2021 Coastal 5th-Cycle Candidate Selection Analysis

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Objective

This document describes the creation of a list of candidate 5th-Cycle selections for in-field evaluation in the Coastal 4th-Cycle progeny tests during January-February 2021. Input data consist of breeding values predicted from progeny test data measured through Fall 2020 in the series CYCLE4C (tests established 2014-2017). The candidate selection list should satisfy genetic gain and diversity goals for the 5th-Cycle breeding program, which has a target of 142 Coastal 5th-Cycle selections to be topgrafted through Spring 2021 (69 of which have already been successfully topgrafted at Arrowhead Breeding Center, leaving 73 Coastal selections to target this winter). This document has an associated .Rmd script containing the R code used in the analysis.

Tree Population and Breeding Values

Individual tree breeding values were calculated for height, volume, straightness, rust, and forking/ramicorn, with mid-parent values used for the defect incidence traits (rust and forking). Individual tree breeding value predictions are not recommended for binary traits with only a single observation per tree, so the mid-parent values are preffered.

Members can find the breeding values on TIPRoot under Publications/Annual BLUP. From this list, non-selection candidates (checklots, pollen-mix families, open-pollinated families, and filler trees) and trees not marked as status 1 (alive and healthy) were removed. There were 16986 progeny on 25 test sites from 376 crosses (361 after lumping reciprocals) among 294 parents.

The distribution of breeding values by trait are presented in Figure 1.

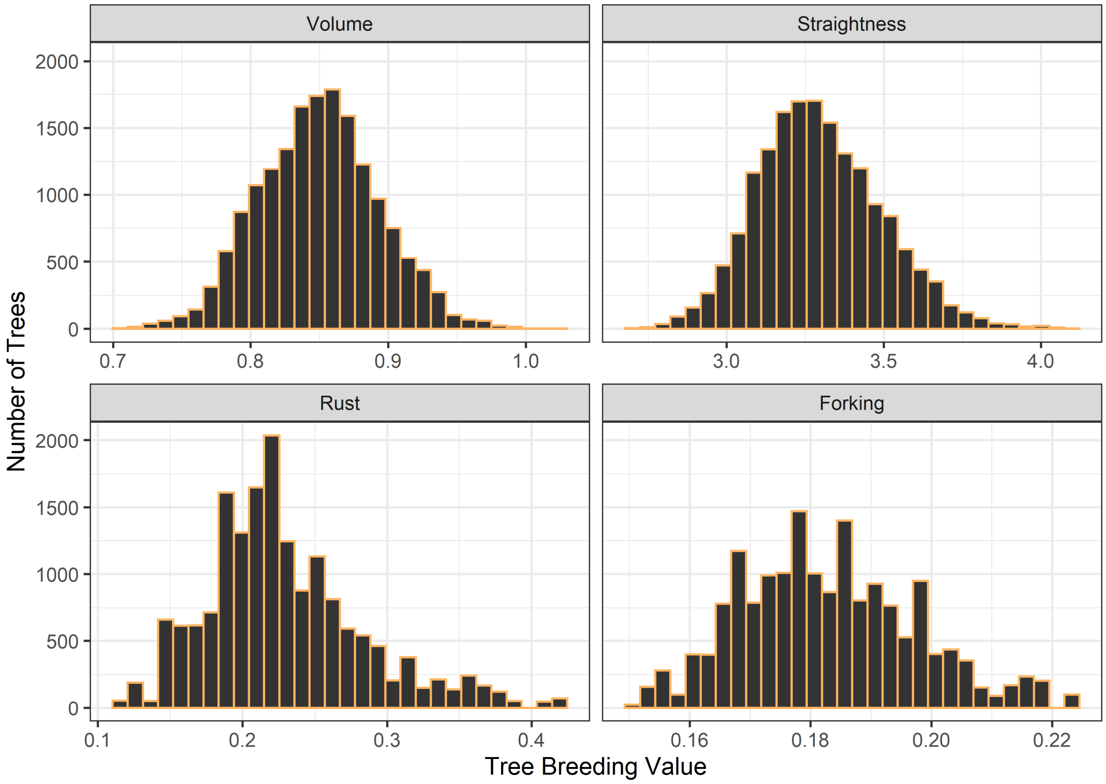

Figure 1. Distribution of individual tree breeding values by trait. Volume is in cubic feet per tree and straightness is on the 1-6 scale (lower is better). Rust and forking values are on the probability scale and are centered on the mean incidence across the progeny test sites. Forking probability includes the probability of ramicorn branches.

Figure 2 shows the correlations among the trait breeding values, which were low and not impactful for breeding/selection decisions.

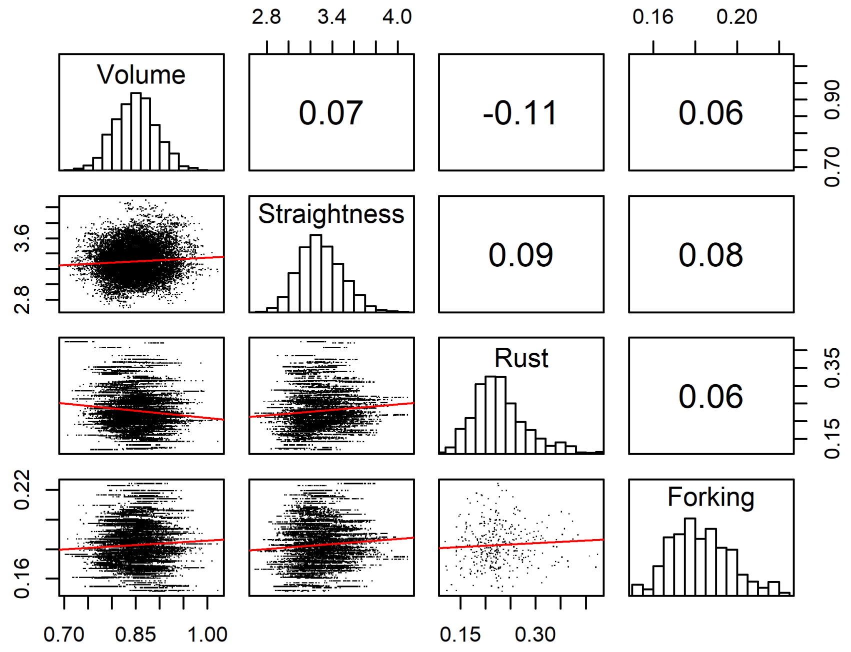

Figure 2. Relationship among individual tree breeding values with scatterplots and simple linear regression line on the lower triangle, Pearson correlation coefficients on the upper triangle, and the trait distributions are on the diagonal. Note there appear to be fewer points for Rust vs Forking because only mid-parent values were used for these two traits, so trees from the same family appear on top of each other.

Index Breeding Value Calculation

An index breeding value was calculated by combining volume, straightness, and rust probability breeding values. Forking was not included in the index, but was used for independent culling of selection candidates as described in the Independent Culling section below.

Standardization

To calculate index breeding values, the breeding value were standardized to Z-scores (standard normal) by subtracting the mean and dividing by the standard deviation. In 2019 and 2020, a different standardization method was used that was found to be sensitive to the mean of the trait: namely, the scale of the rust breeding values caused rust resistance to have more influence on the index than desired. Figure 3 displays the distribution of standardized values for the three traits. Note the straightness and rust breeding values are better when they are lower, but the standardized scores are calculated so that larger values for all three traits are desirable.

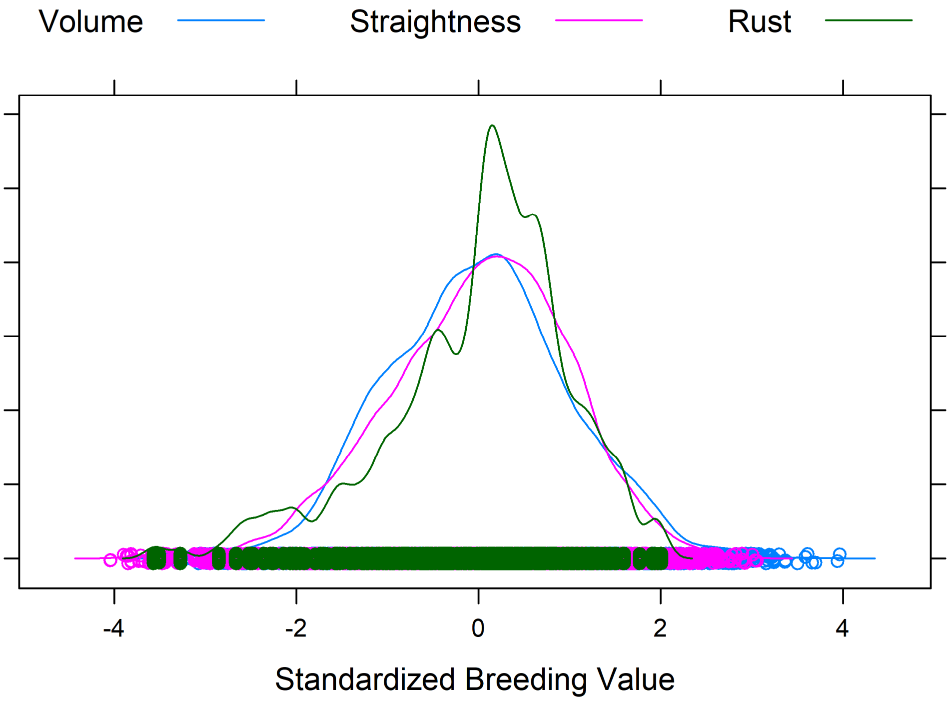

Figure 3. Distribution of standardized breeding values for each trait.

Economic Weights

The following weights were used to calculate the index breeding value:

- 60% volume
- 20% straightness
- 20% rust resistance

The equation below calculates the index scores with the weights and standardized scores.

$$BV_{index} = 0.6 * BV_{Volume_{std}} + 0.2 * BV_{Straightness_{std}} + 0.2 * BV_{Rust_{std}}$$

Figure 4 shows the distribution of index breeding values and Figure 5 shows how the index depends on the trait breeding values.

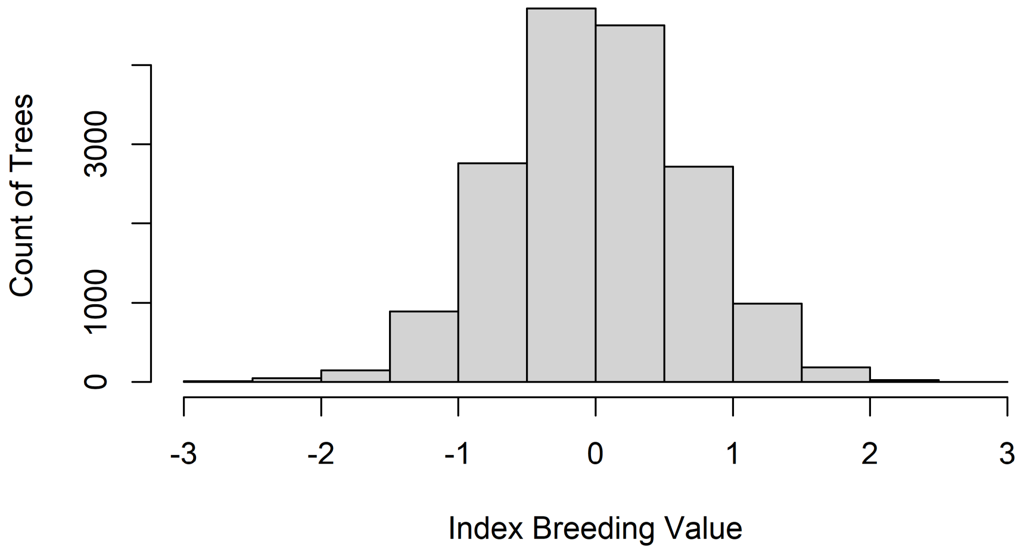

Figure 4. Distribution of index breeding values.

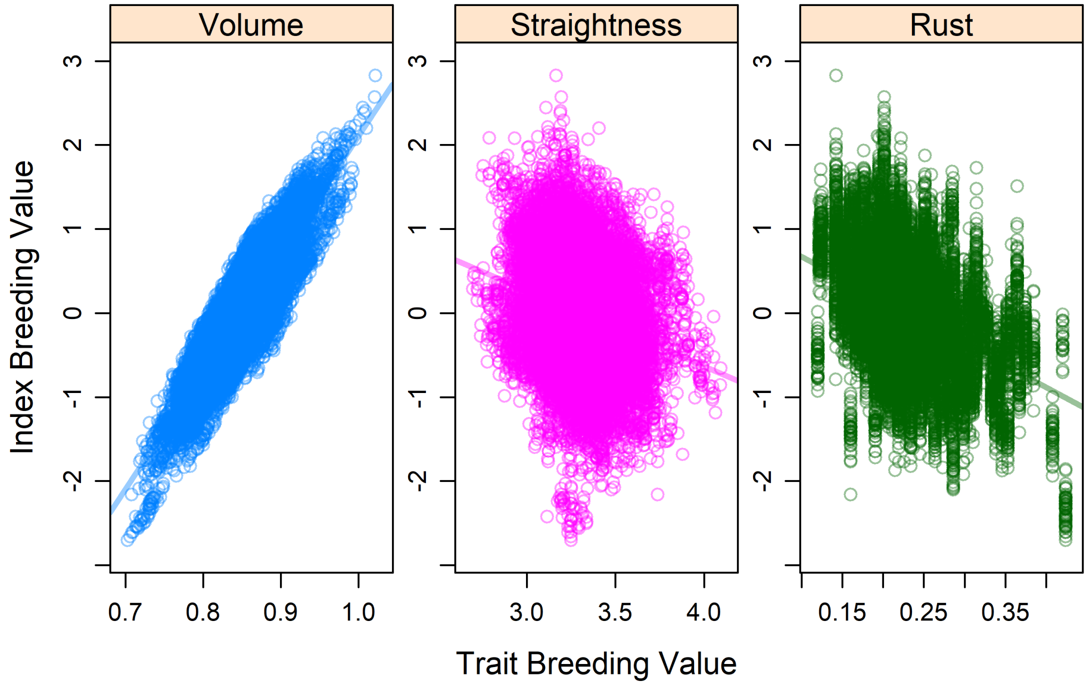

Figure 5. Scatterplot of index breeding values versus the individual trait breeding values (in their natural units) with simple linear regression lines to indicate the dependence.

Selection Candidates

Independent Culling

Trees with unacceptable defects at the individual and/or family level were removed from the list of candidates prior to the selection algorithm using independent culling as described below.

Forking

Family Level

There were 14 families with poor forking/ramicorn mid-parent breeding values (> 0.2094) that were omitted from the pool of selection candidates. These crosses correspond to the poorest 5% of forking breeding values, as illustrated in Figure 6.

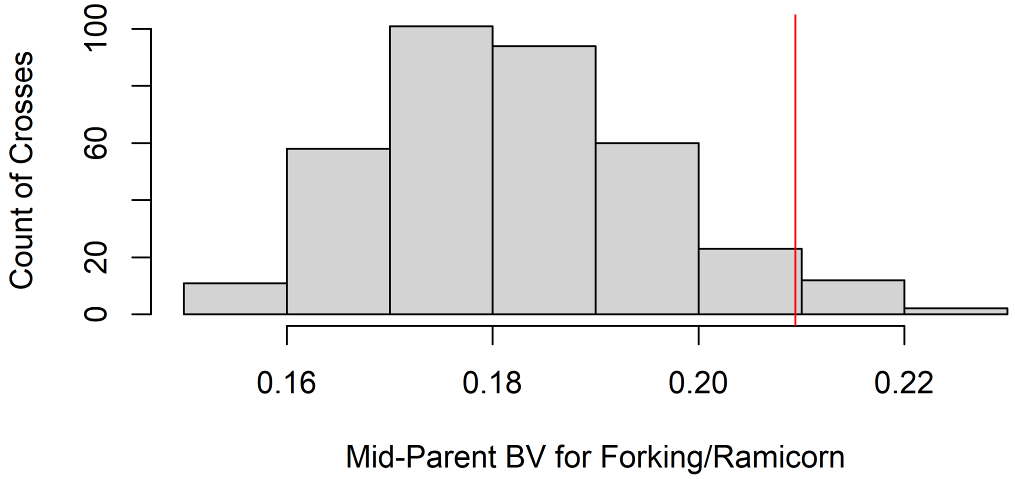

Figure 6. Distribution of forking breeding values with a red line to indicate family culling threshold (worst 5% of families).

Tree Level

Furthermore, all trees with a fork or ramicorn were flagged for removal from the candidate list. There were 3842 trees with a fork or ramicorn at time of measurement.

Rust - Tree Level Culling

There were 3441 trees with rust observed during measurement that were also flagged for removal from the candidate list.

Straightness - Tree Level Culling

There were 2368 trees with straightness scores of 5 or poorer that were also flagged for removal from the candidate list.

Trees Already Visited and Determined Inadequate for Selection

There were some trees that were determined to be unsuitable for selection in previous in-field evaluations (2019-2020) due to reasons not apparent from their original measurement data. The count of trees by reason for removal is provided in Table 1.

Table 1. Count of trees determined to be inadequate for selection after in-field verification in 2019-2020.

Reason	Tree Count
EXCESSIVE MISSING NEIGHBORS	12
FORK PRESENT	9
INCORRECT DBH MEASUREMENT	2
INCORRECT HEIGHT MEASUREMENT	4
INCORRECT STRT SCORE	11
RAMICORN PRESENT	9
RUST PRESENT	13
UNDESIREABLE BRANCHING	5
VARIABLE TEST DUE TO WET SITE AND WASHED OUT BEDS	1046

In total, there were 9009 trees removed from the candidate list due to independent trait culling and previous in field evaluations, leaving 7977 trees as selection candidates. The Venn diagram in Figure 7 shows the counts of trees in each category for removal.

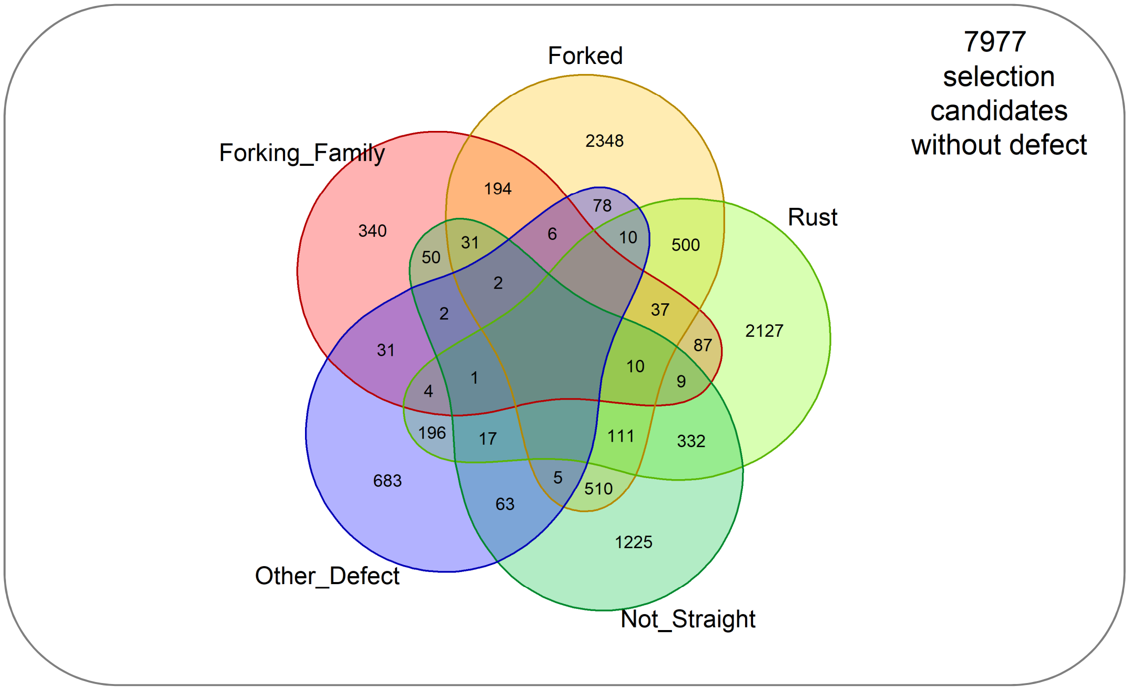

Figure 7. Count of trees removed from the selection candidate population due to independent culling or in-field verification. The count of trees remaining appears outside the colored sets.

MateSel Candidate Selection Algorithm

The commercial version of **MateSel** was used to identify the highest ranking selection candidates while maintaining constraints on diversity. The MateSel program inputs a list of candidate parents and outputs a crossing list (breeding plan), but here we are inputting progeny test trees and then reducing the breeding plan to get a candidate selection list. The driving parameter for the MateSel algorithm is the **Target Degrees**, which ranges from 0 to 90, and corresponds to the amount of weight placed on diversity among the progeny in the next generation and their genetic gain, with 0 degrees selecting only the very best few individuals for breeding (higher gain) and 90 degrees selecting individuals from many different families with no weight on genetic merit (greater diversity).

Development of the MateSel Input Files

MateSel Main Data File

The process used to develop the MateSel **Main Data File** is described here. The following inputs were required:

- A pedigree of the breeding candidates, including ancestors through the founders
- Index breeding values to use for selection
- A designation of trees as candidates for selection and specification of maximum and minimum times they can be used for mating

A pedigree file was downloaded from TIPRoot that was pruned to contain the ancestors of candidate trees for selection. Next, the selection candidates (progeny in the tests) were added to the pedigree. A preview of the pedigree format is given below (the first and last 6 rows).

```
##     Tree Parent1 Parent2
##   119519       0       0
##   1621292      0       0
##   1173760      0       0
##   1487936      0       0
##   11038493     0       0
##   138245       0       0

##          Tree Parent1 Parent2
##       3564093  2178087 NAG034
##       3564092  NB2052  NAG029
##       3564090  NR2056  NC3054
##       3564088  NAB766  NR2056
##       3564087  NAG045  NAI002
##       3564085  NBB051  NB2052

## [1] "Pedigree dimensions: 17718 x 3"
```

Next, the index breeding values were merged to the expanded pedigree. The column names were changed to the livestock convention (Id, Sire, Dam) to be consistent with the software manual. The individual trait breeding values (Volume, Height, Straightness, Rust, and Forking) were also merged to the last columns of the file for monitoring purposes.

A column named *Maxuse* was used to indicate which trees are 5th-Cycle selection candidates, and the maximum number of 5th-Cycle matings allowed for the candidate. Note that the objective was to identify a list of selection candidates rather than a mating list, but the values of Maxuse have a strong influence on how many selection candidates are identified for 5th-Cycle mating. For high values of Maxuse, fewer trees will be selected to participate in 5th-Cycle breeding, and there will be many more crosses assigned to the selections with the highest index breeding value. The developers of MateSel suggest supplying biological/logistical limits for Maxuse rather than specifying values to meet diversity constraints, as the Target Degrees parameter should reflect the weighting on diversity/gain. A biological constraint on breeding that was observed in the 4th-Cycle was the limited number of flowers available on young topgrafted forward selections, which then required multiple years of breeding in order to achieve the planned number of crosses. For this reason, the maximum number of matings per 5th-Cycle selection was set to 5 times as a female. In the same vein, the maximum use as a male was set to 5, which can be supplied to MateSel as a Maxuse value of 50005. Values of 0 for Maxuse indicate the tree is not a candidate (e.g. ancestors). This field corresponds to the retired *CandStat* field in older versions of MateSel.

The *Minuse* column specifies that if a tree is selected for mating, it must be used a certain number of times. For example, in order to obtain robust general combining ability estimates, we may require that a selection is used in a minimum number of crosses. Also, one may require a minimum number of crosses to increase the opportunities for among-family selection, and reduce the risk of a single-pair mating between an outstanding parent and a mediocre one (which would not yield excellent 6th-Cycle selections). Presently, Minuse values of 20002 were used, which indicates that if the tree is chosen as a male, it must be used at least twice as a male, and if it is chosen as a female, it must be used at least twice as a female. While these sex use designations are arbitraty for loblolly pine and rather clunky, this is how the current version of the MateSel software handles Maxuse and Minuse.

A column named *AbsMinuse* indicates that a tree must be included in the mating (i.e. mandatory selection). In this analysis, we considered using this field to require mating with 5th-Cycle selections that have already been successfully topgrafted. Our motivation was to deter the algorithm from choosing a new selection with slightly better index breeding value that is closely related to selections that have already been topgrafted, as this would add additional years to the breeding cycle for perhaps little improvement in genetic gain. Similarly, if two trees have comparable breeding values, it would be preferable for the algorithm to select the tree that is less related to genotypes that have already been topgrafted. There have been 69 5th-Cycle Coastal selections successfully topgrafted in springs 2019-2020. AbsMinuse values of 10001 were used to indicate these trees, and 0 otherwise. Note that the value of Minuse specified in the above section will override the AbsMinuse values greater than 0.

Finally, to reduce the run time of MateSel, only the 4 best trees per cross were allowed as breeding candidates, as it is undesirable in the mainline breeding population to make numerous selections from a sinlge cross.

A preview of the MateSel input file is shown in Table 2.

Table 2. Preview of the MateSel main data file (first 6 rows and last 10 rows).

Id	Sire	Dam	Sex	Index	Maxuse	Minuse	Absminuse	Volume	Height	Strt	Rust	Fork
119519	0	0	0		0	0	0					
1621292	0	0	0		0	0	0					
1173760	0	0	0		0	0	0					
1487936	0	0	0		0	0	0					
11038493	0	0	0		0	0	0					
138245	0	0	0		0	0	0					
3564265	150187	2751739	0	0.747	50005	20002	0	0.863	18.092	2.989	0.161	0.197
3564621	1103086	1412064	0	-0.381	50005	20002	0	0.833	18.228	3.196	0.296	0.188
3564200	X112038	3210310	0	0.553	50005	20002	0	0.885	18.310	3.356	0.195	0.182
3564198	1973363	2146028	0	-0.455	50005	20002	0	0.845	17.707	3.446	0.292	0.169
3564141	2570633	271124	0	0.382	50005	20002	0	0.836	18.146	2.986	0.158	0.161
3564129	1857822	216059	0	-0.042	50005	20002	0	0.881	18.037	3.243	0.375	0.187
3564127	150187	2751739	0	0.739	50005	20002	0	0.859	18.274	2.933	0.161	0.197
3564124	2190369	2446494	0	1.086	50005	20002	10001	0.924	19.310	3.227	0.234	0.219
3564117	1940090	1378159	0	1.125	50005	20002	10001	0.931	18.969	3.319	0.222	0.174

3564107	2311895	2193637	0	-0.564	50005	20002	0		0.787	17.506	3.106	0.198	0.197
3564106	2311895	139150	0	-0.064	50005	20002	0		0.825	17.985	2.932	0.255	0.155

InpOneGroups.txt

The *InpOneGroups.txt* file is necessary for the program to run, but no changes were made to the default values, as Maxuse and Absminuse will be read from the Main Data file.

Committed Matings

In this analysis, we considered the use of the *CommittedMatings.txt* file to account for juvenile progeny that are not yet eligible for selection. This represents 4th-Cycle tests that were planted in 2018 - 2021 and are not yet old enough for measurement. The purpose for accounting for the juvenile population in CommittedMatings.txt is to apply some negative pressure on selection candidates that have close relatives that have not yet been measured, unless their index breeding value is outstanding. Ideally, if two individuals have the same index breeding value, the tree that is less related to the juvenile population should be preferred.

The CommittedMatings.txt file is tab delimited, with a single header line with columns *Sire* and *Dam* as shown below. We excluded crosses with fewer than 20 progeny from the file. Table 3 shows a preview of the CommittedMatings.txt file.

Table 3. Preview of the first and last 6 rows of the CommittedMatings.txt file.

Sire	Dam
S138245	2232855
S238245	289540
S238245	1162449
S238245	1141560
S238245	X78108
ZZ0993	1198287
NZ44404	NZ44306
NZ44406	NZ44223
NZ44708	NZ44223
NZ44910	NZ44223
NZ44223	NZ44112
NZ44223	N0Z4018

There were 428 crosses in the juvenile population represented in the CommittedMatings.txt file.

MateSel.ini Parameters

The *MateSel.ini* file holds values for the algorithm parameters. The following values were changed from their defaults to represent the targets for the present analysis:

- Target Degrees: 45
  - This puts an equal weight on short term and long term gain
- Number of matings: 213 crosses
  - This value was based on the target number of Coastal 5th-Cycle selections to be topgrafted through Spring 2021 (142 selections). The breeding target is 3 crosses per selection to obtain robust GCA estimates and increase opportunity for among-family selection, which results in 213 crosses (142 selections * 3 crosses per selection / 2 parents per cross). Note that not all selected trees will be bred 3 times, and some might not be bred at all due to grafting success, incompatibility, or selection during the breeding plan development. Hence this value was chosen to meet current selection targets and will be revisited during development of the breeding plan.
- Switch for BiSexCands = 1 to allow individuals to be used as both male and female
- Switch to avoid duplicate, reciprocal, and self matings = 111 to simplify the output
- Switch for Committed Matings = 1 to include CommittedMatings.txt

Scenarios Evaluated

To test the influence of the *Absminuse* column for selections already made and the *CommittedMatings.txt* for accounting for the juvenile population, three MateSel runs were made:

- Scenario 1 Include Absminuse and CommittedMatings.txt
- Scenario 2: Include Absminuse, but not CommittedMatings.txt
- Scenario 3: Do not use Absminuse or CommittedMatings.txt

MateSel Scenario Comparisons

Population Diversity Summary

Table 4 shows the number of individuals chosen for mating in each scenario (which are considered as the candidate selections to make this winter) and information about their diversity, such as the number of 4th-Cycle parents and families they come from. The table also gives the average numerator relationship (**A** matrix values, which are the additive genetic relationship and twice the inbreeding coefficient) among individuals in the population, the average number of unrelated crosses possible per selection, and the number of founders represented.

In terms of mean genetic relationship, Scenario 1 resulted in the most diverse population, followed closely by Scenario 2 and finally Scenario 3. Scenario 2 included more selections than Scenario 1, and thus included selections from more 4th-Cycle parents and crosses; however, the mean relationship was not improved, which is reflected in the similar number of founders represented. Note that Scenario 3 statistics do not include topgrafts that were made in 2019-2020 but not selected again, and including those topgrafts in the calculations would increase the mean genetic relationship and only slightly benefit the number of families, parents, and founders represented. Note also that there were 16 selections already topgrafted that were mandatory in Scenarios 1 and 2 but were not allowed to appear in Scenario 3 due to defect culling that was not implemented in 2019 and 2020.

Table 4. Candidate 5th-Cycle breeding population diversity summary by MateSel scenario.

Scenario	Number of New/Existing Selections	Cycle-4 Parents Selected From	Cycle-4 Crosses Selected From	Mean **A** Among Selections	Mean Number of Unrelated Crosses Possible per Selection	Number of Founders Represented
1	67 / 69	126	104	0.01605	9.6	132
2	76 / 69	131	111	0.01680	11.6	131
3	101 / 22	105	79	0.01894	10.5	116

The Venn diagram in Figure 8 indicates the amount of overlap in the selection candidates in each scenario (excluding those that have already been topgrafted). There is considerable overlap in the trees chosen among the three scenarios. Scenario 3 has the most trees not included in the other scenarios.

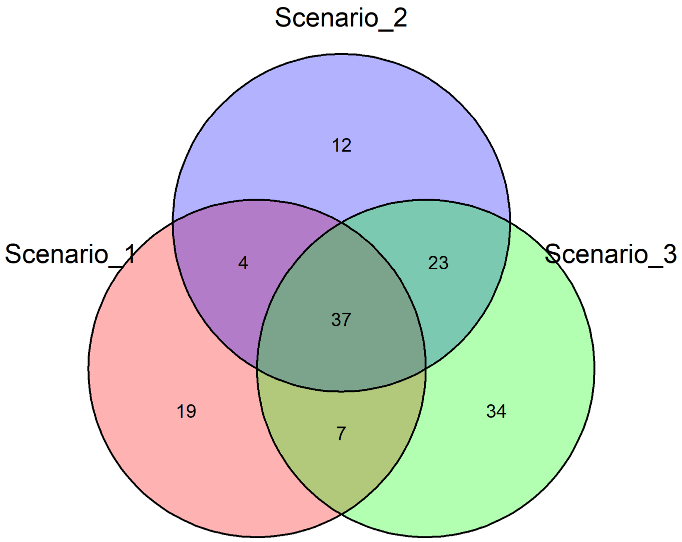

Figure 8. Count of trees in common and unique to the three MateSel scenarios evaluated.

Genetic Gain

The distribution of index breeding values for the selected trees compared to the entire 4th-Cycle population (with measurements through Fall 2020) are shown for each scenario in Figure 9. As should be expected, Scenario 3 (which had the fewest constraints) produced the largest average index breeding value (1.32), followed by Scenario 2 (1.14) and lastly Scenario 1 (1.07).

The difference between Scenario 3 and Scenario 2 indicates that using the Absminuse column to require mating of individuals already topgrafted comes with a considerable penalty in expected genetic gain. This is because there are individuals in recently measured progeny tests that are closely related to the topgrafted population but have better index breeding values. Selection of these individuals would increase the mean index breeding value, but would increase the population size without adding meaningful diversity, and potentially extend the time to complete the breeding cycle.

Scenarios 1 and 2 had more similar gain values than Scenario 3. This indicates that considering relatedness among new selections and the juvenile population (tests not yet measured) had less impact on the expected genetic gain than when forcing the algorithm to include individuals already topgrafted. Using the CommittedMatings.txt to account for the juvenile population in future MateSel runs is expected to reduce the disparity in mean index breeding value observed when comparing Scenario 3 and Scenario 2, because there would be less relatedness between the juvenile and grafted population.

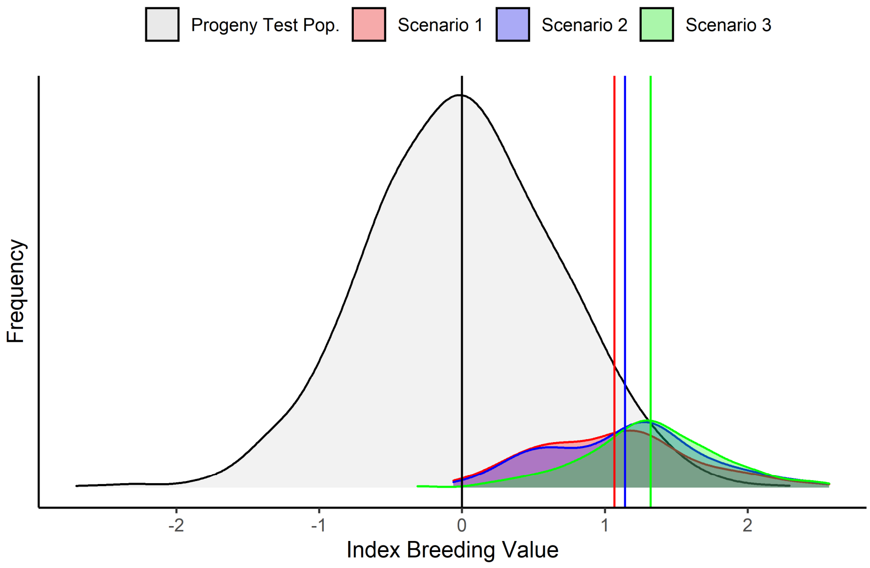

Figure 9. Distribution of index breeding values for the entire 4th-Cycle population (gray) and trees selected by different MateSel scenarios, with vertical lines indicating the mean for each population

Number of Selections per 4th-Cycle Parent

Figure 10 displays the number of selections candidates from each 4th-Cycle parent by selection scenario, with those parents having the greatest index breeding values appearing at the top. As expected, parents with a higher index breeding value tended to have more trees selected. Scenarios 1 and 2 had more parents with only one selection compared to Scenario 3. Parents common to all three scenarios tended to have more selections within a given scenario, with the maximum being 11 selections from a single 4th-Cycle parent. Not all parents had a selection made and the parents with selections differed slightly among the scenarios.

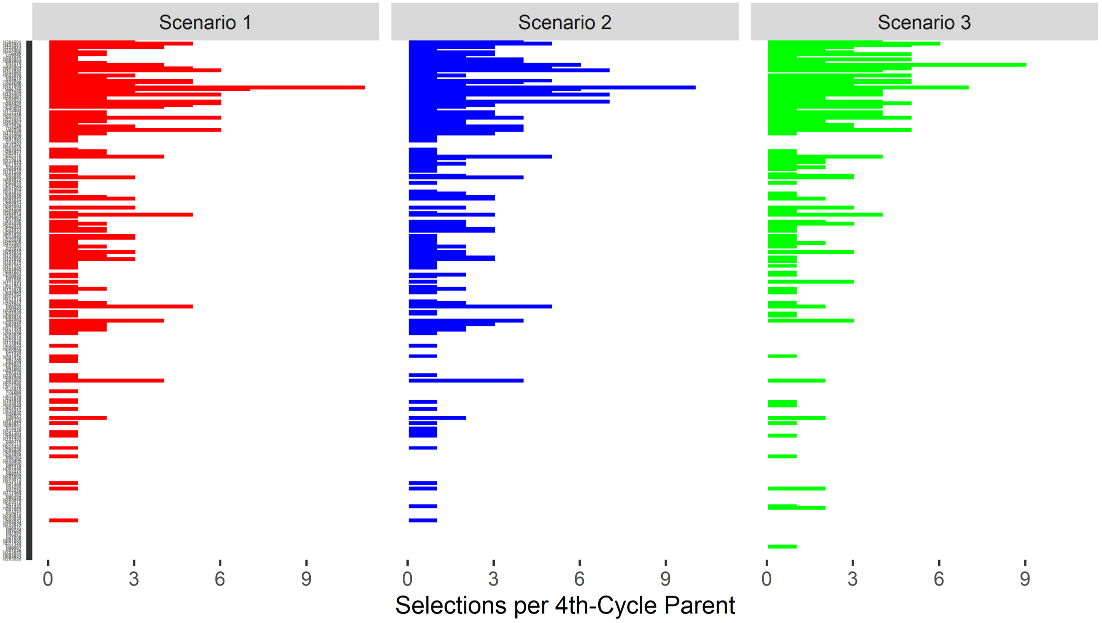

Figure 10. Number of trees proposed for selection per 4th-Cycle parent by MateSel scenario. Trees chosen by the algorithm but already topgrafted are not included. The highest ranked parents are sorted at the top.

Relatedness Among New Candidates and 5th-Cycle Selections Already Topgrafted

Recall that Scenarios 1 and 2 required MateSel to use 5th-Cycle selections that had already been successfully topgrafted, whereas Scenario 3 did not. Figure 11 displays the additive genetic relationship values among the 69 existing 5th-Cycle selections topgrafted at Arrowhead (on y-axis) and the list of new proposed selection candidates for each scenario. The trees are ordered so that those with the highest index breeding value appear towards the top and right. In all three scenarios, there is relatedness among the new selection candidates and those already topgrafted, although there is a higher incidence of relatedness in Scenario 3. The mean genetic relationship is shown below the scenario titles. In the figure Scenario 1 and 2 were slightly more similar to each other than when compared to Scenario 3, which had the highest mean relationship, indicating that the new selections candidates in Scenario 3 are more related to those already topgrafted.

Figure 11. Additive genetic relationship between 5th-Cycle selections already topgrafted and proposed new selections by MateSel scenario. Highest ranking trees are sorted to the top and right.

Relatedness with Juvenile Population

In Scenario 1, we used the CommittedMatings.txt file to inform MateSel about crosses that are in the juvenile 4th-Cycle progeny test population (not yet measured), while Scenarios 2 and 3 did not consider those crosses coming down the measurement pipeline. Figure 12 shows the additive genetic relationship among the new selection candidates (on the x-axis) and the crosses in the 4th-Cycle progeny tests that are still too young to measure (y-axis with only 1 row per cross). For the selection candidates, those with higher index breeding values are on the right. While all three scenarios contain relatedness among these two populations, Scenario 1 had more pairs of unrelated individuals. The mean additive relationship values are below the scenario titles in the figure. Scenario 2 and 3 were very similar, while Scenario 1 had considerably lower mean relationship, indicating that the new selections candidates are much less related to the juvenile population. Thus, the reduction in relatedness with trees not yet measured when using the CommittedMatings.txt was substantial.

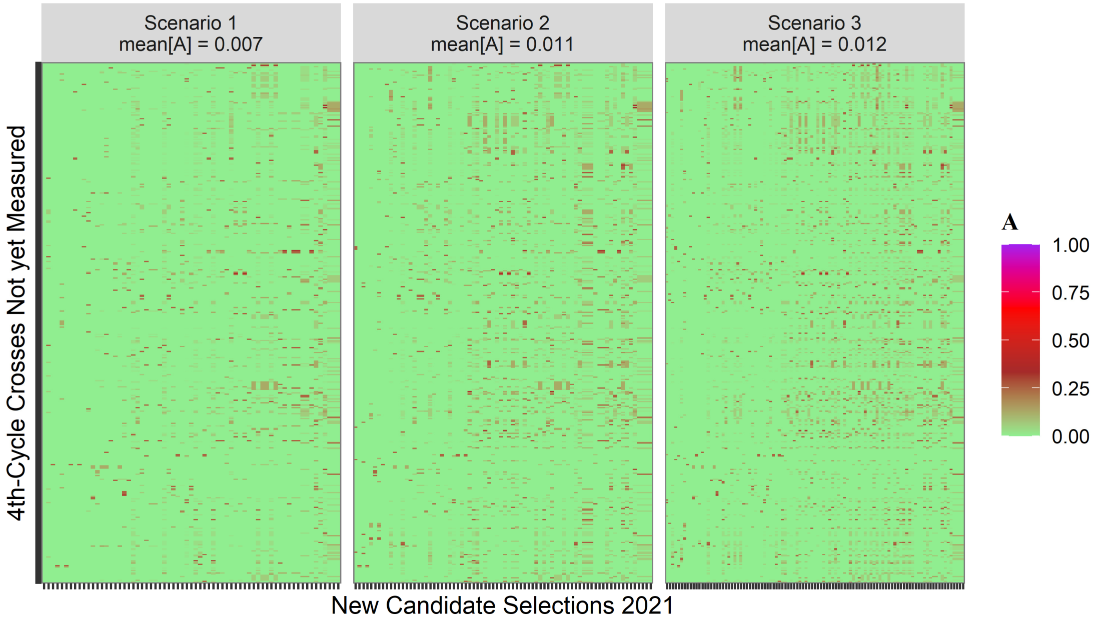

Figure 12. Additive genetic relationship between 4th-Cycle crosses not yet measured (planted in 2018-2021) and proposed new selections by MateSel scenario. The trees with the highest index breeding values are sorted to the right.

Conclusions

Findings from MateSel Input Parameters

MateSel has proven to be a useful tool for identifying potential 5th-Cycle selections, and will be used to create a selection candidate list for January 2021. However, the output is sensitive to the Maxuse, Minuse, and CommittedMatings.txt parameters, even when the balance on gain and diversity is fixed at Target Degrees 45 (equal weight on short term and long term gain). While not elaborated here, the decision for Maxuse and Minuse values was partly guided by evaluating how the count of new selections compared to the targets set forth in the 5th-Cycle breeding plan (142 Coastal selections topgrafted through Spring 2021).

The candidate output list was very sensitive to the requirement of including selections already made (via Absminuse) and accompanied by a noteworthy loss of expected genetic gain in the mean index breeding value. The candidate list was also sensitive to the consideration of the juvenile population (young progeny tests via CommittedMatings.txt), with a considerable increase in diversity among the candidate selections accompanied by only a slight sacrifice in expected genetic gain. Had the CommittedMatings.txt been considered during selection in 2019-2020, it is possible that the impact of the Absminuse requirement would have been less. Unfortunately, the free version of MateSel was used in 2019-2020 and it did not include this functionality.

While the current version of MateSel presents excellent new features, the Maxuse and Minuse for bisexual species (like loblolly pine) are limited in flexibility. In our present use of the software, it would be preferable for these to ignore sex altogether rather than place separate limits by gender.

Next Steps for Spring 2021 5th-Cycle Selections

We recommend that a blended list of Scenario 1 and Scenario 3 be used to guide the in-field selection evaluations. All of the trees in Scenario 1 are recommended, and we recommend including those trees in Scenario 3 that have a significantly better index breeding value when accounting for their relatedness with trees in Scenario 1. Figure 14 shows the trees that are in Scenario 3 but not in Scenario 1, and has their index breeding value plotted against their mean additive relationship with the trees in Scenario 1. There were 6 trees that were more than 0.5 index breeding value points greater than the mean index breeding value adjusted for relatedness with Scenario 1, which appear above the dashed line in the plot. All of these trees had a much higher index breeding value than the average for Scenario 1, and will increase the mean genetic merit of the 5th-Cycle Coastal breeding population. These were added to the list of trees to evaluate for selection in 2021 to bring the total to 73.

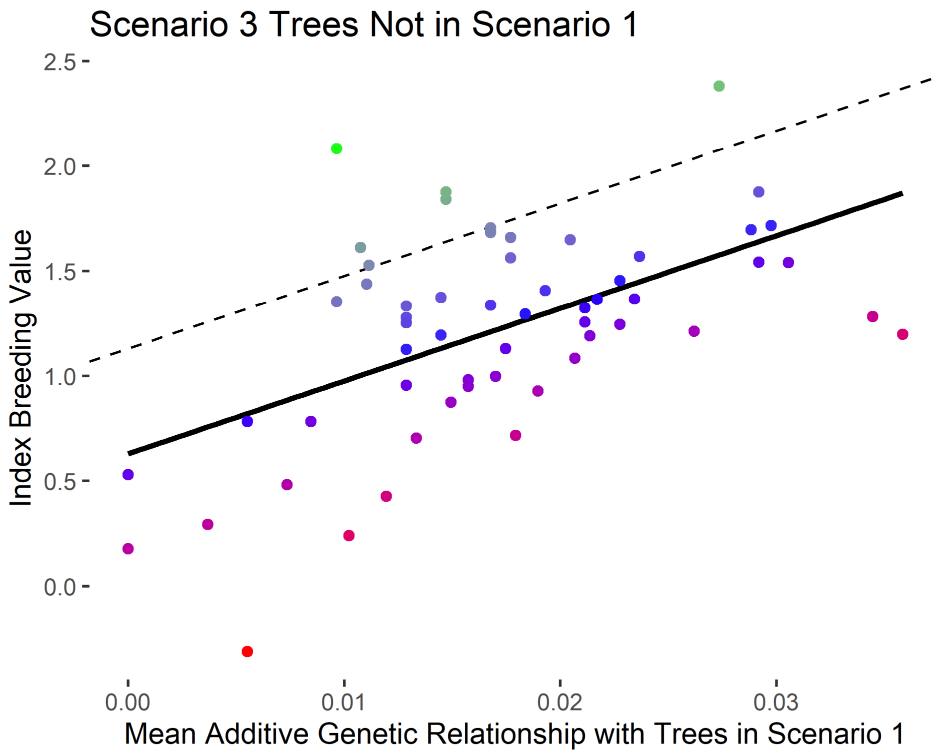

Figure 14. Index breeding values for trees in Scenario 3 that are not included in Scenario 1, plotted against their mean additive genetic relationship with the trees in Scenario 1. The solid line is the simple linear regression and the dashed line was used as a threshold to choose trees from Scenario 3 with strong index values given their relatedness with trees in Scenario 1.

Proposed Selections by Cross

Figure 13 shows the distribution of index breeding values for 4th-Cycle trees by cross, with the crosses with the highest mean index breeding value appearing at the top. The 73 trees recommended for evaluation (blend of Scenarios 1 and 3) are highlighted red and the trees that were selected in 2019-2020 and successfully topgrafted are blue. The non-selected trees are black and a 'X' indicates the tree was removed from the selection list due to culling.

The individual with the highest breeding value within a family is preferred unless it was culled from the candidate selection list due to forking, poor straightness, the presence of rust, too many missing neighbors, etc. There are no new selections with an index breeding values less than 0 (the population average), although there were two individuals that have already been topgrafted with index less than 0, which come from families whose ranking dropped with the addition of more progeny test measurements in Fall 2020. While the vast majority of crosses have only one tree proposed for selection, there were many crosses where the algorithm insisted that more than one selection was appropriate, with one cross having as many as 5 selections suggested including those already topgrafted. Instead of mandating a maximum number of selections per cross allowed, the MateSel algorithm considers the relatedness among crosses and will choose more individuals from a family when justified by their index breeding values and diversity contribution.

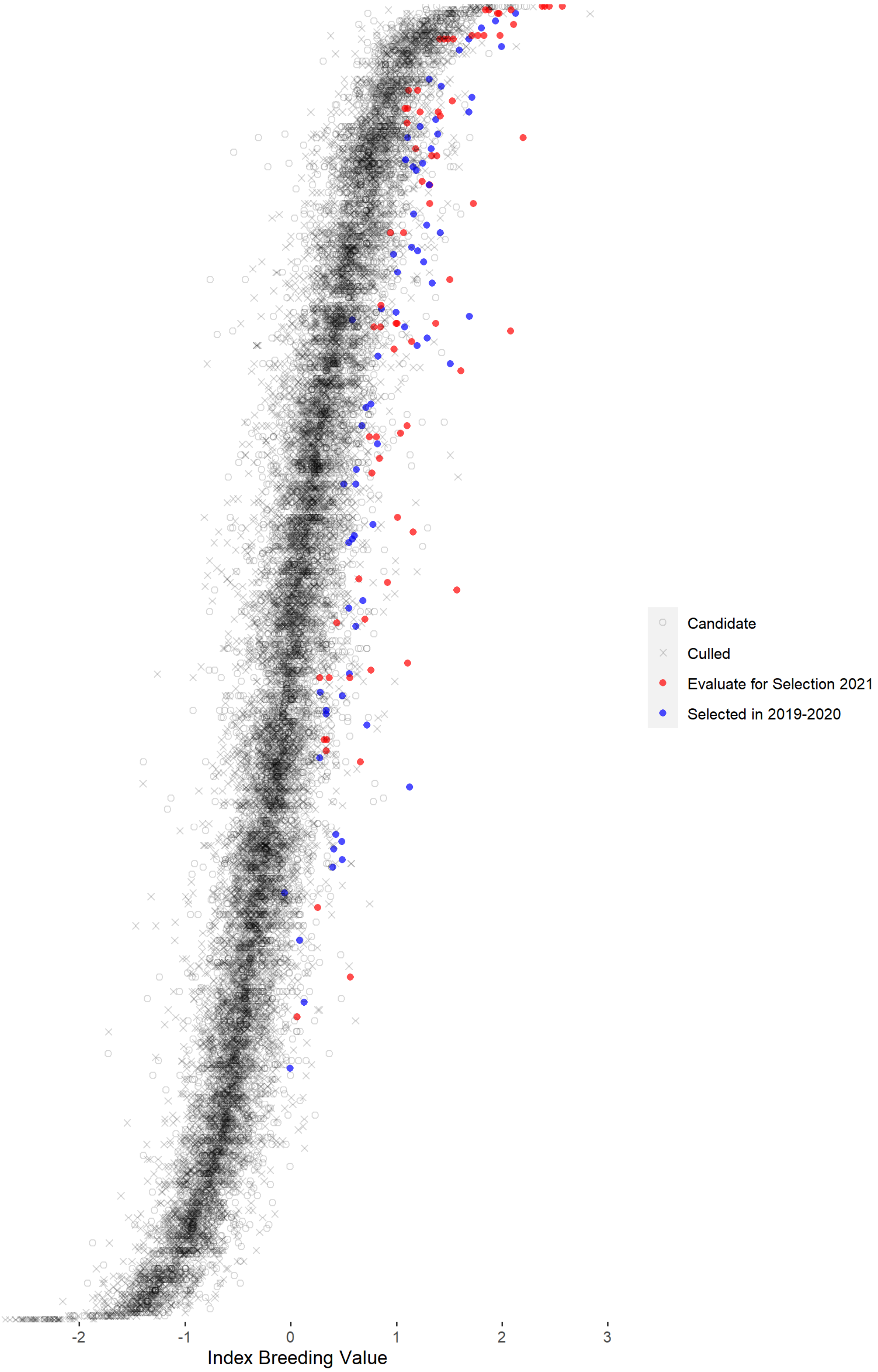

Figure 13. Index breeding values by cross (y-axis) with the proposed selections (blend of Scenarios 1 and 3) highlighted red, existing selections highlighted blue, and non-selected trees black. The best ranking crosses appear at the top.

Coastal Evaluation List

Note that the MateSel run creates a candidate list of selections that will be evaluated in the field in January-February 2021, and changes to the actual selections made can happen due to findings of incorrect measurement data or field conditions not adequately accounted for by the models used (e.g. missing neighbors). Therefore, an in-field evaluation list was made that included the 73 trees identified by MateSel as well as the up to two “backup” trees per cross with the next highest index breeding values within the cross. Should a backup tree be chosen, the diversity values presented here will be maintained, but the nominal gain values will be reduced. We also included 11 trees to the evaluation list that had superior index breeding values but were previously excluded due to culling or diversity constraints, with the motivation that these should be candidates for open-pollinated testing to supplement the number of parents for deployment (seed orchard) candidates, but not necessarily contribute to the breeding program. Table 5 shows the number of trees to evaluate in each test site.

Table 5. Number of selection candidates (and backup trees) to evaluate by progeny test site in the CYCLE4C population. Some of these numbers changed slightly after switching trees for logistical reasons and based on previous tree evaluations.

	1st Choice	Backup 1	Backup 2	OP Candidate
2014ABC16	2	0	0	1
2014ABC17	1	2	1	0
2014DEF19	1	0	0	0
2014GHI20	1	0	0	0
2014GHI21	0	1	0	1
2014JKL23	0	0	1	0
2015DEF01	1	1	2	0
2015DEF02	0	2	3	2
2015GHI03	0	0	0	2
2015JKL06	0	1	1	0
2016DEF02	3	1	2	0
2016GHI03	6	2	1	1
2016MNO04	8	5	4	1
2016JKL05	1	0	0	0
2017ABC01	2	1	2	0
2017QRS02	0	1	3	1
2017QRS08	2	5	8	0
2017GHI05	5	4	5	0
2017MNO04	7	4	5	1
2017MNO07	32	13	7	1
2017GHI09	1	5	3	0

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