How heritable is growth, branch score and sonic velocity in Douglas-fir?

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NZ Douglas-fir Cooperative

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ABSTRACT

Douglas-fir is the most important plantation softwood after radiata pine in New Zealand and has wood properties well suited for structural purposes. Recent work has indicated that there is good genetic variation available for improving stiffness in Douglas-fir in New Zealand. Good variation in density has been shown within provenances across a number of sites and recent studies in Oregon have shown that sonic velocity and MoE are highly heritable, and have low genotype × environment interaction.

A selection index was constructed in 2006 using the heritability estimates obtained in Oregon as a guide. The index constructed assumed a heritability for sonic velocity in New Zealand of 0.45. This study was initiated to validate this number.

The Douglas-fir '871' and '869' series trial at Whakarewarewa was assessed in 2006 for sonic velocity using the IML hammer. This data was analysed, along with a recent branch size score, and diameter at breast height from ages 16 and 32. Heritability and genotypic and phenotypic correlations were estimated for all these traits.

Sonic velocity was found to be moderately heritable (0.51±0.12) at Whakarewarewa. However, no knowledge is available on the extent of genotype × environment (g×e) interaction for this trait. Indications from MoE and sonic velocity across-site correlations in Oregon are that g×e is likely to be small. An additional study of sonic velocity at one more site to determine g×e has been approved for next financial year. At this stage, the heritability estimate used in the selection index for Douglas-fir by Knowles and Lee (2006) of 0.45 appears reasonable

Diameter was found to be moderately heritable for all ages analysed and moderately negatively correlated with sonic velocity. Correlations estimates therefore indicate that selection for sonic velocity will reduce the diameter in Douglas-fir considerably at this site. Care will need to be taken in selection for sonic velocity to ensure the diameter growth is not compromised in future generations.

Branch size was not very heritable (0.20±0.07) and was positively correlated with growth.

Gains estimated using a selection index for the top-ranked family indicated that a gain of 15.4% DBH and 5.9% in sonic velocity was possible over the trial average. When the top 10 families were selected, this reduced to 14.5% and 2.6% respectively. When the top 20 families were selected, gains reduced further to 12.5% and 1.7% respectively. The intensive selection for higher wood density of the '871' series resulted in gains in sonic velocity of 1.8% over the '869' series.

HOW HERITABLE IS SONIC VELOCITY IN DOUGLAS FIR?

INTRODUCTION

Douglas-fir is the most important plantation softwood after radiata pine in New Zealand (Shelbourne and Low 2004) and has wood properties well suited for structural purposes (Knowles et al. 2004). It is expected that improving the species for wood properties will improve the utilisation and price differential of this species even further.

Work in the last ten years has shown that there is potential for genetic variation and genetic improvement of stiffness in Douglas-fir. Lausberg et al (1997) showed that good variation in density exists within provenances (between trees) rather than between provenances. In addition, Knowles et al. (2003) studied variation in wood stiffness and determined that most of the variation was between individual trees (Knowles et al. 2003, Knowles et al. 2004). Knowles et al. (2004) determined that the IML hammer (Anon 2001) gave relatively cheap and reasonably accurate methods for selection in Douglas-fir in two different stands in New Zealand.

Knowles and Lee (2006) constructed a New Zealand Douglas-fir selection index (SI) based on growth (diameter at breast height, DBH) and sonic velocity: SI = (DBH*0.3)*(BH velocity^2*0.45). This index was based on the assumption that the heritability of DBH was around 0.3, which had previously been found to be around this level at some sites (0.14-0.38, Low 1997). The heritability (0.45) estimated for sonic velocity was a conservative one based on experience from Johnson and Gartner (2006), where heritability estimated across four sites ranged between 0.32 and 1.0, with an average of 0.53. This heritability used for the index was, however an estimate only. The next step is therefore to determine the heritability for sonic velocity in New Zealand to ensure the selection index is optimal. The primary aim of this project was to determine the heritability of sonic velocity in Douglas-fir in New Zealand.

In 2006 the IML hammer was used to assess the sonic velocity of the '869'- and '871'-series progeny trial at Whakarewarewa at age 34. Branch size (a subjective score) and diameter at breast height (DBH) were also measured at age 32. This report analyses these traits to determine their heritability, and compares them to previous growth measurements.

MATERIALS AND METHODS

Study material

The trial series tests open-pollinated progeny from 118 'plus trees' from the 869 series, selected originally from parents in Kaingaroa and Whakarewarewa forests in the Central North Island, most likely from the Washington Coastal provenance (Shelbourne 1988). In addition, there were 48 parents known as the '871' series, selected originally in Kaingaroa forest, with all the same selection criteria as the '869' series, but with the addition of high wood density. The 48 parents were selected from a total of 305 candidate trees (Vincent and Birt 1971). An anomaly of this trial is that the 869 series was planted in 1972, leaving gaps for the 871 series, which was planted in 1973. There were originally 5 trial sites, planted at 1666 stems per hectare (spha) of which Naseby was later abandoned due to mortality caused by frost. The other trials are listed and described in Table 1.

Table 1. Extant trials from the progeny tests used in this report. denigrated

Trial name	**Trial code**	**Latitude**	**Longitude**	**Comments**
Golden Downs Cpt 64	NN256	41°30.5’	172°54.3	Sheltered site with initial infestation by gorse, thinned 1992 to 300 stems per ha
Rankleburn Cpt 509	SD245	45°59.5’	169°23.9’	Some damage from exposure, thinned 1992 to 700 stems per ha
Waimihia Cpt 784	RO908/2	38°51’	176°8.1’	Damaged by frost 1974, thinned 1992 to 300 stems per ha
Whakarewarewa Cpt 21	RO1014	38°12.7’	176°16.5’	Initial heavy bracken growth, thinned 1987 to 300 stems per ha

The trial design was sets in replicates, with 8 replicates in total. Within sets, progeny were assigned to 6-tree row plots. Each rep/set comprised 2 columns of 10 plots. Sets 1-5 contained progenies 869-200 – 869-335 planted in 1972. Sets 9-11 contained progenies 871-401 – 871-451 planted in 1973. Progeny details are as follows (Shelbourne 1988):

- 869.200-335 open-pollinated progeny of trees selected in several compartments in Kaingaroa and Whakarewarewa.
- 871.401-451 open-pollinated progeny of trees selected within high wood density populations in Cpts. 1128, 1101, 1103 and themselves selected for high wood density.

Controls used were:

- 395 – FRI 69/1914 Cpt 1154 Kaingaroa (unselected trees equivalent to the ‘869’ series).
- 396 – FRI 69/1917 Cpt 737 Kaingaroa (unselected trees equivalent to the ‘869’ series).
- 498 – Unselected trees from Cpt. 1103, equivalent to the ‘871’ series but unselected.
- 499 – R69/839 Kaingaroa bulk seed collection
- Californian check lot 744: H0 70/744 Swanton, California.

Measurements

The trial at Whakarewarewa was last measured in 2006 at an age of 34 years. The traits measured and analysed in this report are given in Table 2. Branch size was measured as a subjective 1-5 scale relating to the diameter of branches, from small (1) to large (5) and roughly equating to centimetres in branch diameter. Sonic velocity was measured using IML at breast height (Anon 2001).

Table 2. Traits measured at Whakarewarewa.

Trait	**Measurement ages**
DBH	16, 32
Branch size	32
Sonic velocity	34

ANALYSIS

Descriptive analyses

All controls were excluded for the genetic analysis and estimation of variation. Controls were incorporated for the estimation of IML breeding values, based on the previously estimated variance components.

All traits were analysed for normality using PROC Univariate in SAS, based on the Kolmogorov-Smirnov test, for sample sizes larger than 2000 and Shapiro-Wilk test for those samples less than 2000 (SAS Institute 1990).

Series was found to be significant for DBH at age 16, DBH at age 32, branch size at age 32 and sonic velocity (P<0.001, using PROC GLM (SAS Institute 1990) using the following model:

$$y = \mu + R + SER + F(SER) + RSER + RF + e \quad [1]$$

Where y represents individual observations on trees, μ is the site mean, R is the effect of the replicate, SER is series (either 869 or 871), F(SER) is the effect of family within series, RSER is the interaction between replicate and series, RF is the interaction between family and replicate and e is the residual.

The effect of sets was tested using PROC GLM and the following model:

$$y = \mu + R + SER + SET(SER) + e \quad [1]$$

Where y represents individual observations on trees, μ is the site mean, R is the effect of the replicate, SER is the effect of series SET(SER) is the effect of set within series and e is the residual.

Sets were significant for all traits except for branch size at age 32. Sets were therefore left in the model for all remaining analyses.

Table 3. Tests for normality for individual traits at Whakarewarewa. Tests were based on the Kolmogorov-Smirnov (KS) test for sample sizes larger than 2000 and Shapiro-Wilk test for those samples less than 2000 (SW).

Trait	Age	Normality	Test for normality P value
DBH	16	OK	>0.15 (KS)
	32	OK	0.43 (SW)
Branch size	32	Not normal	<0.001 (SW)
Sonic velocity	34	OK	0.05 (SW)

All descriptive statistics (means, minimums, maximums, coefficients of variation), were estimated using the MEANS Procedure in SAS (SAS Institute 1990).

Genetic analyses

Genetic variances, heritabilities and genetic correlations were estimated in ASREML (Gilmour et al. 2002) using model [2] for DBH and form score at age 17.

$$y = \mu + R + Ser + S(Ser) + R*S(Ser) + F(S(Ser) + e \qquad [3]$$

Where y represents individual observations on trees, μ is the site mean, R is the effect of the replicate, Ser is the effect of series, S(Ser) is the effect of the set within series, R*S(Ser) is the interaction between replicate and sets within series, F(S(Ser) is the effect of families within sets within series and e is the residual variance. The replicate and series effect were considered fixed. All other effects were considered random. For the estimation of breeding values, the female within sets within series was replaced with a female within series term.

Genetic correlations ($r_{G_{ab}}$) between traits were estimated using pair-wise sums of traits and [4]

$$r_{G_{ab}} = \frac{(\sigma^2_{a+b} - \sigma^2_a - \sigma^2_b)/2}{\sqrt{\sigma^2_a \sigma^2_b}} \qquad [4]$$

where σ^2_{a+b}, σ^2_a and σ^2_b represented the additive or phenotypic variance components estimated by fitting model [3] above using ASREML as above for traits a+b, a and b respectively. This method of estimation is described in detail in Steele and Torrie (1960) p 78, Falconer and Mackay (1996) and Williams et al. (2002).

RESULTS AND DISCUSSION

Basic statistics

Means, maximums, minimums, number of observations and the coefficient of variation (CV) estimated for controls only are given in Table 4 and statistics estimated across families and series, excluding controls in Table 5. Basic statistics estimated for individual series are given in Table 6.

Diameter at breast height was lower in the control seedlots at both 16 and 32 years-of-age (Table 4) when compared with all other material in the trial (Table 5, e.g at age 32: 347.85 versus 355.10 respectively). DBH was substantially lower in the '871' series than the '869' series (336.67 and 365.29 DBH at age 32 respectively, Table 6). There was little difference in the basic statistics for branch score (controls 3.50 versus all other material 3.45) or sonic velocity (3426 controls versus 34.5 all other material). Sonic velocity was higher in the '871' (3437) series when compared with the '869' series (3375, Table 6). Branch size was, however, reasonably consistent between the series (Table 6: '869' 3.49, '871' 3.39).

Table 4. Basic statistics for diameter at breast height (DBH), branch score (1-5) and sonic velocity at Whakarewarewa for control seedlots.

Variable	Age	Mean	Std Err	Maximum	Minimum	CV	N
DBH	16	144.52	1.25	266	62	23.50	739
DBH	32	347.85	5.16	585	173	20.60	193
Branch score	32	3.50	0.06	5	2	25.15	192
Sonic velocity	34	3426	17	3918	2871	5.67	118

Table 5. Basic statistics for diameter at breast height (DBH), branch score (1-5) and sonic velocity at Whakarewarewa for all material in the trial across series and families excluding control seedlots.

Variable	Age	Mean	Std err	Maximum	Minimum	CV	N
DBH	16	149.13	0.48	277	57	23.45	5259
DBH	32	355.10	1.88	570	161	19.64	1379
Branch score	32	3.45	0.02	5	1	25.59	1378
Sonic velocity	34	3405	7.55	4015	2746	6.28	802

Table 6. Basic statistics for diameter at breast height (DBH), branch score (1-5) and sonic velocity at Whakarewarewa for the separate selection series '869' and '871'. The probability value is given for a difference between series, as tested in ANOVA using GLM. (See page 5).

Variable	Age	Mean	Std err	Maximum	Minimum	CV	N	P test
Series 869								
DBH	16	158.72	0.58	277	60	21.65	3458	<0.001
DBH	32	365.29	2.30	570	192	18.80	888	<0.001
Branch score	32	3.49	0.03	5	1	24.88	887	0.042
Sonic velocity	34	3375	10.35	4015	2746	6.23	413	<0.001
Series 871								
DBH	16	130.73	0.66	231	57	21.49	1801	
DBH	32	336.67	3.06	505	161	20.17	491	
Branch score	32	3.39	0.04	5	1	26.82	491	
Sonic velocity	34	3437	10.83	3998	2788	6.21	389	

*DBH 23 measured only for one series.

Genetic parameters

Variance estimates and individual narrow-sense heritability estimates are given in Table 7. Heritability (h^2) estimates were moderate for diameter at all ages (DBH, 0.38-0.57, Table 7). These estimates are comparable with those given in Low (1997) using SAS (SAS Institute 1990) for the same data at Whakarewarewa: DBH at age 16 0.38 and DBH at age 23 of 0.50.

The heritability estimate for branch size at age 32 was low (0.20±0.07). Although this was not scored directly in previous measurements, the heritability is in the lower end of the range for some other branching traits measured at age 23 and presented in Low (1997): branch angle 0.05 (branch angle score 1 = steep to 9 = flat or drooping), branch size score 0.29 (BRT, branch size score, 1 = large branches to 9 = extremely small branches) and branching category 0.29 (BRY, 1 = uninodal, 2 = bi-nodal, 3 = multimodal).

The heritability estimate for sonic velocity was 0.51±0.12. This is compatible with the previous 'estimate' of heritability of sonic velocity of 0.45 (see Knowles and Lee 2006). This estimate is also comparable with the across-site estimate of 0.53 from Johnson and Gartner (2006) in Oregon.

Table 7. Variance component estimates and individual narrow-sense heritability estimates (h^2) and their approximate standard errors for individual traits at Whakarewarewa.

Trait	Age	Phenotypic	Additive	Sets within series	Replicate × set within series	error	h^2	se
DBH	16	1052	401.8	0.00	43.11	908	0.38	0.05
DBH	32	4697	2680	87.39	96.59	3843	0.57	0.16
Branch size	32	0.77	0.15	0.00	0.04	0.69	0.20	0.07
Sonic velocity	34	43470	22200	264.7	47210	32720	0.51	0.12

Genetic and phenotypic correlations between traits are presented in Table 8. Sonic velocity was moderately-to-strongly negatively correlated with diameter at all ages, at both the genetic and phenotypic levels. Branch size was positively correlated phenotypically and genetically with DBH at all ages.

Genetic correlations between different diameter measurements (16 and 32) were strong and positive (0.84, Table 8). The phenotypic correlation estimate was moderate and positive and slightly lower than the equivalent genetic correlation (0.55, Table 8).

Genetic and phenotypic correlations between branch size and sonic velocity were moderate-to-low and negative. This correlation indicates that larger branch sizes lead to lower sonic velocities. The correlation may be an artefact of how sonic velocity is measured; with larger branches, a clear section for the measurement using the IML tool may be difficult to find, thus introducing more area (i.e. the branches themselves) and reducing the speed of the wave. However, this is purely speculative.

These correlations show that selection for sonic velocity will most likely reduce the diameter in Douglas-fir. Care will need to be taken in selection for sonic velocity to ensure the diameter growth of the crop is not considerably reduced.

Table 8. Genotypic (below diagonal) and phenotypic (above diagonal) correlation estimates for individual traits at Whakarewarewa.

Trait	Age	DBH	DBH	Branch size	Sonic velocity
		16	32	32	34
DBH	16	**1**	0.51	0.26	-0.31
DBH	32	0.84	**1**	0.55	-0.36
Branch size	32	0.62	0.32	**1**	-0.21
Sonic velocity	34	-0.50	-0.64	-0.30	**1**

The genetic parameter estimates are comparable with other previous estimates for growth, but this is the first heritability estimate for sonic velocity in Douglas-fir in New Zealand. The estimate is only from a single site and does not take into account any genotype × environment (g×e) interaction which may or may not exist for this trait. Only measuring other sites and estimating genetic correlations between sites will give an indication of the extent of the gxe interaction.

However, Lausberg (1997) showed that there was very little density gradient for Douglas-fir across a range of sites. This is an indication that g×e may not be important, as density is an important component of stiffness in this species. Johnson and Gartner (2006) also estimated a genetic correlation across sites for MoE of 0.79, and for sonic velocity of 0.85. This is a further indication that g×e for sonic velocity is likely to be low in New Zealand. However, only further studies will give a more accurate picture of g×e in this country. The cost of these further studies will need to be balanced with the need for understanding the genetics of this species.

Gains and breeding values

Breeding values were estimated for both diameter and stiffness (Appendix 1). An index was estimated (see methods) and the seedlots and families were then ranked according to this index.

Gains were estimated for Douglas-fir at this site based on the breeding values estimated. Gains were predicted using the trial mean or over the seedlot 69/839 as the 'unimproved' baseline.

All families showed no gain in stiffness, but an average 6.7% gain in diameter over the 69/839 control (Table 9). When the top family, (when ranked by the index), was compared with the trial average, a gain in diameter of 15.4% and a gain of 5.9% in sonic velocity was predicted (Table 9). When the top 10 families were selected, the predicted gain in diameter dropped to 14.5%, and the gain in sonic velocity to 2.6% when compared with trial averages. When the top 20 families were selected, the diameter gain was still 12.5%, but the gain in sonic velocity dropped to 1.7% (Table 9).

Using the selection index calculated, only one '871' family appeared in the top 10 families and only three '871' families appeared in the top 20.

This ranking was undertaken across two selection series, '869' and '871'. However, in reality, the '871' series was planted one year later than the '869' series and this is likely to have affected trait performance comparisons between series. These breeding values should be used with caution.

The selection index used was also based on giving sonic velocity and DBH a roughly equal weighting. This was not based on any economic weighting. Decisions are needed as to the economic importance of DBH versus stiffness in order to maximise the gains required from the selections. More research is likely to be needed to determine this.

The intensive selection for higher wood density of the '871' series resulted in gains in sonic velocity of 1.8% over the '869' series. Selection for wood density has had some effect on the population mean for sonic velocity. However, direct selection for stiffness is likely to give better results.

Table 9. Gains in stiffness and diameter for family or seedlot groups, Whakarewarewa Douglas-fir progeny trial.

Seedlot	description	Diameter		Stiffness	
		Dbh in mm	% gain	Velocity m/sec	% gain
72/744	Santa Cruz	345	-1.4	3489	0
69/839	Kaingaroa bulk collection	328	-6.7	3450	-1.4
	Average of families	350	0	3498	0
869.212	Top family on index	404	15.4	3703	5.9
	Top 10 families on index	401	14.5	3589	2.6
	Top 20 families on index	394	12.5	3559	1.7

CONCLUSIONS

- Sonic velocity is moderately heritable (0.51±0.12) at Whakarewarewa.
- No knowledge of genotype × environment interaction is available for Douglas-fir in New Zealand.
- It is planned to validate this heritability at one more site during 2007-08, in the same trial series in order to allow the across-site genotype × environment interaction to be estimated. The site will be one of the following:
    - Rankelburn (Cpt. 509, ST245)
    - Golden Downs (Cpt. 64, NN256)
    - Waimihia (Cpt. 784 Kaingaroa, RO908/2)
- Although previous studies indicate that g×e may not be very large, it is important to determine their magnitude to allow for confidence in breeding and deployment of Douglas-fir across a wide range of site types.
- At this stage, the heritability estimate proposed and used in the selection index for Douglas-fir by Knowles and Lee (2006) of 0.45 appears reasonable.
- Diameter is moderately heritable, as has been found previously, and is well correlated between the measurements at different ages at this site.
- Branch size is not very heritable and is positively correlated with growth. Correlations between branch size and sonic velocity were not strong, but were still positive, indicating that sonic velocity may increase with increasing branch size.
- Correlations estimates here show that selection for sonic velocity will reduce the diameter in Douglas-fir considerably at this site. Care will need to be taken in selection for sonic velocity to ensure the diameter growth is not compromised in future generations.
- Gains estimated using a selection index for the top-ranked family indicated that a gain of 15.4% DBH and 5.9% in sonic velocity was possible over the trial average. When the top 10 families were selected, this reduced to 14.5% and 2.6% respectively. When the top 20 families were selected, gains reduced further to 12.5% and 1.7% respectively.
- The intensive selection for higher wood density of the '871' series resulted in gains in sonic velocity of 1.8% over the '869' series.

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APPENDIX 1: FAMILY BREEDING VALUES FOR DBH, BRANCH SCORE AND SONIC VELOCITY WHAKAREWAREWA.

The index was built using the heritabilities and standard deviations for sonic velocity at age 34 (vel34) and diameter at breast height at age 32 (DBH32):
Index = $((bv_{sonic}\text{- site mean}_{sonic})/s.d_{sonic})*h^2_{sonic} + ((bv_{dbh}\text{- site mean}_{dbh})/s.d_{dbh})*h^2_{dbh}$

Heritability and standard deviations used for sonic velocity – 0.51 and 213.8
Heritability and standard deviations used for DBH (age 32) – 0.57 and 69.8

Series	Clone	DBH 32	Branch score 32	Sonic velocity 34	Index
869	**212**	403.8	3.94	3703	0.9872
869	**267**	368.1	3.97	3754	0.8173
871	**447**	396.9	3.99	3634	0.7666
869	**319**	433.2	4.11	3503	0.7520
869	**295**	401.4	4.09	3579	0.6739
869	**290**	356.9	3.95	3719	0.6424
869	**300**	432.6	4.01	3439	0.5946
869	**312**	422.2	4.01	3466	0.5722
869	**293**	381.4	3.97	3601	0.5605
869	**313**	412.3	3.95	3494	0.5580
869	**318**	397.8	4.11	3525	0.5144
869	**247**	345.7	3.91	3701	0.5082
869	**323**	401.0	3.96	3500	0.4817
871	**405**	410.0	4.05	3443	0.4178
869	**304**	419.3	4.03	3410	0.4171
869	**299**	401.1	4.08	3472	0.4144
869	**250**	365.9	3.97	3590	0.4089
869	**308**	375.7	3.90	3556	0.4077
871	**416**	368.5	3.92	3576	0.3962
869	**294**	383.1	4.01	3521	0.3839
869	**314**	347.5	3.82	3643	0.3837
869	**243**	353.5	3.86	3620	0.3789
871	**429**	368.8	3.94	3566	0.3760
871	**408**	346.3	3.93	3622	0.3262
871	**443**	379.7	4.01	3505	0.3188
871	**442**	405.6	4.16	3410	0.3042
871	**411**	326.2	3.89	3668	0.2710
871	**427**	383.2	4.02	3471	0.2654
871	**401**	357.9	3.95	3555	0.2613
871	**407**	357.5	3.93	3549	0.2421
869	**286**	356.1	3.87	3550	0.2337
871	**441**	356.3	3.74	3544	0.2203
869	**396**	335.9	4.02	3605	0.1993
869	**268**	350.7	3.82	3553	0.1967
869	**328**	366.4	4.00	3499	0.1959
869	**241**	370.5	4.00	3481	0.1854
869	**291**	342.5	3.94	3572	0.1753
871	**438**	353.3	4.02	3535	0.1745
869	**333**	379.4	4.02	3445	0.1728
869	**281**	366.9	3.96	3487	0.1717

869	**234**	283.0	3.91	3773	0.1673
871	**434**	372.3	3.96	3465	0.1638
871	**410**	343.5	3.91	3563	0.1613
869	**316**	400.9	4.06	3360	0.1454
869	**274**	329.6	3.88	3603	0.1426
869	**288**	368.7	3.88	3468	0.1399
869	**324**	390.8	4.04	3389	0.1338
869	**310**	378.4	3.98	3430	0.1290
869	**327**	380.8	3.84	3419	0.1233
869	**297**	361.4	4.02	3484	0.1196
869	**255**	354.5	3.85	3502	0.1052
871	**414**	348.3	4.10	3514	0.0838
871	**428**	338.5	3.91	3545	0.0788
871	**451**	370.0	4.07	3437	0.0776
871	**403**	354.4	3.99	3490	0.0758
871	**406**	382.0	3.98	3393	0.0712
869	**292**	349.0	3.93	3506	0.0704
869	**311**	354.9	4.07	3485	0.0684
869	**395**	361.2	3.92	3458	0.0567
871	**424**	308.3	3.72	3639	0.0561
871	**426**	345.0	4.01	3513	0.0550
871	**430**	348.0	3.90	3502	0.0545
869	**236**	328.1	3.87	3571	0.0542
871	**436**	336.5	4.05	3541	0.0513
871	**445**	364.2	3.96	3439	0.0363
869	**200**	328.2	3.95	3563	0.0354
869	**258**	325.8	3.91	3568	0.0295
869	**331**	393.8	4.00	3335	0.0277
869	**302**	388.5	3.94	3348	0.0174
869	**296**	336.6	4.02	3520	0.0028
744	**744**	345.3	3.93	3489	0.0000
871	**440**	346.9	3.95	3478	-0.0126
871	**498**	329.8	3.98	3537	-0.0133
869	**276**	286.3	3.89	3685	-0.0148
871	**435**	331.3	4.14	3527	-0.0228
869	**240**	309.9	3.76	3600	-0.0236
871	**431**	401.9	4.02	3285	-0.0241
871	**423**	342.8	3.97	3482	-0.0359
869	**280**	343.2	3.90	3473	-0.0563
869	**270**	311.5	3.91	3581	-0.0564
871	**422**	384.0	4.00	3328	-0.0676
869	**301**	355.1	4.09	3421	-0.0812
869	**279**	310.9	3.94	3573	-0.0817
869	**251**	333.2	3.77	3492	-0.0928
871	**413**	305.8	3.88	3584	-0.0961
871	**409**	315.6	3.78	3541	-0.1182
869	**257**	316.6	3.92	3536	-0.1232
869	**213**	331.2	3.86	3484	-0.1266
869	**277**	353.9	3.93	3404	-0.1320
869	**264**	268.8	3.77	3686	-0.1544
871	**402**	322.4	3.91	3498	-0.1649
869	**325**	356.3	3.76	3381	-0.1684

869	**307**	375.9	3.98	3313	-0.1692
869	**263**	307.2	3.90	3546	-0.1755
869	**305**	357.6	4.01	3372	-0.1795
869	**329**	341.1	3.90	3426	-0.1840
871	**417**	354.6	3.87	3376	-0.1924
871	**432**	320.3	3.96	3491	-0.1983
869	**282**	311.7	3.86	3519	-0.2018
869	**321**	354.4	4.13	3371	-0.2063
871	**437**	342.3	3.84	3412	-0.2076
869	**322**	338.7	3.85	3423	-0.2114
869	**239**	318.1	3.85	3486	-0.2288
871	**499**	328.2	3.87	3450	-0.2327
869	**326**	387.7	3.91	3242	-0.2428
871	**415**	311.8	3.88	3501	-0.2446
869	**249**	334.0	3.92	3423	-0.2489
871	**404**	337.6	3.80	3408	-0.2549
869	**273**	317.2	3.95	3463	-0.2908
871	**433**	340.7	3.80	3365	-0.3337
871	**419**	308.8	3.88	3470	-0.3422
871	**420**	303.0	3.72	3487	-0.3505
871	**439**	375.3	3.98	3221	-0.3950
869	**269**	300.7	3.98	3472	-0.4050
871	**418**	265.9	3.73	3588	-0.4129
871	**425**	297.6	3.89	3477	-0.4173
869	**287**	294.4	3.88	3484	-0.4270
869	**315**	323.0	3.86	3385	-0.4305
869	**262**	289.9	3.86	3489	-0.4521
869	**265**	287.0	3.97	3468	-0.5269
871	**421**	265.4	3.86	3519	-0.5822
871	**412**	321.3	4.01	3326	-0.5858
869	**261**	291.9	3.77	.	.
869	**260**	288.5	3.75	.	.
869	**248**	321.9	3.89	.	.
869	**245**	332.3	3.90	.	.
869	**238**	298.6	4.00	.	.
869	**235**	347.6	3.89	.	.
869	**233**	291.6	3.89	.	.
869	**232**	332.7	3.92	.	.
869	**229**	266.0	3.80	.	.
869	**225**	375.9	4.00	.	.
869	**215**	294.7	3.86	.	.
869	**211**	292.3	3.91	.	.
869	**210**	341.7	4.06	.	.
869	**209**	311.7	4.00	.	.
869	**207**	338.6	4.06	.	.
869	**206**	295.8	3.83	.	.
869	**202**	273.0	3.85	.	.
869	**201**	327.5	3.96	.	.