ac) (plantation)
  Top Ht @ bh age 50 (m) = 17.50 (base); 19.42 (incl. GW)
  Stock ht = 21cm
  Genetic Worth: 18.0% (total vol. gain 80 years after planting: 15.8%)
```

```
                  |   Volume    |  MAI   |   BA   | DBHq| TI
                  |   (m3/ha)   | (m3/ha)| (m2/ha)| (cm)| (#/
                  |-------------|--------|--------|-----|---
  TIPSY      Top  |             |        |        |     |
   Age        Ht  | Gross Merch | Merch  |        |     |
   (yr)      (m)  | 0.0+  12.5+ | 12.5+  |  0.0+  | 0.0+| 0
------------------------------------------------------------
   0.0       0.2      0      0    0.00       0    0.0
  10.0       1.9      0      0    0.00       0    0.0
  20.0       5.8      6      0    0.00       3    4.9
  30.0      10.0     42     17    0.55      13   10.8
  40.0      14.0    137    109    2.73      29   16.2
  50.0      17.6    248    218    4.37      41   19.5
  60.0      20.7    346    313    5.22      50   21.6
  70.0      23.5    447    410    5.86      57   23.5
  80.0      25.8    532    488    6.10      62   25.3
  90.0      27.8    594    536    5.95      64   26.8
 100.0      29.4    647    571    5.71      64   28.2
 110.0      30.9    692    599    5.44      65   29.4
```


IDAHO
1A DK390


CANADA
Wallowa Mountains

CLOSED

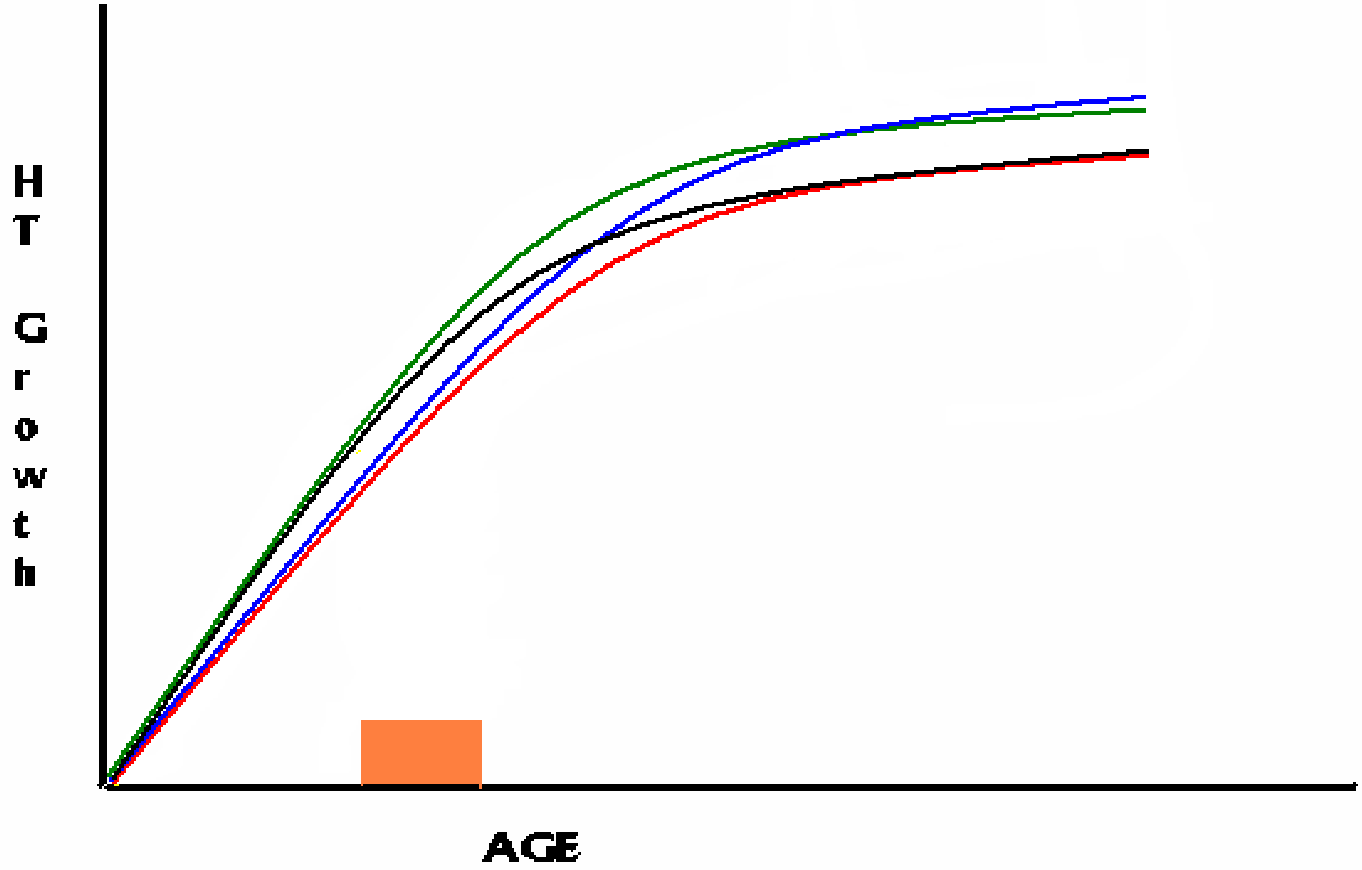
TO

MOTOR VEHICLES

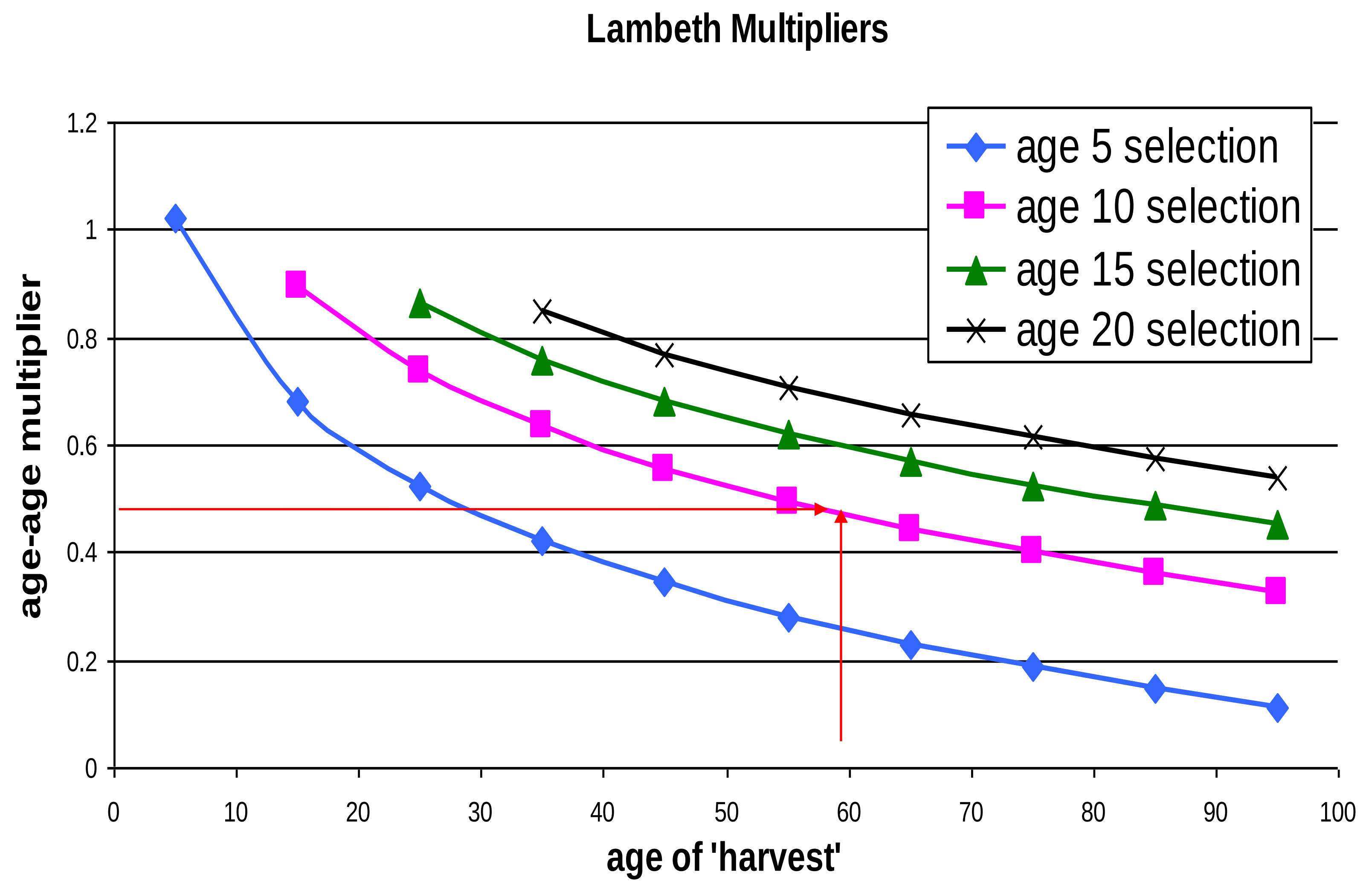
3 DAYS PRIOR TO
FIRST RIFLE BULL THROUGH LAST
DAY OF THE SECOND RIFLE BULL SEASON

OREGON DEPARTMENT OF FISH AND WILDLIFE

Gain and Breeding Value ‘Math’



Genetic Worth ‘math’



Genetic Worth example

Let:

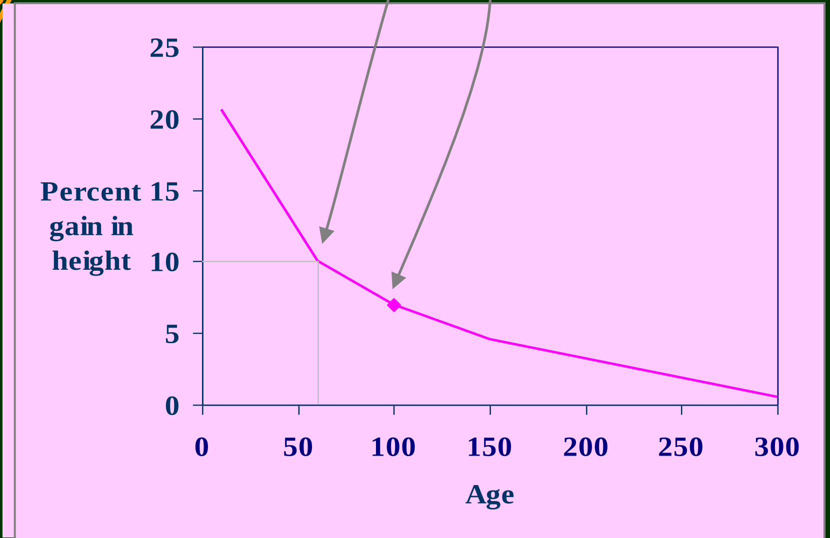
a_s = 12 years (selection age)
a_i = 60 years (index rotation age)
a_y = 100 years (harvest age)
GW= 20% (genetic worth)
GH_i= 20/2=10

Then

$$R_i = 1.02+0.308 \cdot \ln(12/60) = 0.524$$
$$R_y = 1.02+0.308 \cdot \ln(12/100) = 0.367$$
$$GH_{100} = GH_i \cdot (R_i/R_y)$$
$$= 10 \cdot (0.367/0.524)$$
$$= 10 \cdot (0.700) = 7.00\%$$

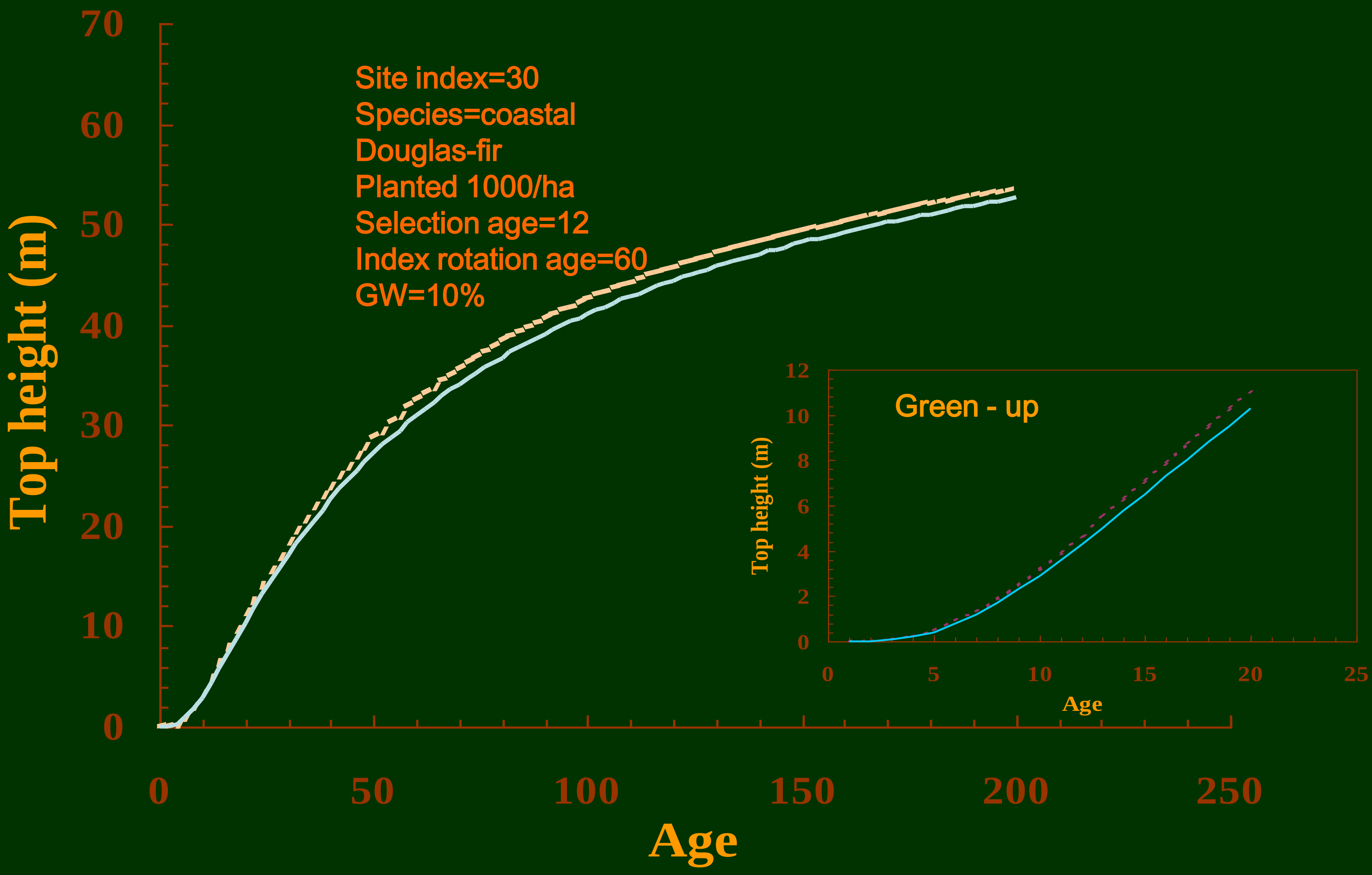
Additionally,

GH_{10}=20%
GH_{60}= 10%
GH_{100}= 7%
GH_{150}= 8%
GH_{300}= 3%



Xie, C-Y. and A. D. Yanchuk. 2003. West. J. Appl. For. 18:88-100.

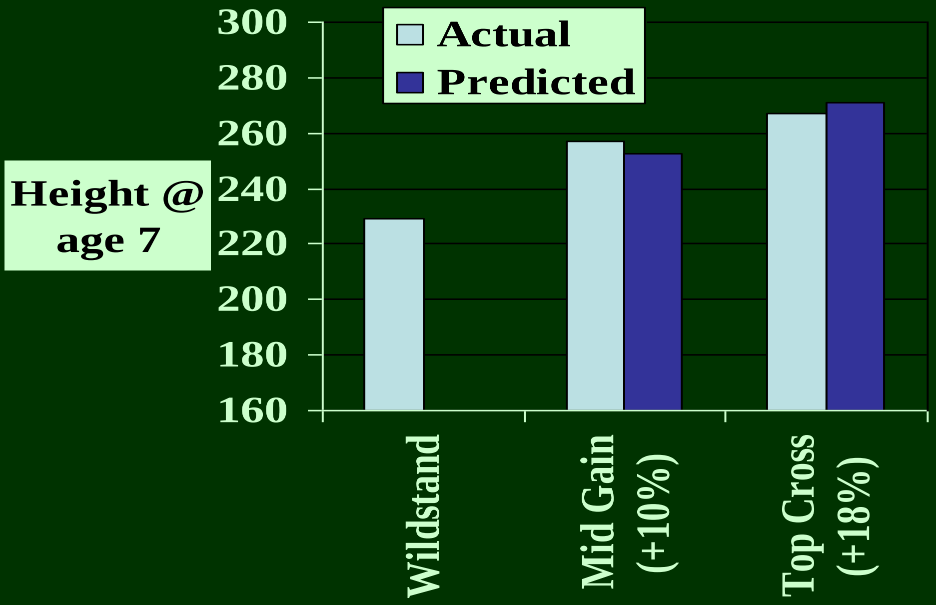
Effects of GW on yield as modelled in TIPSY



Site index=30
Species=coastal
Douglas-fir
Planted 1000/ha
Selection age=12
Index rotation age=60
GW=10%

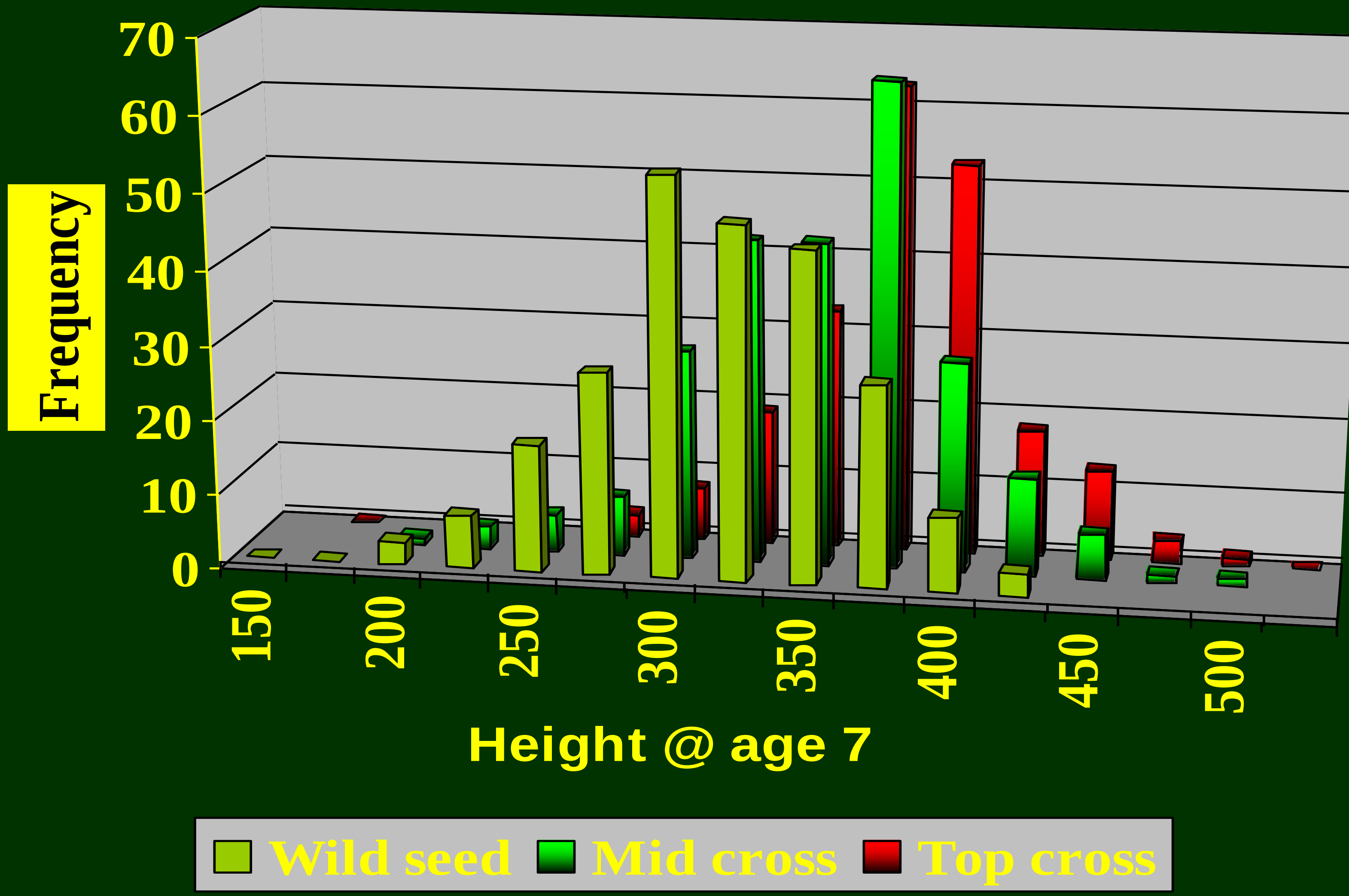
Realized Gain Trials

- **Realized gain trials needed to validate juvenile age selections in single-tree plots**
  - ***(everything up to now is model based!)***
  - **established realized gain trials for most commercial species, starting in 1991**
  - **trials include:**
    - 3-4 genetic entries
    - 4 spacings
    - 4 sites per series
    - 4 replications /site
    - 144-tree square plots



Realised gain early results

(Douglas-fir Norrish site, Spacing=1.6m)



Spatially Explicit Genetic Gain Estimates in Timber Supply Analyses for the “Arrow” and “Golden” Timber Supply Areas

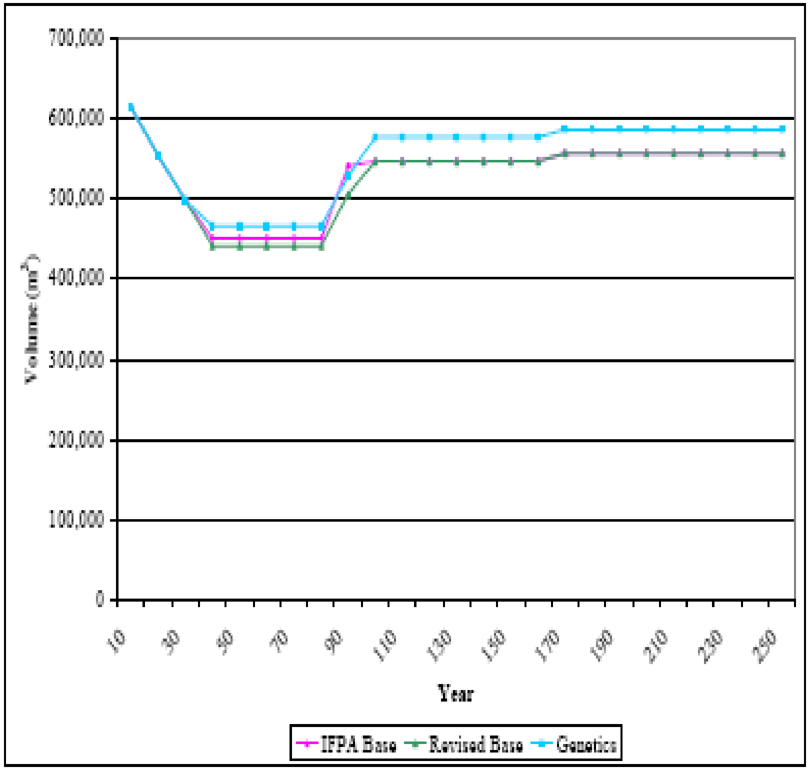


Figure 2.1 Harvest forecasts, Arrow genetics analysis

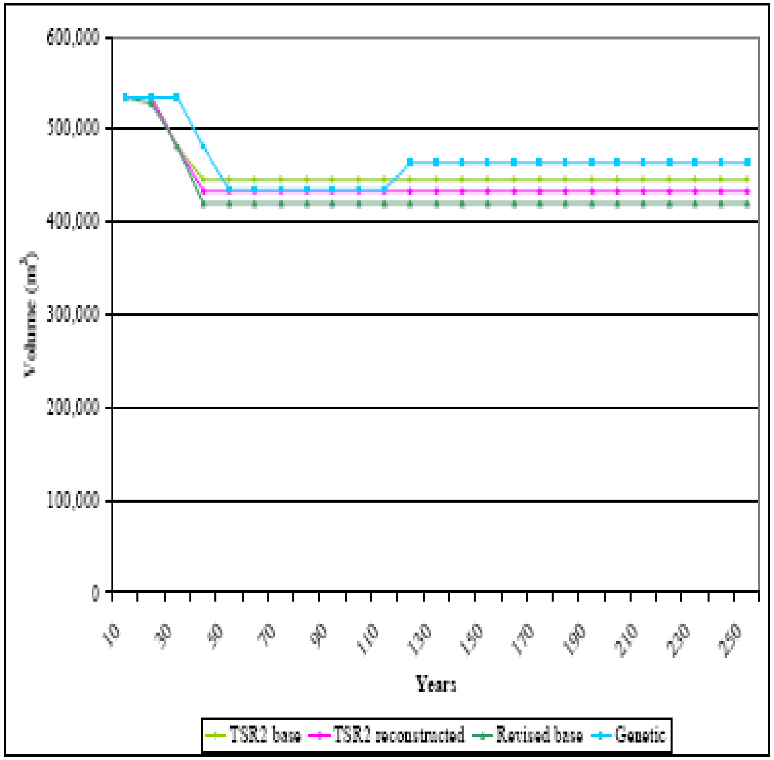
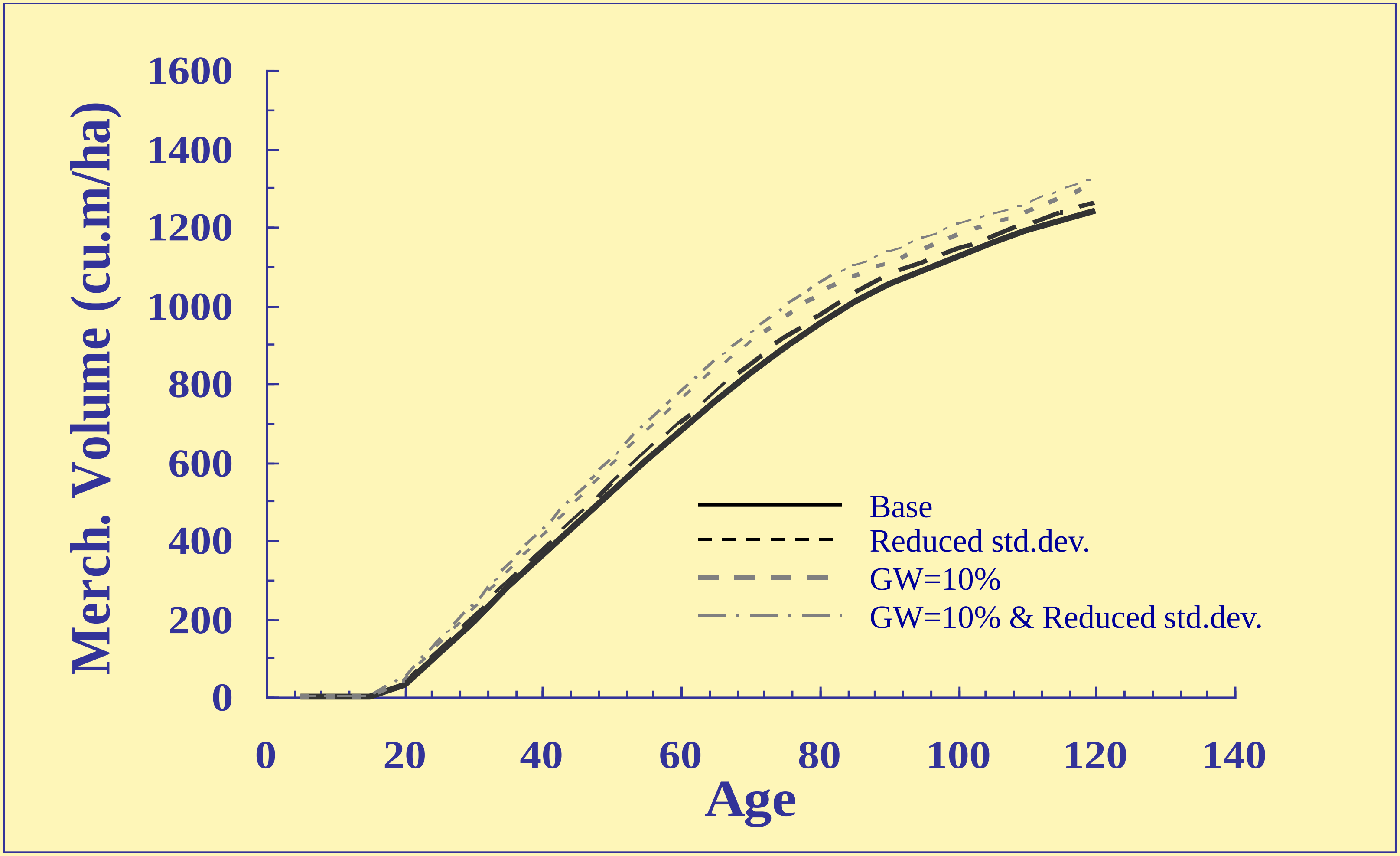


Figure 2.2 Harvest forecasts, Golden genetics analysis

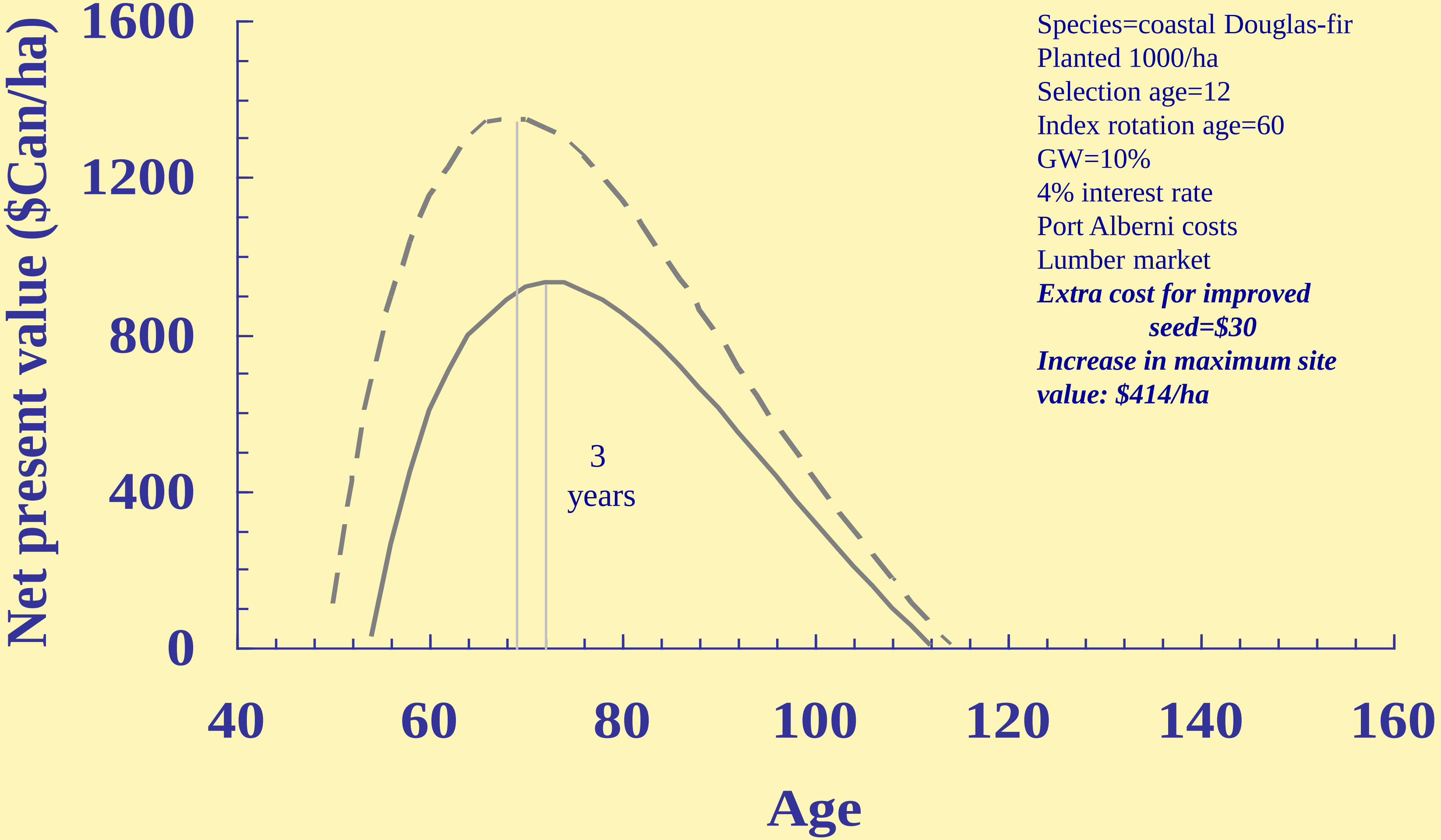
Conclusions

- **genetic theory has served us well in most areas of predicting genetic gain across many organisms**
- **while we can be ‘out’ on any individual stand, the mean of many stands will likely be very close to our predictions**
  - ***e.g., loblolly pine (B.D. Shiver and S. Logan)***
  - **theory and models can only provide general guidance to managers dealing with a system driven by great variability**
- **with climate change / more pest disease epidemics likely, future research may be best focussed on inter- and intra-specific performance of select populations over wider environments**

Thank you!


Merch. Volume (cu.m/ha)
1600
1400
1200
1000
800
600
400
200
0
0
20
40
60
80
100
120
140
Age
Base
Reduced std.dev.
GW=10%
GW=10% & Reduced std.dev.

Effects of genetic worth on *discounted* stand value



Site index=30
Species=coastal Douglas-fir
Planted 1000/ha
Selection age=12
Index rotation age=60
GW=10%
4% interest rate
Port Alberni costs
Lumber market
Extra cost for improved seed=$30
Increase in maximum site value: $414/ha