Comparison of Maximum Stand Density Index (SDI) in Genetically Improved and Unimproved Douglas-fir

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Genetic improvement and stand density

- Genetic improvement in Douglas-fir has emphasized breeding-zone matching, faster growth, better form, and improved wood quality.

- The influence of genetic gain on stand carrying capacity is less well understood, yet it directly informs planting density, thinning schedules, and rotation length.

Introduction

Maximum Stand Density Index (SDI_{MAX})

- “Managed stands are seldom allowed to develop along the actual self-thinning line, at least once they have reached a commercial size. This presents a challenge to observing maximum levels of competition and assessing their influence on productivity”. *(Chivhenge et al. 2024)*

- SDI_{MAX} defines the upper boundary of the size-density relationship under intense competition.

Evidence from Other Species

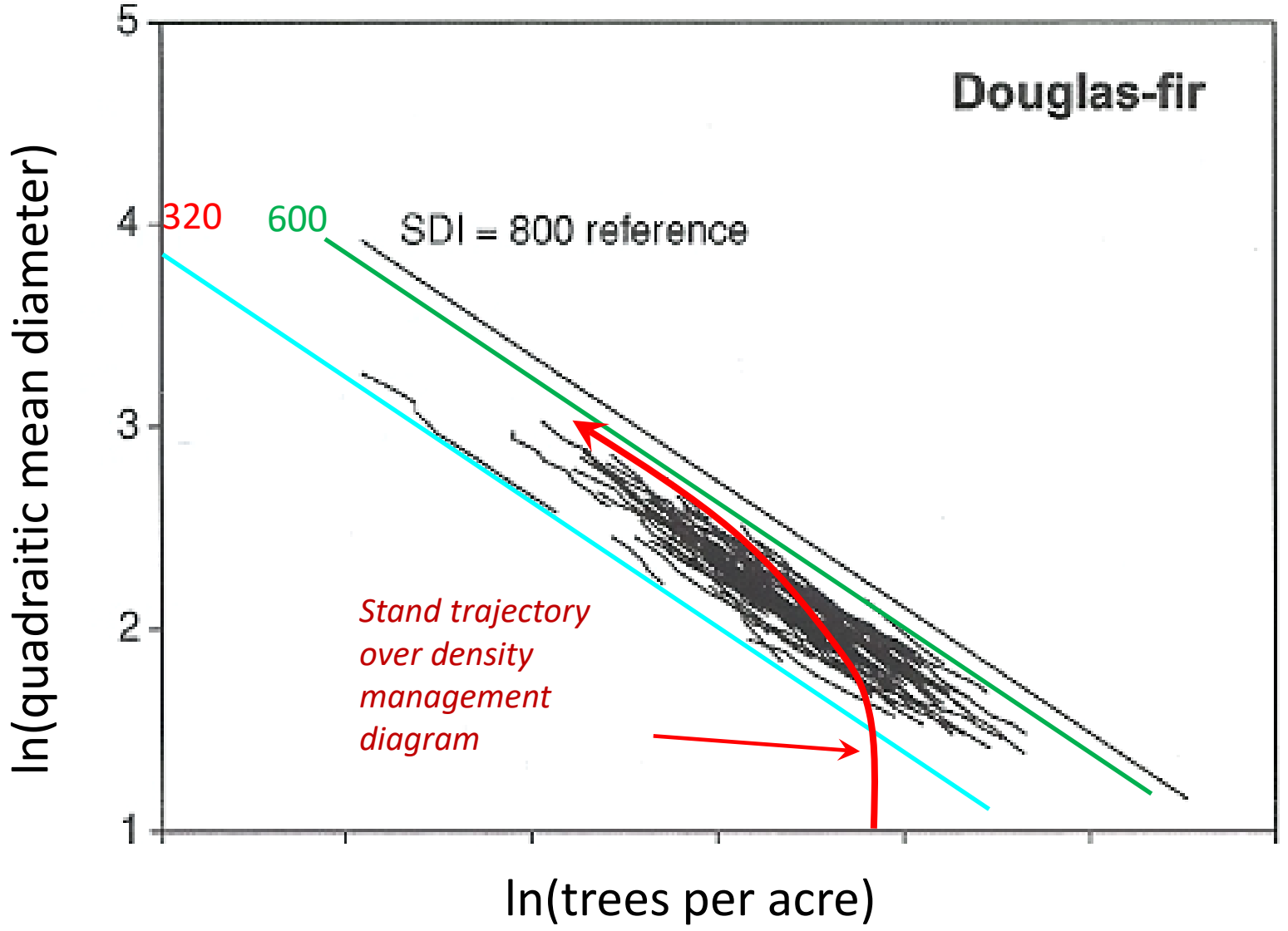
- Loblolly pine - Walker et al. (2020)
  - Lost Pines provenance had a higher predicted carrying capacity than Atlantic Coastal Plain stock
    - But showed slower growth and poor form.

Growth and Yield Models Insights

- Fertilization effect in ORGANON/CIPSANON
  - Nitrogen additions increased diameter and height growth rates, but does not raise the intercept of the SDI_{MAX} line.
  - Faster growth pushes the stand along its existing size density trajectory more quickly
    - Sukachev effect
  - As a result of Sukachev effect, mortality rate increases with fertilization treatment.

Objective

- To test whether SDI_{MAX} increases for genetically improved Douglas-fir.



Materials

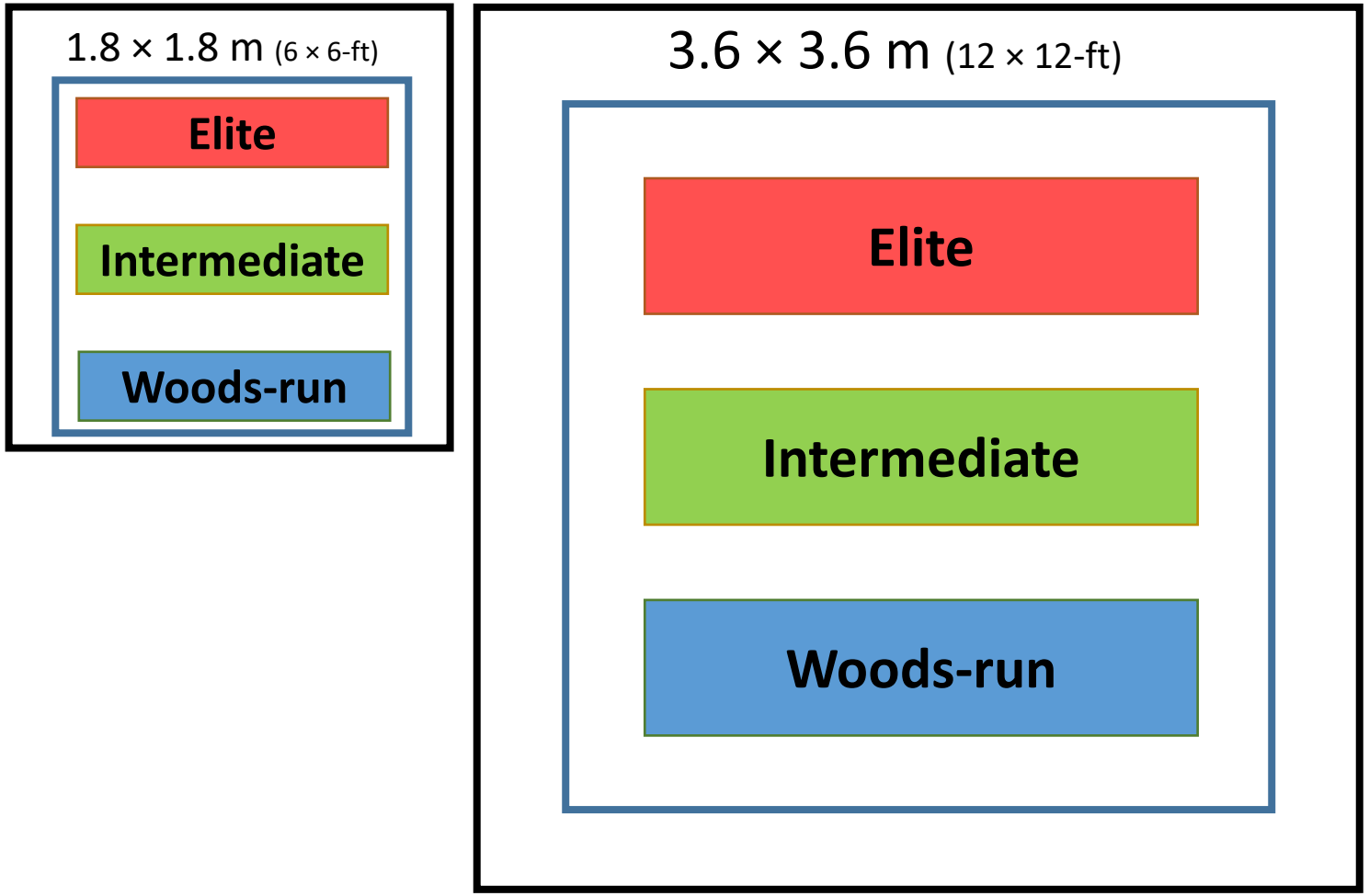
- Molalla realized gain trials

- Three genetic improvement levels
  - **Elite**
  - **Intermediate**
  - **Woods-run (control)**

- Measured DBH at plantation age 26 and 27 years
  - ~10,600 trees
  - Only 6-ft spacing plots
    - SDI = 443
    - Relative density = > 80%

Experimental design

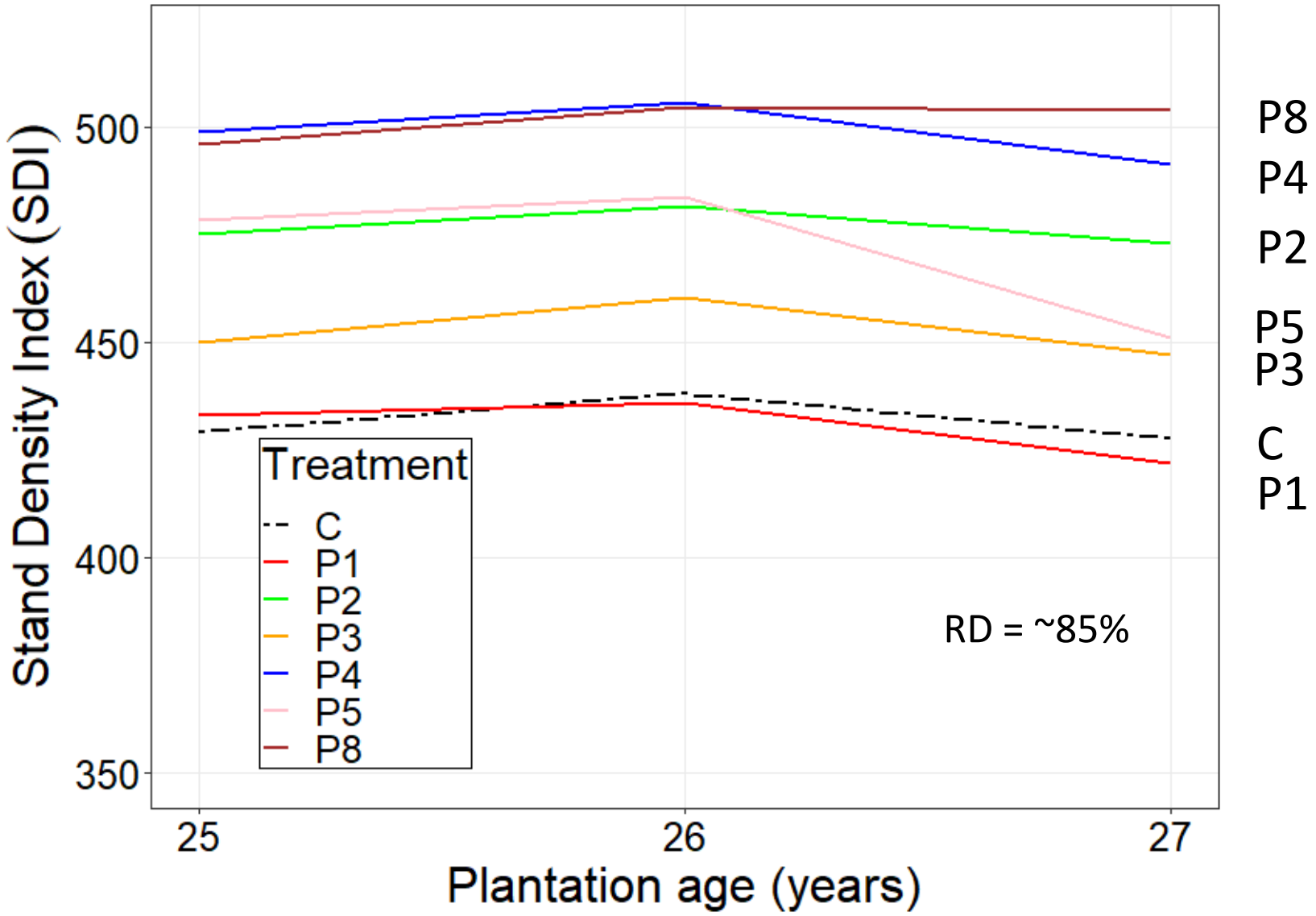
- Split plot design
  - Whole Plot: planting density
  - Split Plot: genetic level
- Three genetic improvement levels
  - **Elite**
  - **Intermediate**
  - **Woods-run (control)**
- Elite & Intermediate
  - Single pair matings of 20 parents (10 families)
- Woods-run (control)
  - Random selection of 50 trees
- 100 trees/plot (10 x 10)



- The whole Colton site and some other plots were excluded in this study due to ice and snow damages

	Elite	Intermediate	Woods-run
Site index (ft)	127.3 (103 – 143)	128.5 (109 – 154)	125.7 (103 – 144)

SDI in family deployment study



Results

- From Molalla realized gain trials

Stand density and stocking

- **Stand Density Index (SDI)**
  - The number of trees (TPA) when quadratic mean diameter (QMD) is 10 inches.

$$SDI = TPA \cdot \left(\frac{QMD}{10}\right)^{1.605}$$

where,

SDI = Stand Density Index

TPA = Number of trees per ace

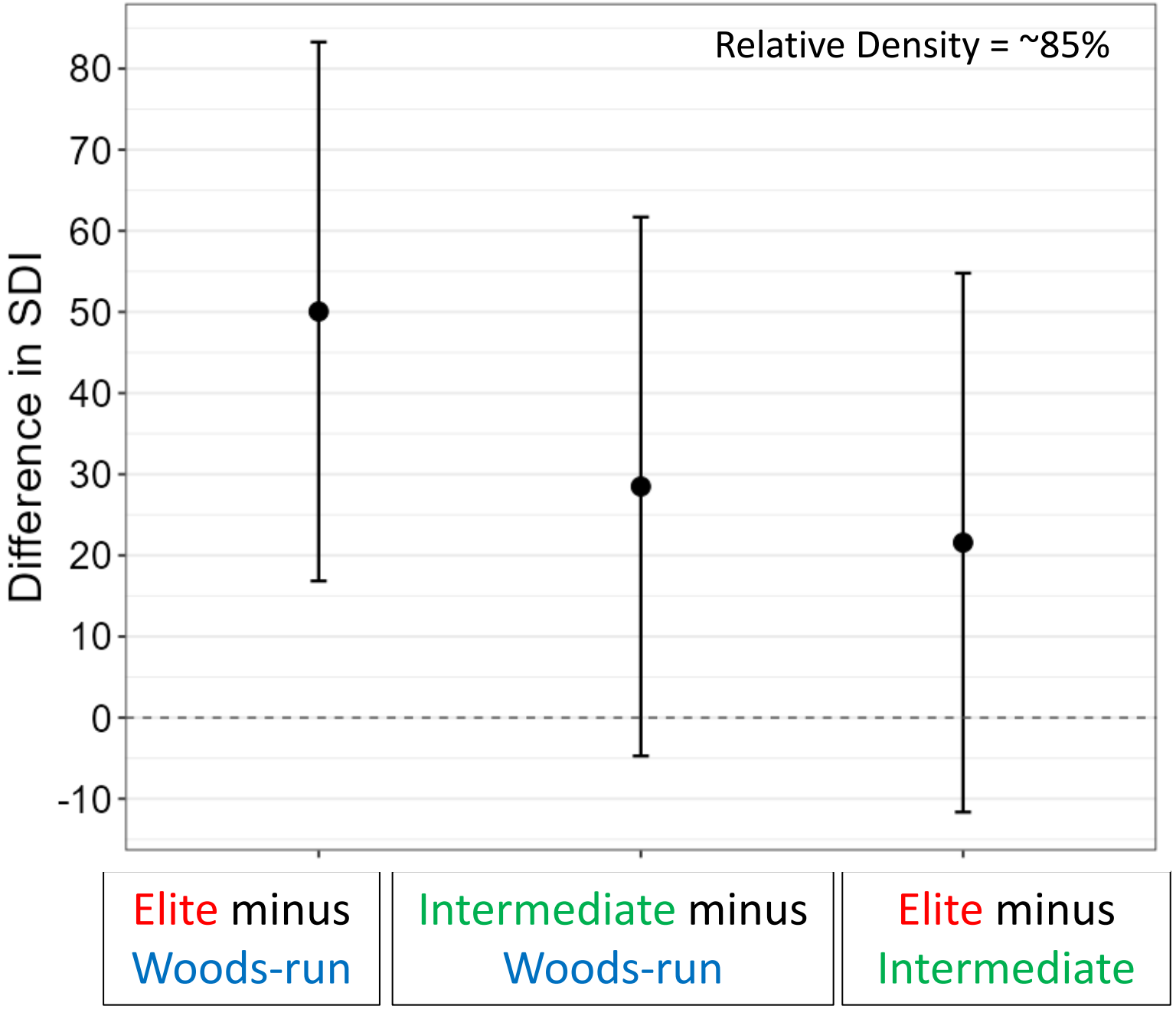
QMD = Quadratic Mean Diameter (inches)

- Stand density index (SDI) difference by genetic-level
  - Elite minus Intermediate
  - Elite minus Woods-run
  - Intermediate minus Woods-run

- SDI = f(site, genetic, site*genetic) + ε

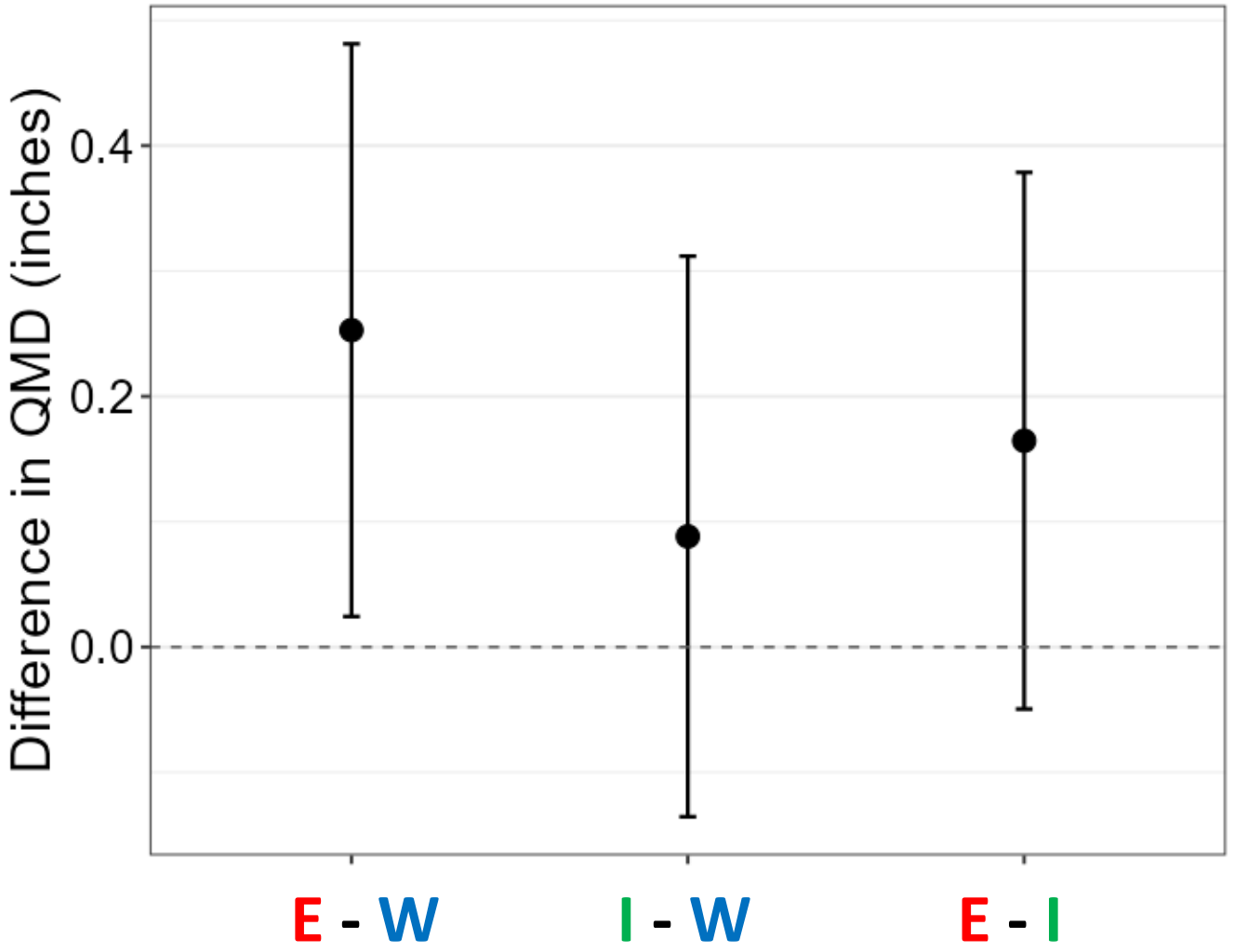
- 95% confidence interval

SDI: the number of trees (TPA) when quadratic mean diameter (QMD) is 10 inches.



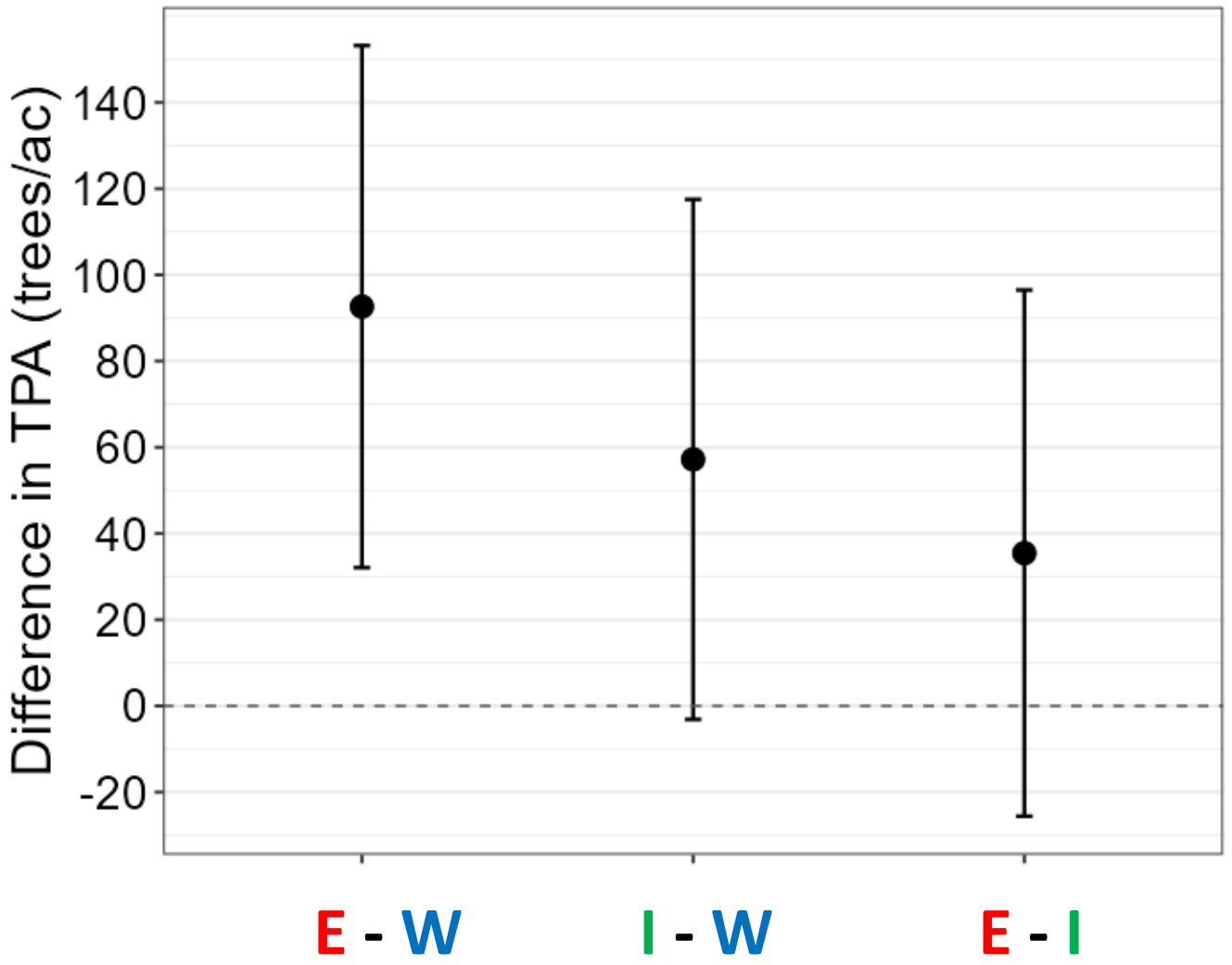
Quadratic Mean Diameter

- QMD = f(site, genetic, site*genetic, TPA) + ε
- 95% confidence interval
- Significant QMD difference between Elite and Woods-run

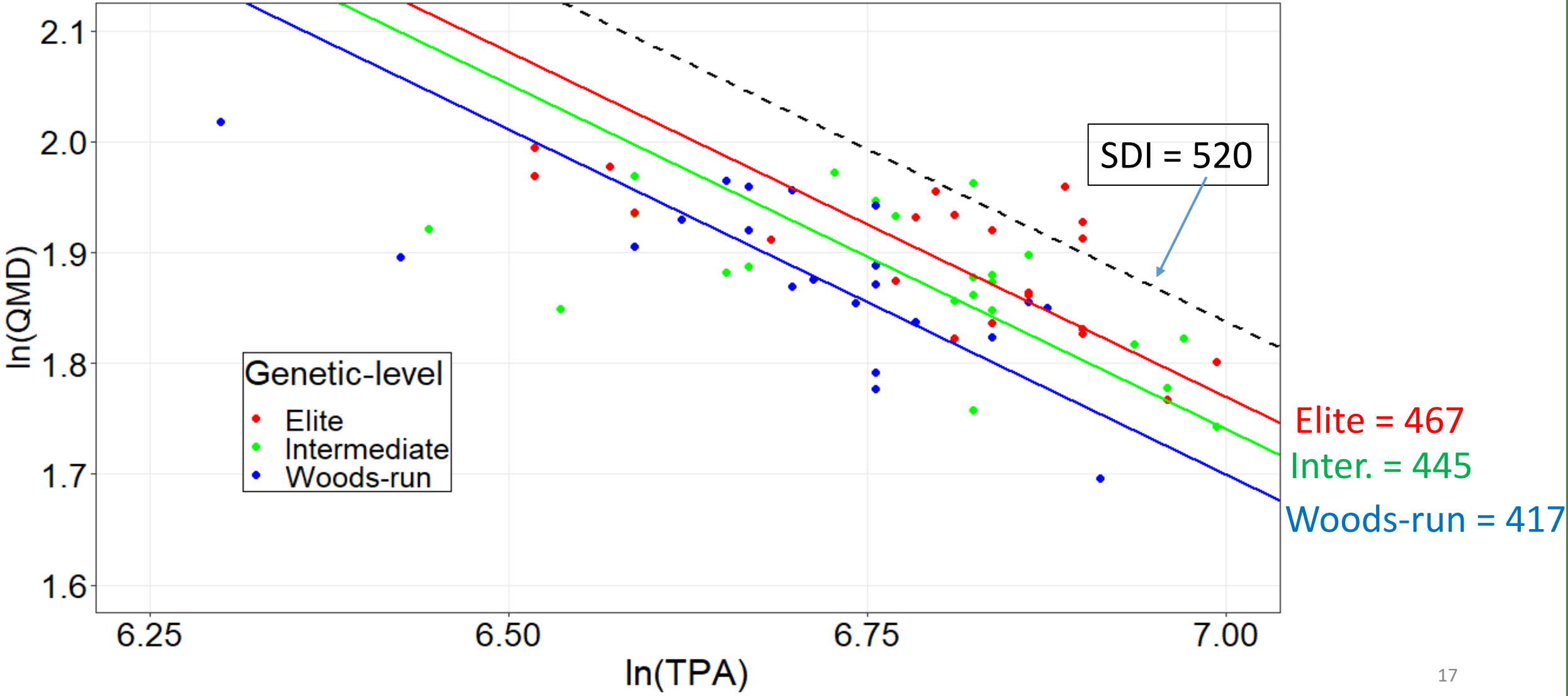


Trees per acre

- TPA = f(site, genetic, site*genetic, QMD) + ε
- 95% confidence interval
- Significant TPA difference between Elite and Woods-run



QMD vs. TPA

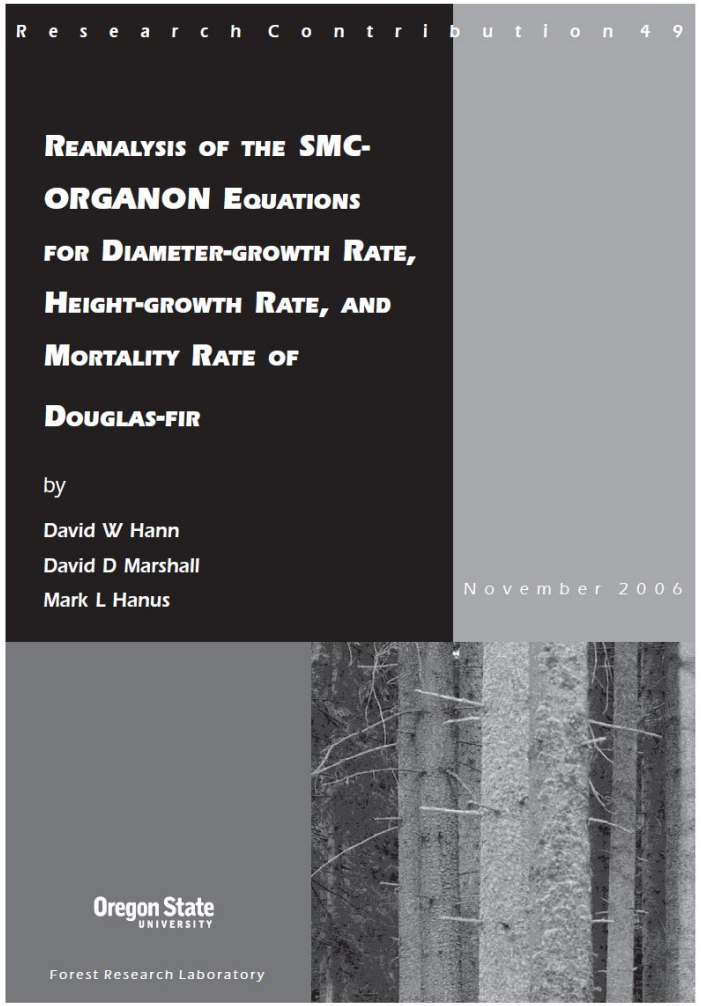

2.1
2.0
1.9
1.8
1.7
1.6
ln(QMD)
6.25
6.50
6.75
7.00
ln(TPA)
Genetic-level
Elite
Intermediate
Woods-run
SDI = 520
Elite = 467
Inter. = 445
Woods-run = 417

Results

- Increasing maximum carrying capacity for genetically improved Douglas-fir
  - **Molalla realized gain trials (at ages 26 and 27)**
    - Elite compared to Woods-run (on average)
      - 50 SDI gains → 12.0% SDI gains
      - 0.25 inches QMD gain → 11.3% QMD gains
      - 93 TPA gain → 3.9% TPA gains
    - Intermediate compared to Woods-run
      - Marginal SDI and TPA gains

Test with ORGANON/CIPSANON equations

Hann et al. (2003)



Hann et al. (2006)

Model for stands at maximum density

- Reineke (1933)

$$MLQ_i = a_1 + a_2 LT_i$$

- MLQ_i = natural log of maximum QMD at the *i*th measurement for a given number of trees per acre
- LT_i = natural log of number of trees per acre at the *i*th measurement

Our maximum density line model

- Genetic effect + random intercept

$$LQ = (b_1 + b_{1,E} I_{Elite} + b_{1,I} I_{Inter}) + b_2 LT + u_{site} + u_{block(site)}$$

- LQ = Natural log of maximum QMD
- LT = Natural log of number of trees per acre at the same measurement
- I_{Elite} = Indicator variable (1 when Elite; 0 otherwise)
- I_{Inter} = Indicator variable (1 when Intermediate; 0 otherwise)
- u_{site} = Random intercept for each site, $u_{site} \sim N(0, \sigma^2_{site})$
- $u_{block(site)}$ = Random intercept for each block within site, $u_{block} \sim N(0, \sigma^2_{block})$

Our maximum size density trajectories

- Hann et al. (2003)

$$LQ = (g_1^* + g_2 LT) - \frac{[(g_1^* \ g_2)\, g_4]^2}{g_1^* + g_2\, LT_1 - LQ_1} e^{-g_3 (LT_1 - LT)}$$

$$g_1^* = (g_1 + u_{site} + u_{block(site)} + g_{1,E}\, I_{Elite} + g_{1,I} I_{Inter})$$

- LQ = Natural log of QMD
- LT = Natural log of number of trees per acre at the same measurement
- LQ_1, LT_1 = Natural log of QMD and TPA for the first measurement on the plot

Use Reineke's slope (-0.62305)

- Followed Hann et al. (2003)

$$LQ + 0.62305 \cdot LT = h_0 + h_{1,E}\, I_{Elite} + h_{2,I} I_{Inter} + u_{site} + u_{block(site)}$$

- The slope of -0.62305 is the reciprocal of Reineke's (1933) Stand Density Index slope of -1.605, representing the maximum size-density relationship for Douglas-fir.

Results – Maximum density line

$$LQ = (b_1 + b_{1,E}I_{Elite} + b_{1,I}I_{Inter}) + b_2 LT + u_{site} + u_{block(site)}$$

Parameter	Estimate	Std. Error	P-value
b_1	3.3938	0.2130	< 0.0001
$b_{1,E}$	0.0285	0.0085	0.0011
$b_{1,I}$	0.0136	0.0088	0.1235
b_2	-0.2247	0.0317	< 0.0001

Results – maximum size density trajectories

$$LQ = (g_1^* + g_2 LT) - \frac{[(g_1^* \; g_2)\, g_4]^2}{g_1^* + g_2\, LT_1 - LQ_1} e^{-g_3(LT_1 - LT)}$$

$$g_1^* = (g_1 + u_{site} + u_{block(site)} + g_{1,E}\, I_{Elite} + g_{1,I} I_{Inter})$$

Parameter	Estimate	Std. Error	P-value
g_1	4.5533	0.5450	< 0.0001
$g_{1,E}$	0.0391	0.0153	0.0122
$g_{1,I}$	0.0240	0.0156	0.1265
g_2	-0.3993	0.0829	< 0.0001
g_3	-9.2673	3.3258	0.0065
g_4	-0.1441	0.0307	< 0.0001

Results - Use Reineke's slope (-0.62305)

$$LQ + 0.62305 \cdot LT = h_0 + h_{1,E} I_{Elite} + h_{2,I} I_{Inter} + u_{site} + u_{block(site)}$$

Parameter	Estimate	Std. Error	P-value
h_0	6.0627	0.0137	< 0.0001
$h_{1,E}$	0.0427	0.0137	0.0025
$h_{2,I}$	0.0327	0.0141	0.0223

- Elite showed 6.5% SDI_{MAX} gain
- Intermediate showed 5.1% SDI_{MAX} gain

Simulation

- In ORGANON/CIPSANON the default SDI_{MAX} for Douglas-fir is 520.
- With genetic SDI_{MAX} gain,
  - Elite = 554
  - Intermediate = 547
- Simulations with and without SDI_{MAX} gain
- There was no economical significance
  - Simulations to age 60 showed < 1 bf/ac difference in volume when only SDI_{MAX} was altered, suggesting limited economic benefit.

Conclusion

- Genetic improvement increases SDI_{MAX} :
  - +6.5 % for Elite, +5.1 % for Intermediate families.

- Despite the higher SDI_{MAX}, simulations indicate minimal volume gain at conventional rotation ages (~50 years).

- Further simulation work is needed to test volume gains from early stand development through biological rotation, using a range of SDI_{MAX} values
  - SDI = 350, 450, and 520
  - Try genetic effects into mortality rate equation (ORGANON/CIPSANON)

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