A Time and a Place for Everything: Phylogenetic history and geography as joint predictors of oak plastome phylogeny

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A Time and a Place for Everything:**Phylogenetic history and geography as joint predictors of oak plastome phylogeny**

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Abstract

Due to high rates of introgressive hybridization, the plastid genome is poorly suited to fine-scale DNA barcoding and phylogenetic studies of the oak genus (*Quercus*, Fagaceae). At the tips of the oak plastome phylogeny, recent gene migration and reticulation generally cause topology to reflect geographic structure, while deeper branches reflect lineage divergence. In this study, we quantify the simple and partial effects of geographic proximity and nucleome-inferred phylogenetic history on oak plastome phylogeny at different evolutionary scales. Our study compares pairwise phylogenetic distances based on complete plastome sequences, pairwise phylogenetic distances from nuclear restriction site-associated DNA sequences (RADseq), and pairwise geographic distances for 34 individuals of the white oak clade representing 24 North American and Eurasian species. Within the North American white oak clade alone, phylogenetic history has essentially no effect on plastome variation, while geography explains 11–21% of plastome phylogenetic variance. However, across multiple continents and clades, phylogeny predicts 30–41% of plastome variation, geography 3–41%. Tipwise attenuation of phylogenetic informativeness in the plastome means that in practical terms, plastome data has little use in solving phylogenetic questions, but can still be a useful barcoding / phylogenetic marker for resolving questions among major clades.

Keywords: gene flow, hybridization, partial Mantel test, plastome sequencing, restriction-site associated DNA (RADseq)

Introduction

Oaks have long been notorious among biologists for both high intraspecific morphological variation and low reproductive barriers (e.g. Wiegand 1935; Muller 1952; Burger 1975; Hardin 1975). Van Valen (1976) famously wrote, “It may well be that *Quercus macrocarpa* in Quebec exchanges many more genes with local *Q. bicolor* than it does with *Q. macrocarpa* in Texas” (Van Valen 1976: 235). Other studies have since confirmed that while oak species with overlapping ranges exchange alleles through introgressive hybridization (Whittemore & Schaal 1991; Cavender-Bares & Pahlisch 2009; Peñaloza-Ramírez et al. 2010), these events are rare relative to the rate of intraspecific gene flow (Muir et al. 2000; Hipp and Weber 2008; Cavender-Bares et al. 2009; Gerber et al. 2014). This asymmetry of rates helps to maintain species boundaries even in sympatry and the genetic coherence of oak species over large geographic ranges. It appears that high rates of intraspecific gene exchange ensure that introgressant alleles remain at low frequencies (Petit and Excoffier 2009), increasing their chance of loss through drift. Thus gene flow among conspecific populations counterbalances the homogenizing effect of hybridization in the oak nuclear genome, making nuclear DNA a reliable source of phylogenetic data (Eaton et al. 2015; Hipp 2015).

The plastid genome, long the workhorse of angiosperm phylogenetics (Chase et al. 1993; Ruhfel et al. 2014; Shaw et al. 2014 and references therein), is haploid and non-recombinant, and it has a smaller effective population size than nuclear alleles. These factors increase the rate of fixation of haplotypes within populations and species via drift. Moreover, maternally inherited plastids typically have lower rates of among-population migration, reducing their effectiveness in maintaining species cohesion (Petit and Excoffier 2009). For these reasons, the plastome often tracks patterns of geographically structured interspecific gene flow that dominates in lineages at

recent phylogenetic scales (e.g. Rieseberg and Soltis 1991; Rieseberg et al. 1991; Whittemore and Schaal 1991; Sang et al. 1997; Petit and Excoffier 2009) and can reveal evidence of hybridization history at even deep phylogenetic scales (Folk et al. 2016). These and related studies demonstrate that while phylogeny frequently tracks geography at broad scales, localized interspecific gene flow is often detectable at finer scales through conflict between plastomic and genomic phylogenies. Forest trees in particular frequently demonstrate plastome divergence patterns that conflict with known lineage divergence history (phylogeny), reflecting either the sorting of plastome lineages in large populations across large geographic regions or contemporary hybridization among interfertile species (Hamzeh and Dayanandan 2004; Shaw et al. 2012). Numerous studies of oaks have demonstrated that plastome haplotypes are shared freely among species of the same section, and that these haplotypes tend to cluster by geography instead of population divergence history or phylogenetic relationships (Whittemore and Schaal 1991; Petit et al 1993; Dumolin-Lapegue 1997; Simeone et al. 2016). At deeper phylogenetic scales, however, the plastome appears to track the monophyly of species within the major oak clades, whereas nuclear data provide evidence for higher order relationships among those clades (Manos et al. 1999; Oh and Manos 2008). The plastome may be thought of as complementary to the nuclear genome in oaks (Manos et al. 1999), providing resolution for ambiguous nuclear relationships near the base of the clade while reconstructing patterns of contemporary interspecific gene flow and introgression. The latter may be more weakly captured in the nuclear genome, where recombining loci differentially track segregation of ancestral alleles, population divergence, and ongoing gene flow (Via and West 2008).

Phylogeny and gene flow are typically considered separate targets of inquiry: studies investigating phylogeny generally treat gene flow as a nuisance factor, while studies of gene

flow frequently ignore the contribution of phylogenetic history to variation observed in their molecular genetic datasets. Our study presents a novel approach to estimating the relative contributions of both phylogenetic signal and geographic proximity (a covariate of local gene flow) to patterns of oak plastome variation at different phylogenetic levels. We use whole plastome assemblies, nuclear restriction site-associated DNA sequencing (RADseq) data, and geographic source information to examine the joint and partial effects of population divergence history and local gene flow on the plastome phylogeny in white oaks (*Quercus* L. section *Quercus*) and intermediate oaks (*Quercus* section *Protobalanus* (Trelease) A.Camus).

Materials and methods

Sampling

43 RADseq and 45 plastome samples were drawn from the distribution of white and intermediate oaks (sections *Quercus* and *Protobalanus* respectively) across North America to detect phylogeographic structure at a continental scale; 33 of these samples overlapped between datasets. Three Eurasian white oak species (*Quercus mongolica* Fisch. ex Ledeb.; *Q. petraea* (Mattuschka) Libel.; *Q. robur* L.) were included for both datasets to assess geographic and phylogenetic structure between North America and Eurasia based on RADseq and plastome data. An additional 51 white oak samples focused predominantly on four Eurasian white oak species (the three aforementioned, plus *Q. dentata* Thunb.) were also surveyed for plastome variation to more exhaustively assess plastome phylogenetic and geographically-structured genetic variation among North American, European, and Asian white oaks. The total number of plastome sequences reported here is 91. A previously published red oak plastid genome (*Quercus rubra*

L.; NCBI NC_020152) was included as an outgroup, and one RADseq sample from a different individual was added as the RADseq outgroup. Thus the total number of RADseq samples presented in this paper is 47. Geographic coordinates (latitude and longitude) were collected for source trees using a GPS.

Restriction-site associated DNA sequencing

RADseq DNA extraction, library preparation, and sequencing were conducted as presented previously by ALH and colleagues (Hipp et al. 2014; Eaton et al. 2015; Cavender-Bares et al. 2015). Briefly, DNA for all RADseq samples was extracted from fresh or frozen material using the DNeasy plant extraction protocol (DNeasy, Qiagen, Valencia, CA). DNA extractions were gel-quantified in agarose by visual comparison with the New England BioLabs 100 bp DNA Ladder (NEB, Ipswich, MA). Extraction concentrations ranged from 5–10 ng DNA / μ l extraction. RAD sequencing library preparation was conducted at Floragenex, Inc. (Portland, OR, USA) following the methods of Baird et al. (2008) with *Pst*I. RAD libraries were barcoded by individual and multiplexed on an Illumina Genome Analyzer IIx. Sequencing reads were 100 bp in length; after removal of the barcode and recognition sequence, analyzed sequences were 85 bp long. Quality, read lengths, and base composition of FASTQ data were assessed in R v. 3.3.1 (“Bug in your hair”; R Core Team 2016) using the ShortRead package (Morgan et al. 2009).

RADseq clustering

Data were analyzed using the PyRAD pipeline (Eaton 2014; www.dereneaton.com/software). In this pipeline, sequences were clustered first by individual, and highly similar sequences are clustered into “stacks.” In pyRAD, these stacks were generated using VSEARCH (Rognes et al. 2016), which allows sequences within clusters to vary in indels, nucleotide polymorphisms, and sequencing strand (direction). After clustering, heterozygosity

and sequencing error were jointly estimated from the base counts observed across all sequences, sites, and clusters using the likelihood equation of Lynch (2008). Heterozygotes were inferred by a binomial probability based on these parameters. Bases that could not be assigned with $\geq 95\%$ probability were treated as unknown (*N*). Any locus possessing more than 2 haplotypes within individuals after correcting for sequencing errors was discarded, under the assumption that it included one or more paralogous sequences. For each individual, each locus was summarized as a consensus sequence, and consensus sequences were clustered among individuals to generate a data matrix for each locus. Due to variation in sequencing coverage and mutation at the restriction site defining RAD loci, the resulting data matrix was not complete for all loci in all individuals. The following parameters were specified for pyRAD: Minimum depth of reads per within-sample cluster: 6; maximum number of sites in a read which can have a quality score of less than twenty: 4; clustering threshold (percent similarity): 0.85; minimum number of samples in each across-sample cluster: 4; maximum number of individuals with a shared heterozygous site in an across-sample cluster: 3. All other settings used default values.

RADseq data matrix

After clustering, consensus sequences of resulting RADseq loci were produced in R (R Core Team 2016) using the RADami package (Hipp 2014) and mapped to a complete *Quercus rubra* oak plastome using Bowtie2 (Langmead and Salzberg 2012) with default settings. Loci with a positive match to the plastome were removed using RADami. Samples of the western North American *Q. gambelii* Nutt. were initially included, but preliminary analyses of the dataset demonstrated that *Q. gambelii* samples in combination with *Q. macrocarpa* Michx. destabilize the white oak RADseq phylogeny, suggesting a complex genomic composition that could be the product of hybridization and that is beyond the scope of the current paper. This issue is

addressed in a separate paper in this volume (McVay et al., current issue), but in brief, inclusion of *Q. gambelii* has the effect of pulling *Q. lobata* Née toward *Q. macrocarpa* and relatives, at odds with all nuclear data. Samples of *Q. gambelii* were therefore removed from the RADseq dataset for final analyses. RADseq loci were subsetted for alternative analyses presented below and concatenated for analysis in RAxML (Stamatakis 2014) using RADami and exported as a FASTA file. Concatenation order was the numerical sort order of the locus names, which are assigned arbitrarily during the clustering pipeline implemented in pyRAD.

Plastome sequencing and plastome assembly

Individual DNA aliquots (0.5–1 g) were sheared to a median length of ca. 300 bp and converted into individually indexed sequencing libraries using Illumina TruSeq v.2 kits at the USDA Forest Service (Corvallis, OR, USA), as described in Schroeder et al. (2016). Briefly, sequencing was performed using: the Illumina MiSeq with 2×150 bp paired-end reads to produce individual *de novo* genome reference assemblies for representative North American, European and Asian species (*Quercus alba*, *Q. petraea* and *Q. mongolica* respectively); and the Illumina HiSeq with 100 bp single-end reads to sequence individual samples for reference-guided read mapping and genome assembly. All reactions used version 3 sequencing chemistry. Information on raw clusters, sequence yield, and approximate target sequence (plastid genome) coverage depth is provided in the supplements section (Supplement S2).

Plastome data matrix

Raw read quality filtering, *de novo* assembly, and reference guided assembly for these samples are described in Schroeder et al. (2016). Briefly, raw read quality filtering was

accomplished using Trimmomatic v0.30 (Bolger et al. 2014) to remove reads with a mean Phred score less than 33. Reference guided read mapping and plastome assembly were performed using CLC Genomics Workbench v. 7.5.1 (CLC-Bio; Aarhus, Denmark) and the 135,258 bp *Quercus mongolica* draft plastid genome reference (accession MOR360 / QUMO5_CH_1; Schroeder et al. 2016). This chloroplast genome reference contains only one of the two inverted repeat regions that are present red oak chloroplast genomes (Alexander and Woeste 2014), so our reference size (135.2 kb) is smaller than a complete oak chloroplast genome (~161 kb). Reads were mapped to the reference using a length fraction of 0.9, a similarity fraction of 0.94, a mismatch cost of 2, and insertion/deletion costs of 6. A minimum depth of 5 or greater was applied to call reference and non-reference bases; sites with a depth less than 5 were coded as N. Ingroup plastome assemblies were aligned in MAFFT v7.149b (Katoh and Standley 2013), using gap opening and extension penalties of 2.0 and 0.1, respectively. The ingroup matrix was aligned to the *Quercus rubra* outgroup using MAFFT profile-profile alignment. The resulting alignment was edited manually in Geneious version R8 (<http://www.geneious.com>, Kearse et al. 2012), primarily to remove large insertions present in the ingroup plastome alignment. The resulting alignment was processed in gblocks (Castresana 2000), using default parameters for DNA to remove positions where differences in the ingroup and outgroup sequences resulted in erroneous or ambiguous alignments. Ambiguous positions (Ns) were retained in alignments and analysis except where gblocks removed them. Unlike in the RADseq matrix, *Q. gambelii* was retained in the plastome matrix, as intragenomic recombination / genealogical discordance is not an issue in the plastome.

Phylogenetic analyses

Phylogenetic analyses were conducted under maximum likelihood using RAxML v. 8.2.4 on the RADseq and plastome alignments separately. Given the size and complexity of the

genomic data, we utilized the relatively parameter rich GTR+gamma model, under the GTRCAT approximation. For each dataset, bootstrap proportions were generated from 100 non-parametric bootstrap replicates and mapped to the internal branches of the ML tree. For computational reasons, we utilized fast bootstrapping (-f a option in RaxML) for all analyses presented in this paper. A comparison of fast bootstrapping with thorough bootstrapping (-b in RAxML) on the full plastome tree (Fig. 1) shows no systematic difference between bootstrapping methods (Supplement S1). Trees were rooted using *Quercus rubra* for both datasets.

Modeling the effect of geography and population divergence history on plastome phylogeny

The relative predictive power of phylogeny and geography on plastome similarity was estimated in R using the packages ape (Paradis et al. 2004) and phytools (Revell 2012) and the morton R library (<https://github.com/andrew-hipp/morton>). Cophenetic pairwise distances (branch length distances, estimated in RAxML according to the GTR+gamma nucleotide substitution model as described under *Phylogenetic Analyses* above) between all tips on a single tree were calculated for both the RADseq and plastome trees as our estimates of plastome pairwise dissimilarity (Δ_{plast}) and nuclear DNA pairwise dissimilarity (Δ_{nuc}). Latitude and longitude data for the samples were used to calculate the geographic distance between samples (Δ_{geog}) using the Haversine formula as implemented in the morton library. Multiple and partial correlation coefficients were estimated, with Mantel permutations to assess significance (Mantel 1967; Smouse et al. 1986; Diniz-Filho 2013), on the following regression models: plastome variation predicted by both gene flow and nuclear genetic variation ($\Delta_{\text{plast}} \sim \Delta_{\text{geog}} + \Delta_{\text{nuc}}$); plastome variation predicted by gene flow alone ($\Delta_{\text{plast}} \sim \Delta_{\text{geog}}$); plastome variation predicted by nuclear genetic variation alone ($\Delta_{\text{plast}} \sim \Delta_{\text{nuc}}$); and nuclear genetic variation predicted by gene flow alone ($\Delta_{\text{nuc}} \sim \Delta_{\text{geog}}$). Only the position of samples in the response matrix was permuted,

under the assumption that the prediction matrices were known without error (Smouse et al. 1986).

To assess how a dataset's phylogenetic depth affects the partial effects of lineage divergence history and gene flow on plastome variation, the dataset was pruned to several different phylogenetic levels and the Mantel tests described above were performed on each. The pruned datasets are: (1) **all oaks sampled** (N = 33 samples), in which trees are pruned to only tips shared between the RADseq and plastome trees. This dataset contains both Eurasian and North American oaks in sections *Quercus* (the white oaks) and *Protobalanus* (the intermediate oaks). It spans the widest geographic range and largest phylogenetic scale. (2) The **North American oaks** (N = 30 samples): excludes the Eurasian white oaks from all oaks sampled. This exclusion set allows us to test whether geographic signal in the plastome is amplified by studying populations separated an ocean. (3) The **North American white oaks** (N = 25 samples): excludes the intermediate oaks (section *Protobalanus*) from the North American oak dataset. This exclusion set allows us to examine the effects of removing a large source of phylogenetic signal in the plastome. While there is one North American white oak (*Q. engelmannii* Greene) that has been shown to harbor a *Protobalanus* plastome (Manos et al. 1999), there is no evidence of ongoing gene flow between these two, and we know of no other cases of interbreeding between white oaks and intermediate oaks. (4) The **North American oaks without California white oaks** (N = 21 samples): excludes California oaks from the North American oak dataset. The California white oaks excluding *Q. engelmannii* are a well defined clade (Sork et al. 2016) unlikely to exchange alleles with eastern North American oaks, making the California oaks another potential source of phylogenetic signal in the plastome. This exclusion set is analogous to the North American white oak dataset, *q.v.* The inclusion of the intermediate oaks but

exclusion of California oaks tests whether gene flow and phylogenetic signal is comparable with either of the two western North American clades present in our dataset. (5) The **eastern North American white oaks** (N = 19 samples): excludes the Californian oaks and a clade of derived Mexican and southwestern North American oaks (represented in our study by *Q. arizonica* Sarg., *Q. engelmannii*, *Q. vaseyana* Buckley, and *Q. mohriana* Buckley ex Rydb.) from the North American white oak dataset. This exclusion set is paraphyletic but concentrates the partial Mantel tests on just the potentially interbreeding eastern North American oaks, one that has been particularly challenging to oak systematists (e.g. Hardin 1975). All exclusion sets are summarized in Supplement S3.

Results

RADseq clustering and data matrix

RADseq sequencing runs produced 8.43×10^5 to 3.49×10^6 sequences per individual, with a mean of $2.16 \times 10^6 \pm 1.87 \times 10^6$ (s.d.). Sequencing quality averages nearly 40 (out of 40) across bases 1-60, with high quality averaged across all runs (mean quality score = 36.7 ± 0.536 s.d.). Including the outgroup *Quercus rubra*, the RADseq library comprises 48 individuals and 6.92×10^4 loci, spanning 80 to 118 bp, with an average length of $87.6 \text{ bp} \pm 2.90$ s.d. The number of loci returned for single individuals ranges from 1.81×10^4 to 3.58×10^4 , with a mean of $2.66 \times 10^4 \pm 4.07 \times 10^3$ s.d. The number of variable sites per locus averages 7.58 ± 5.62 s.d.

Seven loci (loci 508, 5924, 11871, 34638, 23273, 51846, 69261) mapped back to the *Quercus rubra* plastid reference genome and were omitted from locus concatenation. In the *Q. rubra* plastome utilized in this study, there are 13 *Pst*I cut sites, suggesting that closer to 26

RADseq loci ought to have mapped back to the genome. However, several of these are in the inverted repeat region and may as a consequence have been collapsed into loci. Alternatively, our mapping may have underestimated the number of loci mapping back to the plastome. At any rate, even without removal of these seven loci, the plastome is a negligible contributor to the RADseq dataset, which we safely treat as a nuclear dataset in this study. Two *Q. gambelii* individuals (accession numbers MOR-387 and MOR-546) were also omitted from concatenation (see discussion above). Not including the outgroup, the final data matrix contains 45 individuals belonging to 25 species, and 6.06×10^6 nucleotide positions.

Plastome data matrix

Individual shotgun sequencing used for plastome assembly produced between 2.46×10^6 to 18.33×10^6 reads per individual, yielding 109×10^6 to $1,765 \times 10^6$ bases (mean values: 8.17×10^6 reads and 763.5×10^6 bp per individual). Sequencing quality averaged $34.9 \pm 0.1.73$ (s.d.) for 101 bp reads. Reference-guided mapping to the *Quercus mongolica* draft plastid genome reference (MOR360) showed that an average of 3.47% of sequence reads could be mapped to the reference (range: 0.36% to 9.33%); this produced assemblies that averaged 204X depth and were nearly complete, with all sequences showing fewer than 350 N's (mean = 84). Assembly information can be found in the supplements section (S2). Alignment to the *Quercus rubra* reference plastid genome yielded a data matrix with 92 individuals, 26 species, and an overall length of 136,790 bp. Further refinement with gblocks removed 12,854 bp, resulting in a final matrix 132,936 bp in length. Alignments between white oaks (*Quercus* sect. *Quercus*) revealed 1852 ingroup variable sites across all genomes (including ambiguities), while adding members of *Quercus* sect. *Protobalanus* yielded an additional 306 ingroup variable sites (2158 total including ambiguities). The profile-to-profile plastome alignment is 136,790 bp long once

aligned with the *Quercus rubra* outgroup sequence, and contains 91 individuals comprising 26 species not including the outgroup. gblocks removes 3,854 bp from the alignment, resulting in a final matrix that is 132,936 bp long.

Phylogenetic analyses

The plastome ML tree (Fig. 1) exhibits four deep plastome lineages, each supported with 100% bootstrap support, and each confined to either North America (3 lineages) or Eurasia (one lineage). Sections *Quercus* and *Protobalanus* are both non-monophyletic in this tree, and one member of section *Quercus* (*Q. engelmannii* Greene) falls within an otherwise *Protobalanus*-dominated plastome lineage, as reported previously (Manos et al. 1999). Section *Protobalanus* exhibits a deep polyphyly that was also reported in Manos et al. (1999), with two lineages that show no evidence of recent plastome sharing (Fig. 1): species in this section segregate for comparatively ancient plastomes that conflict with sectional circumscription. Numerous species within the white oaks are non-monophyletic in the plastome tree, with accessions clustering coarsely by geography. For example, *Q. muehlenbergii* Engelm. is represented by three individuals in the plastome analysis (Fig. 1), and two of these samples (MOR-632 and MOR-383) do not resolve as closely related to the third sample (MOR-639). While this species together with *Q. prinoides* Willd. form a clade in the RADseq tree (Fig. 2), samples MOR-632 and MOR-383 were collected from the eastern United States (IL, OK) and cluster with other samples from the same geographic region (e.g., *Q. lyrata* from Georgia, *Q. macrocarpa* from Kansas, *Q. alba* from Pennsylvania). In contrast, the outlier sample (MOR-639_ was collected from the Guadalupe Mountains of Texas, and it resolves with other samples (*Q. mohriana* Buckley ex Rydb. and *Q. vaseyana* Buckley) that were collected from the same geographic region in southwest Texas.

The RADseq ML tree (Fig. 3, left) produced by the RADseq matrix shows a clear split between sections *Quercus* and *Protobalanus* (100% bootstrap support for both clades). Within the white oaks (section *Quercus*), the California oaks are sister to the rest of the clade (bootstrap = 100%). The Eurasian oaks form a clade sister to all white oaks except for the California clade (bootstrap = 100%). All taxa but *Quercus macrocarpa* Michx., *Q. stellata* Wangerh., *Q. muehlenbergii*, and *Q. chrysolepis* Liebm. are monophyletic, with 100% bootstrap support for the bipartition grouping accessions representing each species. With the exception of the placement of the Eurasian white oaks, which fall sister to a small clade of eastern North American white oaks in Hipp et al. (2014), the topology of the tree concurs with this previous skeletal phylogeny of the oaks based on RADseq data, and all clades are strongly supported.

Effect of geography and population divergence history on plastome phylogeny

At the broadest phylogenetic and geographic scale (“all oaks”), geography and phylogeny are both strong, significant partial predictors of plastome variation (geography partial correlation: $r^2 = 0.412$, $p < 0.002$; phylogeny partial correlation: $r^2 = 0.382$, $p < 0.002$; phylogeny simple correlation: $r^2 = 0.311$, $p < 0.002$; Table 2). In the North American oaks, geography decreases in predictive power ($r^2 = 0.028$, $p = 0.062$; Table 2), but phylogeny remains a strongly significant predictor of plastome variation ($r^2 = 0.406$, $p < 0.002$; Table 2). The North American white oak dataset and the North American oak dataset without California each excludes one western North American clade (section *Protobalanus* and the California white oaks respectively) that exhibits little hybridization with non-California taxa. The two exclusion sets, however, exhibit different patterns of plastome prediction. Exclusion of section *Protobalanus* alone results in a dramatic decrease in the predictive power of phylogeny ($r^2 = 0.001$, $p = 0.621$; Table 2). However, exclusion of the California white oaks results in an increase in predictive power of phylogeny

from the North American oaks ($r^2 = 0.300$), though both phylogenetic and geographic signal are significant ($p < 0.002$ for both). This result appears, however, to be due solely to the presence of the Mexican clade species *Carex engelmannii*, for its exclusion reduces partial correlations of phylogeny and geography to non-significance (Supplement S4). At the finest phylogenetic scale (the eastern North American white oaks), geographic signal and phylogeny are both non-significant predictors of plastome variation (Table 2).

Discussion

Phylogenetic incongruence between nuclear and plastid genome genealogies have been documented for diverse taxa over decades, using a variety of gene marker systems (Maddison 1997; Wendel and Doyle 1998). One common outcome of these studies is that organelle genome variation often tracks geographic genetic structure, while the nuclear genome appears to track evolutionary relationships as predicted by morphology or ecology (Whittemore and Schaal 1991). Our study is unique in its attempt to partition the effects of phylogeny and geography on the plastome nucleotide variation at varying phylogenetic depths in a lineage that is known to experience contemporary hybridization. We show that increasing the depth of the phylogeny considered increases the partial effect of phylogeny on the plastome topology, and that at the continental scale in North America, geography outweighs phylogeny as a predictor of plastome topology. We find, moreover, that the strong phylogeographic structure found in previous studies of European oaks (e.g. Dumolin-Lapegue et al. 1997) is not demonstrated in the eastern North American oaks, the classic oak syngameon (Hardin 1975; Burger 1975; Van Valen 1976). The deepest unambiguous split in the nuclear phylogeny, the split between the white oaks (section *Quercus*) and the intermediate oaks (section *Protobalanus*), is the single most important factor

explaining concordance between the plastome phylogeny and population divergence history as encoded in the RADseq data. Inclusion of that split with the California species, however, reduces the fit between the RADseq and the plastome data, presumably because historic hybridization between section *Protobalanus* and California white oaks (as evidenced by incongruence in the placement of *Q. engelmannii*) erodes phylogenetic signal. Thus, joint analysis of nuclear and plastome data captures the interaction among biogeography, ancestral lineage divergences, and contemporary gene flow in the oaks, but within major clades of the genus, combined analysis is a poor method of inferring phylogenetic history.

Phylogenetic analyses

The recovery of phylogenetic structure among major clades and geographic signal at fine scales in the plastome tree is consistent with past studies, which have also found non-monophyly of species but geographic structuring of populations at fine scales based on plastome sequences (Dumolin-Lapegue 1991; Petit et al. 1993; Manos et al. 1999). The RADseq tree also returned expected relationships at fine interspecific levels, confirming relationships and monophyly of most species inspected (Pearse and Hipp 2009; Hipp et al. 2014). The paraphyly of *Q. stellata* in the RADseq tree derives, we suspect, from a relatively high rate of hybridization in this species (cf. Nixon and Muller 1997) that we do not investigate further in the current paper.

Effect of geography and population divergence history on plastome phylogeny

Hybridization in oaks is primarily limited to crosses within sections, with the exception of the single inferred case of historical hybridization between western North American *Protobalanus* and *Quercus* first reported in Manos et al. (1999) involving the white oak *Q. engelmannii* and corroborated in our study. We therefore expect the plastome to track deeper

(more ancient) phylogenetic relationships, as seen in our results by the predictive power of the RADseq tree on the plastome topology in the all oaks sampled dataset. At the scale of all oaks sampled, the plastome topology is significantly predicted by geography in both simple and partial regressions, with the partial correlation coefficient ($r^2 = 0.406$) slightly larger than the simple correlation coefficient ($r^2 = 0.338$). This increase of 7% in variance explained from the simple to partial regression may reflect the fact that at the broadest phylogenetic scale in this study, there is substantial geographic structure embedded within the phylogenetic structure, and that a portion of this variation is only captured when phylogeny is controlled for using partial regression.

Removing Eurasian white oaks from this analysis has minimal effect on the proportion of plastome variation explained by the RADseq phylogeny (from $r^2 = 0.382$ to $r^2 = 0.407$). The phylogenetic placement of Eurasian white oaks has varied among published studies, with the group resolving as monophyletic sister to a subset of eastern North American white oaks (RADseq nuclear markers; Hipp et al. 2014), weakly monophyletic within the white oaks (six nuclear genes; Hubert et al. 2014), or strongly monophyletic and sister to the remainder of the white oaks (AFLP markers; Pearse and Hipp 2009; also plastid genomes in this study). The plastid genome and the nuclear genome consistently recover the Eurasian white oaks as a strongly supported clade; it is their placement within *Quercus* subg. *Quercus* that is uncertain in our study, and the deep divergence between the Eurasian white oaks and their sister taxa in the plastid genome tree (e.g., Fig. 1) contrast the more recent divergences indicated by the nuclear data (Fig. 2, left panel). As a consequence of these long branches, removing the Eurasian white oaks has the effect of focusing comparisons on the deepest divergences in both trees, such as the

divergence of *Protobalanus* and the white oaks, and between Californian and Eastern North American oaks.

The deepest plastome divergences distinguish the two *Protobalanus* lineages, the Eurasian white oak lineage, and the North American white oak lineage. Thus, excluding both *Protobalanus* and the Eurasian white oaks from analysis removes the effect of nuclear phylogeny on the plastome topology (partial effect of RADseq variance on plastome variance decreases from $r^2 = 0.382$ to $r^2 = 0.001$). Major clades are recoverable in the plastome tree because there are stronger reproductive barriers among sections than within sections and among geographic regions. Removing both the strongest geographic outliers (viz., the Eurasian white oaks) and the members of the section *Protobalanus* restricts comparisons to a single major clade on a single continent. The plastome divergence between the California and eastern North American white oaks, which presumably have a very limited history of gene flow, is not nearly as deep as the break with either *Protobalanus* or the Eurasian white oaks, perhaps reflecting a history of gene flow among clades that postdates initial divergence. Thus the North American oaks, even with California included, shows much weaker correlation between the plastome topology and the RADseq phylogeny than the datasets that include the deepest plastome divergences.

An interesting finding from our genome-scale survey is evidence for two comparatively ancient plastome lineages in section *Protobalanus*. This recapitulates a finding of Manos et al. (1999) with far greater genome-scale resolution, albeit with shallower taxon sampling. In the prior study, members of *Protobalanus* formed two monophyletic lineages that were incompletely resolved in a basal polytomy. Sampling of *Protobalanus* in Manos et al. (1999) was sufficient to demonstrate that two divergent plastome types were segregating in at least two of the sampled species (*Quercus chrysolepis*, *Q. palmeri* Engelm.). This unusual level of polymorphism may

reflect a very ancient gene exchange event between *Protobalanus* and a white oak lineage, or lineage sorting of ancient haplotypes: in our study, the divergence between *Protobalanus* plastomes corresponds to the crown node of the entire ingroup, and in Manos et al. (1999: 337), the two plastome clades differed by 13 restriction sites. The origin and taxonomic distribution of these two ancient plastome clades bears further study. Our plastome tree is also congruent with Manos et al. (1999) in placing *Q. engelmannii* Greene, a California white oak, in the same plastome group as *Q. tomentella* Engelm. Given the crown depth of each *Protobalanus* plastome clade (much younger than the divergence time between the *Protobalanus* plastomes), this placement almost certainly reflects more recent gene flow between white oaks and intermediate oaks. Stronger within-species sampling in a geographic context within the intermediate and California white oaks will be needed to evaluate how prevalent gene flow is between these sections.

Our analysis of the eastern North American white oaks contrasts sharply with previous studies on the European oaks (e.g. Dumolin-Lapegue et al. 1997), which have found strong phylogeographic signal. In the eastern North American oaks, plastome variation correlates poorly with both geographic and phylogeny (Table 2), unlike at the largest phylogenetic scales, where both geographic and phylogenetic signal are strong predictors because of the geographic structure embedded in phylogenetic signal (congruence of the two signals). In this classic eastern North American oak syngameon, it is remarkable that we do not find consistent geographic clustering across deep splits in the plastome tree within North America (Fig. 3). While our sampling should be sufficient to detect, for example, the Mississippi River discontinuity exhibited by numerous animals and a few plant species (Soltis et al. 2006), no node on the plastome tree supports a clean east-west phylogeographic split. The capacity for long-distance

gene flow in oaks and their large population sizes may blur any signal of such phylogeographic breaks in eastern North America, where Pleistocene refugia were likely less discrete than in Europe.

In this study, we quantified the proportion of evolutionary history explained by plastome variation and contemporary geographic distributions. It is important to note, however, that for oaks and other temperate zone trees, current geographic distributions can be accurately modeled as a response to climatic variables (Rehfeldt et al. 2006 ; Roberts and Hamann 2012). This suggests that the correlations we observe between phylogeny and geography most likely have their origins in both adaptation to climate and the biogeography of diversification. The distributions of oaks and other temperate zone tree species have been in a continuous state of flux during Pleistocene-era climate change (Hewitt 1996 ; Roberts and Hamann 2015), with some species moving continental-scale distances of latitude and longitude (e.g., *Quercus alba*; Gugger et al., 2013; *Q. petraea* and *Q. robur*, Taberlet et al., 1998), and others migrating shorter geographic distances across elevational gradients (e.g. *Q. garryana*; Crookston 2016; *Q. lobata*, Gugger et al. 2013). This climate-driven migratory history is likely to be a major source of the ‘geographic signal’ and ‘phylogenetic noise’ we observe in eastern North American white oaks. Geographic signals may be enhanced via changes in population sizes (e.g., contraction during glacial maxima; expansion during interglacial episodes) or the exchange of haplotypes via rare hybridization events between species as they migrate into and out of common refugia (e.g., Taberlet et al. 1998). Climate envelope modelling and paleoclimate reconstructions are now being integrated to understand the role of past climates on contemporary species diversity (Roberts and Hamann 2015), and such analyses may help to dissect the individual contributions

of phylogeny, geography and climate to contemporary genetic variation in such complex groups as the white oaks.

Finally, our findings have relevance to ongoing efforts to identify DNA barcodes (Hollingsworth et al. 2016), informative genetic markers that are diagnostic for oak species and related hybrids. Due to the ecological and economic importance of *Quercus* globally, there have been a few attempts to develop simple diagnostic markers for oak species identification for use in ecological/landscape inventories (Simeone et al. 2012), conservation management, and screening oak wood products suspected as being derived from exploited sources (Schroeder et al. 2016). For example, *Q. mongolica* is listed as a CITES Appendix III species due to pressure from illegal logging in the far-east of the Russian Federation (U.S. Department of Justice 2015); this status restricts trade of *Q. mongolica*, and brings all commercial species of white oak under greater scrutiny for labeling accuracy. Due to their high similarity, *Q. mongolica* cannot be discriminated from other white oak species by wood anatomy, leaving DNA-based detection as one of the few available tools for identifying the taxonomic source of wood and enforcing illegal logging laws (Dormontt et al. 2015).

Our survey of 91 complete plastid genomes (Fig. 1) shows that organelle genomes are frequently shared across diverse evolutionary lineages and species. Indeed, of the 15 species represented by multiple sequences in our study, plastome monophyly was only observed in one case (*Q. gambelii*), and this seems likely to be a consequence of limited sampling. This result, combined with other barcoding efforts in *Quercus* (Piredda et al. 2010; Simeone et al. 2012), suggest that plastid genome sequences – either as subsets of barcode genes, or as the complete genomic ‘ultrabarcode’ (Coissac et al. 2016) – are highly unlikely to offer the precision required for confident identification of source species, unless they are accompanied by additional

information from the nuclear genome. In this regard, oak joins a growing list of woody species that cannot be “barcoded” with a single genome (Arca et al. 2012; Clement and Donoghue 2012; Parks et al. 2012; Percy et al. 2014) and that will require additional information from multiple genomes and multiple loci for accurate species identification. Our study does, however, confirm that a substantial proportion of variation in the plastome can be explained by geography (e.g., Table 2; Figs. 1, 2). This should make it possible to develop markers and databases that can address questions of geographic origin, as has recently been accomplished for the Asian white oaks *Q. mongolica* and *Q. dentata* (Schroeder et al. 2016).

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Table 1. Samples metadata. SRA BioSample ID references NCBI sample ID for each sequence.

<u>Specimen code</u>	<u>Species</u>	<u>Herbarium accession</u>	<u>Latitude</u>	<u>Longitude</u>	<u>Section</u>	<u>Continent</u>	<u>Country</u>	<u>State/Province</u>	<u>RADseq SRA BioSample ID</u>	<u>cpDNA SRA BioSample ID</u>
OAK-MOR-359	Quercus alba L.	174462	45.367983	-93.219304	Q	NA	USA	Minnesota	SAMN06446142	SAMN03264816
PM-19	Quercus alba L.	177669	36.021818	-79.016068	Q	NA	USA	North Carolina	SAMN06446143	
OAK-MOR-204	Quercus alba L.	175336	39.9347718	-89.8016103	Q	NA	USA	Illinois	SAMN06446144	
OAK-MOR-76	Quercus alba L.	174513	41.866545	-86.349921	Q	NA	USA	Michigan	SAMN06446145	
QUAL_NC_2	Quercus alba L.		35.25357	-82.19709	Q	NA	USA	NC		SAMN03264817
QUAL_PN_1	Quercus alba L.		41.38389	-79.054	Q	NA	USA	PN		SAMN03264818
QUAL_PN_4	Quercus alba L.		41.50643	-79.24511	Q	NA	USA	PN		SAMN03264819
OAK-MOR-413	Quercus arizonica Sarg.	174229	31.44959506	-109.2431153	Q	NA	USA	Arizona	SAMN06446146	SAMN03264796
OAK-MOR-508	Quercus berberidifolia Liebm.	174692	38.41167	-122.04917	Q	NA	USA	California	SAMN06446147	SAMN03264799
OAK-MOR-342	Quercus bicolor Willd.	174534	41.740864	-87.860335	Q	NA	USA	Illinois	SAMN06446148	SAMN03264820
OAK-MOR-289	Quercus bicolor Willd.	175338	38.9048	-94.8926	Q	NA	USA	Illinois	SAMN06446149	SAMN03264821
OAK-MOR-436	Quercus boyntonii Beadle	175278	34.014264	-86.00664	Q	NA	USA	Alabama	SAMN06446150	SAMN03264814
OAK-MOR-415	Quercus chrysolepis Liebm.	174230	31.43347498	-109.2431153	P	NA	USA	Arizona	SAMN06446151	SAMN03264797
OAK-MOR-474	Quercus chrysolepis Liebm.	174682	38.757996	-120.548892	P	NA	USA	California	SAMN06446152	SAMN03264807
Qd_01	Quercus dentata Thunb.		42.801233	131.245433	Q	EU	RUS			SAMN03653768
Qd_03	Quercus dentata Thunb.		42.801267	131.245467	Q	EU	RUS			SAMN03653764
Qd_04	Quercus dentata Thunb.		42.801283	131.245483	Q	EU	RUS			SAMN03653765
Qd_05	Quercus dentata Thunb.		42.8013	131.2455	Q	EU	RUS			SAMN03653766
Qd_06	Quercus dentata Thunb.		42.801317	131.245517	Q	EU	RUS			SAMN03653769
Qd_09	Quercus dentata Thunb.		42.801367	131.245567	Q	EU	RUS			SAMN03653767
Qd_10	Quercus dentata Thunb.		42.801383	131.245583	Q	EU	RUS			SAMN03653762
OAK-MOR-531	Quercus douglasii Hook. & Arn.	174681	38.696153	-120.887322	Q	NA	USA	California	SAMN06446153	SAMN03264808
OAK-MOR-406	Quercus engelmannii Greene	174583	32.594883	-116.843812	Q	NA	USA	California	SAMN06446154	SAMN03264801
OAK-MOR-387	Quercus gambelii Nutt.	174463	38.861158	-105.172682	Q	NA	USA	Colorado	SAMN06446155	SAMN03264809
OAK-MOR-546	Quercus gambelii Nutt.	174218	31.75663448	-109.2431153	Q	NA	USA	Arizona	SAMN06446156	SAMN03264795
QUGA4_OR_1	Quercus garryana Douglas ex. Hook.		43.3050	-123.2412	Q	NA	USA	OR		SAMN03264824
OAK-MOR-422	Quercus garryana Douglas ex. Hook.	174699	38.678479	-120.812513	Q	NA	USA	California	SAMN06446157	SAMN03264823
OAK-MOR-123	Quercus lobata Née	174703	36.61667	-120.85	Q	NA	USA	California	SAMN06446158	SAMN03264805
OAK-MOR-385	Quercus lyrata Walter	174540	36.720972	-90.112917	Q	NA	USA	Missouri	SAMN06446159	SAMN03264826
OAK-MOR-611	Quercus lyrata Walter	174529	30.7084	-84.8564	Q	NA	USA	Georgia	SAMN06446160	SAMN03264825

OAK-MOR-356	Quercus macrocarpa Michx.	174544	37.149225	-94.443003	Q	NA	USA	Missouri	SAMN06446161	
OAK-MOR-357	Quercus macrocarpa Michx.	174520/174521	41.486798	-87.799832	Q	NA	USA	Illinois	SAMN06446162	
OAK-MOR-673	Quercus macrocarpa Michx.	175524	45.5129	-73.5506	Q	NA	CAN	Quebec	SAMN06446163	SAMN03264829
OAK-MOR-672	Quercus macrocarpa Michx.	175314	33.6	-105.4	Q	NA	USA	New Mexico	SAMN06446164	SAMN03264812
QUMA2_KS_1	Quercus macrocarpa Michx.		39.0286	-94.9404	Q	NA	USA	KS		SAMN03264827
QUMA2_WI_3	Quercus macrocarpa Michx.		42.8751	-88.3276	Q	NA	USA	WI		SAMN03264830
OAK-MOR-420	Quercus margarettae (Ashe) Small	174705	29.616474	-97.572742	Q	NA	USA	Texas	SAMN06446165	SAMN03264804
OAK-MOR-353	Quercus michauxii Nutt.	174516	36.644722	-89.285	Q	NA	USA	Missouri	SAMN06446166	SAMN03264833
OAK-MOR-694	Quercus michauxii Nutt.	174537	38.905693	-86.035881	Q	NA	USA	Indiana	SAMN06446167	SAMN03264832
OAK-MOR-700	Quercus michauxii Nutt.	175231	37.15382	-89.34699	Q	NA	USA	Illinois	SAMN06446168	SAMN03264831
PM143	Quercus michauxii Nutt.		35.99555	-79.05416	Q	NA	USA	North Carolina	SAMN06446169	
PM155	Quercus michauxii Nutt.		36.015223	-78.923317	Q	NA	USA	North Carolina	SAMN06446170	
OAK-MOR-125	Quercus mohriana Buckley ex Rydb.	174704	31.979167	-104.754722	Q	NA	USA	Texas	SAMN06446171	SAMN03264800
OAK-MOR-360	Quercus mongolica Fisch. ex Ledeb.	174518	40.58	116.7375	Q	EU	CHI	Beijing Shi	SAMN06446172	SAMN03264834
Opb_13	Quercus mongolica Fisch. ex Ledeb.		50.187167	138.591	Q	EU	RUS			SAMN03653770
Opb_21	Quercus mongolica Fisch. ex Ledeb.		50.187167	138.591	Q	EU	RUS			SAMN03653771
Opb_26	Quercus mongolica Fisch. ex Ledeb.		50.187167	138.591	Q	EU	RUS			SAMN03653772
Opl_19	Quercus mongolica Fisch. ex Ledeb.		43.374833	133.892	Q	EU	RUS			SAMN03653773
Opl_20	Quercus mongolica Fisch. ex Ledeb.		43.374833	133.892	Q	EU	RUS			SAMN03653774
Opl_21	Quercus mongolica Fisch. ex Ledeb.		43.374833	133.892	Q	EU	RUS			SAMN03653775
Oto_03	Quercus mongolica Fisch. ex Ledeb.		49.0497	131.860333	Q	EU	RUS			SAMN03653777
Oto_14	Quercus mongolica Fisch. ex Ledeb.		49.0497	131.860333	Q	EU	RUS			SAMN03653776
Ovl_02	Quercus mongolica Fisch. ex Ledeb.		43.073167	131.909833	Q	EU	RUS			SAMN03653779
Ovl_04	Quercus mongolica Fisch. ex Ledeb.		43.073167	131.909833	Q	EU	RUS			SAMN03653780
Ovl_14	Quercus mongolica Fisch. ex Ledeb.		43.073167	131.909833	Q	EU	RUS			SAMN03653778
Qkor_02	Quercus mongolica Fisch. ex Ledeb.		37.5667	126.9781	Q	EU	SKO			SAMN03653781
Qkor_07	Quercus mongolica Fisch. ex Ledeb.		37.5667	126.9781	Q	EU	SKO			SAMN03653782
Qkor_08	Quercus mongolica Fisch. ex Ledeb.				Q	EU	SKO			SAMN03653803
Qm_14	Quercus mongolica Fisch. ex Ledeb.		45.083333	133.947194	Q	EU	RUS			SAMN03653784
Qm_18	Quercus mongolica Fisch. ex Ledeb.		46.083028	133.945889	Q	EU	RUS			SAMN03653785
Qm_20	Quercus mongolica Fisch. ex Ledeb.		46.082194	133.945556	Q	EU	RUS			SAMN03653786
Qm_42	Quercus mongolica Fisch. ex Ledeb.		45.429692	127.092031	Q	EU	CHI			SAMN03653800
Qm_44	Quercus mongolica Fisch. ex Ledeb.		45.429531	127.091156	Q	EU	CHI			SAMN03653801

Qm_49	Quercus mongolica Fisch. ex Ledeb.		45.428283	127.090569	Q	EU	CHI			SAMN03653802
Qm_65	Quercus mongolica Fisch. ex Ledeb.		48.619717	135.90783	Q	EU	RUS			SAMN03653787
Qm_68	Quercus mongolica Fisch. ex Ledeb.		48.619717	135.90783	Q	EU	RUS			SAMN03653788
Qm_71	Quercus mongolica Fisch. ex Ledeb.		48.619717	135.90783	Q	EU	RUS			SAMN03653789
Qm_SUW_4	Quercus mongolica Fisch. ex Ledeb.		37.5667	126.9781	Q	EU	SKO			SAMN03653783
OAK-MOR-352	Quercus montana Willd.	174846	37.141444	-79.995722	Q	NA	USA	Virginia	SAMN06446173	SAMN03264838
OAK-MOR-693	Quercus montana Willd.	174514	37.52575	-80.249722	Q	NA	USA	Virginia	SAMN06446174	
OAK-MOR-575	Quercus montana Willd.	175353	35.429102	-82.251822	Q	NA	USA	North Carolina	SAMN06446175	
OAK-MOR-383	Quercus muehlenbergii Engelm.	174533	41.210569	-88.017575	Q	NA	USA	Illinois	SAMN06446176	SAMN03264810
OAK-MOR-632	Quercus muehlenbergii Engelm.	175345	35.623899	-99.008733	Q	NA	USA	Oklahoma	SAMN06446177	SAMN03264815
OAK-MOR-639	Quercus muehlenbergii Engelm.	174690	31.97917	-104.75417	Q	NA	USA	Texas	SAMN06446178	SAMN03264803
OAK-MOR-520	Quercus petraea (Matt.) Liebl.	174539	51.816667	19.883333	Q	EU	POL		SAMN06446179	SAMN03264835
HB_175	Quercus petraea (Matt.) Liebl.		53.700539	10.719256	Q	EU	GER			SAMN03653790
HB_181	Quercus petraea (Matt.) Liebl.		53.700539	10.719256	Q	EU	GER			SAMN03653791
MST_29	Quercus petraea (Matt.) Liebl.		51.909356	7.740925	Q	EU	GER			SAMN03653792
MST_30	Quercus petraea (Matt.) Liebl.		51.909356	7.740925	Q	EU	GER			SAMN03653793
MST_31	Quercus petraea (Matt.) Liebl.		51.909356	7.740925	Q	EU	GER			SAMN03653794
OAK-MOR-532	Quercus prinoides Willd.	175238	40.076297	-95.720956	Q	NA	USA	Nebraska	SAMN06446180	SAMN03264811
QUPR2_NC_1	Quercus prinoides Willd.		35.2535	-82.197	Q	NA	USA	NC		SAMN03264836
QUPR2_PN_1	Quercus prinoides Willd.		41.5073	-79.2442	Q	NA	USA	PN		SAMN03264837
OAK-MOR-392	Quercus robur L.	174567	55.838647	37.600483	Q	EU	RUS		SAMN06446181	SAMN03264839
ARK_15	Quercus robur L.		54.416667	56.666667	Q	EU	RUS			SAMN03653809
B2_01	Quercus robur L.		52.674197	58.742517	Q	EU	RUS			SAMN03653795
PIE_06	Quercus robur L.		44.737028	-0.776389	Q	EU	FRA			SAMN03653797
PIE_10	Quercus robur L.		44.737028	-0.776389	Q	EU	FRA			SAMN03653796
SVT_06	Quercus robur L.		49.052833	37.9295	Q	EU	UKR			SAMN03653807
SVT_11	Quercus robur L.		49.052833	37.9295	Q	EU	UKR			SAMN03653808
TAM_01	Quercus robur L.		59.974439	23.435525	Q	EU	FIN			SAMN03653798
TAM_10	Quercus robur L.		59.974439	23.435525	Q	EU	FIN			SAMN03653799
WR4_01	Quercus robur L.		53.685833	23.792833	Q	EU	BEL			SAMN03653805
WR4_07	Quercus robur L.		53.685833	23.792833	Q	EU	BEL			SAMN03653806
OAK-MOR-498	Quercus rubra L.	174465			L	NA	USA	Illinois	SAMN06446182	
OAK-MOR-388	Quercus stellata Wangenh.	174535	40.5849	-91.2756	Q	NA	USA	Iowa	SAMN06446183	SAMN03264841

OAK-MOR-340	Quercus stellata Wangenh.	174543	38.034944	-91.520306	Q	NA	USA	Missouri	SAMN06446184	
OAK-MOR-616	Quercus stellata Wangenh.	175244	35.4	-82.4	Q	NA	USA	North Carolina	SAMN06446185	SAMN03264813
QUST_GA_2	Quercus stellata Wangenh.		33.9025	-83.3824	Q	NA	USA	GA		SAMN03264840
OAK-MOR-133	Quercus tomentella Engelm.	174688	34.023206	-119.765766	P	NA	USA	California	SAMN06446186	SAMN03264802
OAK-MOR-377	Quercus vaccinifolia Kellogg	174684	38.811462	-120.123212	P	NA	USA	California	SAMN06446187	SAMN03264806
OAK-MOR-397	Quercus vaseyana Buckley	174580	29.970985	-101.109021	Q	NA	USA	Texas	SAMN06446188	SAMN03264798

Draft

Table 2. Partial regressions of plastome variation on nuclear phylogeny and geographic distance, using Mantel permutations to assess significance.

Dataset	<u>plast~nuc+geo</u>	<u>plast~nuc.geo</u>	<u>plast~geo.nuc</u>	<u>plast~geo</u>	<u>plast~nuc</u>	<u>nuc~geo</u>
(1) All oaks sampled	r2 = 0.596	r2 = 0.382, p < 0.002	r2 = 0.413, p < 0.002	r2 = 0.346, p < 0.002	r2 = 0.311, p < 0.002	r2 = 0.011, p = 0.460
(2) North American oaks	r2 = 0.464	r2 = 0.407, p < 0.002	r2 = 0.028, p = 0.062	r2 = 0.097, p < 0.002	r2 = 0.449, p < 0.002	r2 = 0.084, p < 0.002
(3) North American white oaks	r2 = 0.116	r2 = 0.001, p = 0.621	r2 = 0.112, p < 0.002	r2 = 0.115, p < 0.002	r2 = 0.004, p = 0.517	r2 = 0.077, p < 0.002
(4) North American oaks without California	r2 = 0.526	r2 = 0.301, p < 0.002	r2 = 0.162, p < 0.002	r2 = 0.322, p < 0.002	r2 = 0.435, p < 0.002	r2 = 0.204, p < 0.002
(5) Eastern North American white oaks	r2 = 0.013	r2 = 0.011, p = 0.188	r2 = 0.003, p = 0.779	r2 = 0.002, p = 0.817	R2 = 0.011, p = 0.156	r2 = 0.002, p = 0.588

Note: Models tested are represented using ~ to indicate “is predicted by” and “.” to indicate partial regression, where the predictor before the “.” is the partial coefficient being estimated, and the predictor after the “.” is the covariate. Abbreviations: Plast = the plastome phylogenetic pairwise distances; nuc = nuclear (RADseq) phylogeny pairwise distances; geo = geographic (great circle) pairwise distances. Shaded cells are significant at $p < 0.002$.

FIGURE CAPTIONS

Figure 1. Plastome phylogeny, all samples. Maximum likelihood phylogeny with non-parametric bootstrap values indicated by branch thickness (thickest branches: bootstrap $> 90\%$; medium thickness: bootstrap $\leq 90\%$, $> 50\%$; thinnest branches: bootstrap $\leq 50\%$). Colored blocks indicate the four main plastome lineages. Sample names follow Table 1.

Figure 2. Nuclear RADseq phylogeny (left panel) and plastome phylogeny (right panel), containing all samples listed in Table 1. Corresponding tips are connected between trees. Bootstrap values are shown in boxes at the nodes of the clades to which they correspond. Tips are color-coded by clade; intermediate oaks are blue, california white oaks are red, and all other white oaks are black.

Figure 3. Plastome phylogeny, all samples except outgroup, mapped to sample locations. Maximum likelihood plastome phylogeny (see Fig. 1), excluding the *Quercus rubra* outgroup. Colored blocks correspond to lineages in Fig. 1.

RADseq

<https://mc06.manuscriptcentral.com/genomepubs>

Plastome

Supplement: Pham et al., Phylogenetic history and geography as joint predictors of oak chloroplast phylogeny

Chloroplast genome sequence information: samples, libraries, and assembly summaries

RAxML tree label	organism	sample_title	bioproject_id	SRA_accn	loc
alba_ _MOR359_ _USA-MN	Quercus alba L.	Quercus alba L. shotgun genomic sequencing, MOR_MH109 QUAL_MN_1	PRJNA269970	SAMN03264816	USA-MN
alba_ _USFSNC2_ _USA-NC	Quercus alba L.	Quercus alba L. shotgun genomic sequencing, USFS_NC2 QUAL_NC_2	PRJNA269970	SAMN03264817	USA-NC
alba_ _USFSPN1_ _USA-PN	Quercus alba L.	Quercus alba L. shotgun genomic sequencing, USFS_PN1 QUAL_PN_1	PRJNA269970	SAMN03264818	USA-PN
alba_ _USFSPN4_ _USA-PN	Quercus alba L.	Quercus alba L. shotgun genomic sequencing, USFS_PN4 QUAL_PN_4	PRJNA269970	SAMN03264819	USA-PN
arizonica_ _MOR413_ _USA-AZ	Quercus arizonica Sarg.	Quercus arizonica Sarg. shotgun genomic sequencing, PM66 AZ-HU-15	PRJNA269970	SAMN03264796	USA-AZ
berberidifolia_ _MOR508_ _USA-CA	Quercus berberidifolia Liebm.	Quercus berberidifolia Liebm. shotgun genomic sequencing, MH47 CA-DAV-MH047	PRJNA269970	SAMN03264799	USA-CA
bicolor_ _MOR289_ _USA-KS	Quercus bicolor Willd.	Quercus bicolor Willd. shotgun genomic sequencing, IL_SH184 QUBI_KS_1	PRJNA269970	SAMN03264821	USA-IL
bicolor_ _MOR342_ _USA-IL	Quercus bicolor Willd.	Quercus bicolor Willd. shotgun genomic sequencing, MH94 QUBI_IL_1	PRJNA269970	SAMN03264820	USA-IL
boyntonii_ _MOR436_ _USA-AL	Quercus boyntonii Beadle	Quercus boyntonii Beadle shotgun genomic sequencing, IL-SH24 IL-SH-24	PRJNA269970	SAMN03264814	USA-AL
chrysolepis_ _MOR415_ _USA-AZ	Quercus chrysolepis Liebm.	Quercus chrysolepis Liebm. shotgun genomic sequencing AZ-HU-17	PRJNA269970	SAMN03264797	USA-AZ
chrysolepis_ _MOR474_ _USA-CA	Quercus chrysolepis Liebm.	Quercus chrysolepis Liebm. shotgun genomic sequencing CA-MH70	PRJNA269970	SAMN03264807	USA-CA
dentata_ _QD01_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_01	PRJNA269970	SAMN03653768	RUS
dentata_ _QD03_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_03	PRJNA269970	SAMN03653764	RUS
dentata_ _QD04_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_04	PRJNA269970	SAMN03653765	RUS
dentata_ _QD05_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_05	PRJNA269970	SAMN03653766	RUS
dentata_ _QD06_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_06	PRJNA269970	SAMN03653769	RUS
dentata_ _QD09_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_09	PRJNA269970	SAMN03653767	RUS
dentata_ _QD10_ _RUS	Quercus dentata Thunb.	Quercus dentata shotgun genomic sequence Qd_10	PRJNA269970	SAMN03653762	RUS
douglasii_ _MOR531_ _USA-CA	Quercus douglasii Hook. & Arn.	Quercus douglasii Hook. & Arn. shotgun genomic sequencing, MH73 CA-MH-073	PRJNA269970	SAMN03264808	USA-CA
engelmannii_ _MOR406_ _USA-CA	Quercus engelmannii Greene	Quercus engelmannii Greene shotgun genomic sequencing, MH35 CA-DAV-MH035	PRJNA269970	SAMN03264801	USA-CA
gambelii_ _MOR387_ _USA-CO	Quercus gambelii Nutt.	Quercus gambelii Nutt. shotgun genomic sequencing, MH92 IL-MOR-MH092	PRJNA269970	SAMN03264809	USA-CO
gambelii_ _MOR546_ _USA-AZ	Quercus gambelii Nutt.	Quercus gambelii Nutt. shotgun genomic sequencing, PM62 AZ-CH-11	PRJNA269970	SAMN03264795	USA-AZ
garryana_ _MOR422_ _USA-CA	Quercus garryana Douglas ex. Hc	Quercus garryana Douglas ex. Hook. shotgun genomic sequencing, MH21 QUGA4_CA_1	PRJNA269970	SAMN03264823	USA-CA
garryana_ _USFSOR1_ _USA-OR	Quercus garryana Douglas ex. Hc	Quercus garryana Douglas ex. Hook. shotgun genomic sequencing, USFS_OR1 QUGA4_OR_1	PRJNA269970	SAMN03264824	USA-OR
lobata_ _MOR123_ _USA-CA	Quercus lobata Nee	Quercus lobata Nee shotgun genomic sequencing, MH53 CA-DAV-MH53	PRJNA269970	SAMN03264805	USA-CA
lyrata_ _MOR385_ _USA-MO	Quercus lyrata Walter	Quercus lyrata Walter shotgun genomic sequencing, MH96 QULY_MO_1	PRJNA269970	SAMN03264826	USA-MO
lyrata_ _MOR611_ _USA-GA	Quercus lyrata Walter	Quercus lyrata Walter shotgun genomic sequencing, MH78 QULY_GA_1	PRJNA269970	SAMN03264825	USA-GA
macrocarpa_ _MOR616_ _USA-NC	Quercus macrocarpa Michx.	Quercus macrocarpa Michx. shotgun genomic sequencing IL-SH-187	PRJNA269970	SAMN03264813	USA-NC
macrocarpa_ _MOR672_ _USA-NM	Quercus macrocarpa Michx.	Quercus macrocarpa Michx. shotgun genomic sequencing IL-SH-186	PRJNA269970	SAMN03264812	USA-NM
macrocarpa_ _MOR673_ _CAN-QU	Quercus macrocarpa Michx.	Quercus macrocarpa Michx. shotgun genomic sequencing, IL_SH190 QUMA2_QU_1	PRJNA269970	SAMN03264829	CAN-QU
macrocarpa_ _USFSKS1_ _USA-KS	Quercus macrocarpa Michx.	Quercus macrocarpa Michx. shotgun genomic sequencing QUMA2_KS_1	PRJNA269970	SAMN03264827	USA-KS
macrocarpa_ _USFSWI3_ _USA-WI	Quercus macrocarpa Michx.	Quercus macrocarpa Michx. shotgun genomic sequencing QUMA2_WI_3	PRJNA269970	SAMN03264830	USA-WI
margarettae_ _MOR420_ _USA-TX	Quercus margarettae (Ashe) Small	Quercus margarettae (Ashe) Small shotgun genomic sequencing CA-DAV-MH50	PRJNA269970	SAMN03264804	USA-TX

michauxii_ _MOR353_ _USA-MO	Quercus michauxii Nutt.	Quercus michauxii Nutt. shotgun genomic sequencing, MH1 QUMI_MO_1	PRJNA269970	SAMN03264833	USA-MO
michauxii_ _MOR694_ _USA-IN	Quercus michauxii Nutt.	Quercus michauxii Nutt. shotgun genomic sequencing, MH79 QUMI_IN_1	PRJNA269970	SAMN03264832	USA-IN
michauxii_ _MOR700_ _USA-IL	Quercus michauxii Nutt.	Quercus michauxii Nutt. shotgun genomic sequencing, IL_SH154 QUMI_IL_1	PRJNA269970	SAMN03264831	USA-IL
mohriana_ _MOR125_ _USA-TX	Quercus mohriana Buckley ex Ryc	Quercus mohriana Buckley ex Rydb. shotgun genomic sequencing, MH51 CA-DAV-MH051	PRJNA269970	SAMN03264800	USA-TX
mongolica_ _MOR360_ _CHI-Be	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica Fisch. Ex Ledeb. shotgun genomic sequencing, MH106 QUM05_CH_1	PRJNA269970	SAMN03264834	CHI-Be
mongolica_ _OPB13_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Opb_13	PRJNA269970	SAMN03653770	RUS
mongolica_ _OPB21_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Opb_21	PRJNA269970	SAMN03653771	RUS
mongolica_ _OPB26_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Opb_26	PRJNA269970	SAMN03653772	RUS
mongolica_ _OPL19_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Opl_19	PRJNA269970	SAMN03653773	RUS
mongolica_ _OPL20_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Opl_20	PRJNA269970	SAMN03653774	RUS
mongolica_ _OPL21_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Opl_21	PRJNA269970	SAMN03653775	RUS
mongolica_ _OTO14_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Oto_14	PRJNA269970	SAMN03653776	RUS
mongolica_ _OTO3_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Oto_03	PRJNA269970	SAMN03653777	RUS
mongolica_ _OVL02_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Ovl_02	PRJNA269970	SAMN03653779	RUS
mongolica_ _OVL04_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Ovl_04	PRJNA269970	SAMN03653780	RUS
mongolica_ _OVL14_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Ovl_14	PRJNA269970	SAMN03653778	RUS
mongolica_ _QKOR2_ _SKO	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qkor_02	PRJNA269970	SAMN03653781	SKO
mongolica_ _QKOR7_ _SKO	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qkor_07	PRJNA269970	SAMN03653782	SKO
mongolica_ _QKOR8_ _SKO	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qkor_08	PRJNA269970	SAMN03653803	SKO
mongolica_ _QM14_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_14	PRJNA269970	SAMN03653784	RUS
mongolica_ _QM18_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_18	PRJNA269970	SAMN03653785	RUS
mongolica_ _QM20_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_20	PRJNA269970	SAMN03653786	RUS
mongolica_ _QM42_ _CHI	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_42	PRJNA269970	SAMN03653800	CHI
mongolica_ _QM44_ _CHI	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_44	PRJNA269970	SAMN03653801	CHI
mongolica_ _QM49_ _CHI	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_49	PRJNA269970	SAMN03653802	CHI
mongolica_ _QM65_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_65	PRJNA269970	SAMN03653787	RUS
mongolica_ _QM68_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_68	PRJNA269970	SAMN03653788	RUS
mongolica_ _QM71_ _RUS	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_71	PRJNA269970	SAMN03653789	RUS
mongolica_ _QMSUW4_ _SKO	Quercus mongolica Fisch. Ex Ledeb	Quercus mongolica shotgun genomic sequence Qm_SUW_4	PRJNA269970	SAMN03653783	SKO
muehlenbergii_ _MOR383_ _USA-IL	Quercus muehlenbergii Engelm.	Quercus muehlenbergii Engelm. shotgun genomic sequencing, MH103 IL-MOR-MH103	PRJNA269970	SAMN03264810	USA-IL
muehlenbergii_ _MOR632_ _USA-OK	Quercus muehlenbergii Engelm.	Quercus muehlenbergii Engelm. shotgun genomic sequencing, IL_SH57 IL-SH-57	PRJNA269970	SAMN03264815	USA-OK
muehlenbergii_ _MOR639_ _USA-TX	Quercus muehlenbergii Engelm.	Quercus muehlenbergii Engelm. shotgun genomic sequencing, MH49 CA-DAV-MH49	PRJNA269970	SAMN03264803	USA-TX
petraea_ _HB175_ _GER	Quercus petraea (Mattuschka) Li	Quercus petraea shotgun genomic sequence HB_175	PRJNA269970	SAMN03653790	GER
petraea_ _HB181_ _GER	Quercus petraea (Mattuschka) Li	Quercus petraea shotgun genomic sequence HB_181	PRJNA269970	SAMN03653791	GER
petraea_ _MOR520_ _POL	Quercus petraea (Mattuschka) Li	Quercus petraea (Mattuschka) Liebl. shotgun genomic sequencing, MH97 QUPE2_PO_1	PRJNA269970	SAMN03264835	POL
petraea_ _MST29_ _GER	Quercus petraea (Mattuschka) Li	Quercus petraea shotgun genomic sequence MST_29	PRJNA269970	SAMN03653792	GER
petraea_ _MST30_ _GER	Quercus petraea (Mattuschka) Li	Quercus petraea shotgun genomic sequence MST_30	PRJNA269970	SAMN03653793	GER
petraea_ _MST31_ _GER	Quercus petraea (Mattuschka) Li	Quercus petraea shotgun genomic sequence MST_31	PRJNA269970	SAMN03653794	GER
prinoides_ _MOR352_ _USA-VA	Quercus prinoides Willd.	Quercus prinoides Willd. shotgun genomic sequencing, MH7 QUPR2_VA_1	PRJNA269970	SAMN03264838	USA-VA

prinoides_ _MOR532_ _USA-NE	Quercus prinoides Willd.	Quercus prinoides Willd. shotgun genomic sequencing, IL_SH96 IL-SH-096	PRJNA269970	SAMN03264811	USA-NE
prinoides_ _USFSNC1_ _USA-NC	Quercus prinoides Willd.	Quercus prinoides Willd. shotgun genomic sequencing QUPR2_NC_1	PRJNA269970	SAMN03264836	USA-NC
prinoides_ _USFSPN1_ _USA-PN	Quercus prinoides Willd.	Quercus prinoides Willd. shotgun genomic sequencing QUPR2_PN_1	PRJNA269970	SAMN03264837	USA-PN
robur_ _ARK15_ _RUS	Quercus robur L.	Quercus robur shotgun genomic sequence ARK_15	PRJNA269970	SAMN03653809	RUS
robur_ _B2_1_ _RUS	Quercus robur L.	Quercus robur shotgun genomic sequence B2_01	PRJNA269970	SAMN03653795	RUS
robur_ _MOR392_ _RUS	Quercus robur L.	Quercus robur L. shotgun genomic sequencing, MH84 QURO2_RU_1	PRJNA269970	SAMN03264839	RUS
robur_ _PIE06_ _FRA	Quercus robur L.	Quercus robur shotgun genomic sequence PIE_06	PRJNA269970	SAMN03653797	FRA
robur_ _PIE10_ _FRA	Quercus robur L.	Quercus robur shotgun genomic sequence PIE_10	PRJNA269970	SAMN03653796	FRA
robur_ _SVT06_ _UKR	Quercus robur L.	Quercus robur shotgun genomic sequence SVT_06	PRJNA269970	SAMN03653807	UKR
robur_ _SVT11_ _UKR	Quercus robur L.	Quercus robur shotgun genomic sequence SVT_11	PRJNA269970	SAMN03653808	UKR
robur_ _TAM01_ _FIN	Quercus robur L.	Quercus robur shotgun genomic sequence TAM_01	PRJNA269970	SAMN03653798	FIN
robur_ _TAM10_ _FIN	Quercus robur L.	Quercus robur shotgun genomic sequence TAM_10	PRJNA269970	SAMN03653799	FIN
robur_ _WR4_1_ _BEL	Quercus robur L.	Quercus robur shotgun genomic sequence WR4_01	PRJNA269970	SAMN03653805	BEL
robur_ _WR4_7_ _BEL	Quercus robur L.	Quercus robur shotgun genomic sequence WR4_07	PRJNA269970	SAMN03653806	BEL
stellata_ _MOR388_ _USA-IA	Quercus stellata Wangenh.	Quercus stellata Wangenh. shotgun genomic sequencing, MH95 QUST_IA_1	PRJNA269970	SAMN03264841	USA-IA
stellata_ _USFSGA2_ _USA-WI	Quercus stellata Wangenh.	Quercus stellata Wangenh. shotgun genomic sequencing QUST_GA_2	PRJNA269970	SAMN03264840	USA-WI
tomentella_ _MOR133_ _USA-CA	Quercus tomentella Engelm.	Quercus tomentella Engelm. shotgun genomic sequencing, MH14 CA-DAV-MH14	PRJNA269970	SAMN03264802	USA-CA
vacciniifolia_ _MOR377_ _USA-CA	Quercus vaccinifolia Kellogg	Quercus vaccinifolia Kellogg shotgun genomic sequencing, MH68 CA-MH068	PRJNA269970	SAMN03264806	USA-CA
vaseyana_ _MOR397_ _USA-TX	Quercus vaseyana Buckley	Quercus vaseyana Buckley shotgun genomic sequencing, MH39 CA-DAV-MH039	PRJNA269970	SAMN03264798	USA-TX

Florigenex	collected_by	collection_date	geo_loc_name	lat_lon	specimen_voucher	biomaterial_provider	platform
MOR359	D. Keiser		USA: Minnesota	45.3 N 93.2 W	MOR 174462	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	P. Berrang	10/1/2013	USA: North Carolina	35.25357 N 82.19709 W		USDA Forest Service, Milwaukee, WI	HiSeq_2000_100PE
	S. Forry	9/20/2013	USA: Pennsylvania	41.38389 N 79.0540 W		USDA Forest Service, Allegheny National Forest, PA	HiSeq_2000_100PE
	S. Forry	9/20/2013	USA: Pennsylvania	41.50643 N 79.24511 W		USDA Forest Service, Allegheny National Forest, PA	HiSeq_2000_100PE
MOR413	Andrew Hipp, Paul Manos, Jeannine	6/4/2012	USA: Arizona	31.4495 N, 109.2431 W	MOR 174229	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR508	R. Gankin & J.B. Jaacov	5/11/2012	USA: California	38.4 N, 122.0 W	MOR 174692	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR289	A. Hipp		USA: Kansas	38.9048 N 94.8926 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR342	M. Hahn, B.G. Budaitis, E.M. Meza	5/24/2012	USA: Illinois	41.7357 N 87.8565 W	MOR174534	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR436	R. Lance & A. Hipp	1999	USA: Alabama	34.0 N 86.0 W	MOR 175278	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR415	Andrew Hipp, Paul Manos, Jeannine	6/4/2012	USA: Arizona	31.4334 N, 109.2431 W	MOR 174230	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR474	unknown		USA: California	unknown	MOR 174682	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.801233 N 131.245433 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.801267 N 131.245467 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.801283 N 131.245483 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.8013 N 131.2455 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.801317 N 131.245517 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.801367 N 131.245567 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	42.801383 N 131.245583 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
MOR531	unknown		USA: California	unknown	MOR 174681	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR406	W. Roderick		USA: California	32.6 N, 116.9 W	MOR 174583	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR387	unknown		USA: Colorado	38.8 N 105.2 W	MOR 174463	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR546	Andrew Hipp, Paul Manos, Jeannine	6/2/2012	USA: Arizona	31.7566 N, 109.2431 W	MOR 174218	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR422	R. Gankin & G.L. Stebbins		USA: California	38.6946 N 120.8149 W	MOR174699	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	T. Jennings		USA: Oregon	43.3050 N 123.2412 W		USDA Forest Service, Corvallis, OR	HiSeq_2000_100PE
MOR123	L. Waters		USA: California	36.5 N 120.9 W	MOR 174703	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR385	A. Hipp		USA: Missouri	36.7209 N 90.1129 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR611	R. Lance		USA: Georgia	30.7084 N 84.8564 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR616	unknown		USA: North Carolina	35.4 N 82.4 W	MOR 175244	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR672	unknown		USA: New Mexico	33.6 N 105.4 W	MOR 175314	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR673			Canada: Quebec	45.5129 N 73.5506 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	R. Cronn		USA: Kansas	39.0286 N 94.9404 W		USDA Forest Service, Corvallis, OR	HiSeq_2000_100PE
	P. Berrang		USA: Wisconsin	42.8751 N 88.3276 W		USDA Forest Service, Milwaukee, WI	HiSeq_2000_100PE
MOR420	D. Cavagnaro	10/27/1963	USA: Texas	29.6 N 97.6 W	MOR 174705	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE

MOR353	P. J. van der Linden		USA: Missouri	36.6447 N 89.2850 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR694	Friesner		USA: Indiana			Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR700	A. Hipp		USA: Illinois	37.1393 N 89.3429 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR125	D. Cavagnaro	10/11/1963	USA: Texas	32.0 N, 104.7 W	MOR 174704	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR360			China	40.5 N 116.7 E		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	B. Degen	2012	Russia	50.187167 N 138.591 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	50.187167 N 138.591 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	50.187167 N 138.591 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	43.374833 N 133.892 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	43.374833 N 133.892 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	43.374833 N 133.892 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	49.0497 N 131.860333 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	49.0497 N 131.860333 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	43.073167 N 131.909833 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	43.073167 N 131.909833 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	43.073167 N 131.909833 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	August 2012	South Korea	37.5667 N 126.9781 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	August 2012	South Korea	37.5667 N 126.9781 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	August 2012	South Korea			Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	16. September 20	Russia	45.083333 N 133.947194 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	16. September 20	Russia	46.083028 N 133.945889 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	16. September 20	Russia	46.082194 N 133.945556 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	19. September 20	China	45.429692 N 127.092031 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	19. September 20	China	45.429531 N 127.091156 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	19. September 20	China	45.428283 N 127.090569 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	48.619717 N 135.90783 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	48.619717 N 135.90783 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2012	Russia	48.619717 N 135.90783 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	July 2014	South Korea	37.5667 N 126.9781 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
MOR383	C. Shaw		USA: Illinois	41.2 N 88.0 W	MOR 174533	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR632	unknown		USA: Oklahoma	35.7 N 98.9 W	MOR 175345	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR639	unknown		USA: Texas	32.00 N 104.8 W	MOR 174690	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	B. Degen		Germany	53.700539 N 10.719256 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen		Germany	53.700539 N 10.719256 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
MOR520			Poland	51.8 N 19.8 E		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	B. Degen	18. May 2005	Germany	51.909356 N 7.740925 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	18. May 2005	Germany	51.909356 N 7.740925 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	18. May 2005	Germany	51.909356 N 7.740925 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
MOR352	A. Hipp		USA: Virginia	37.1414 N 79.9957 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE

MOR532	G. Morgenson		USA: Nebraska	40.0 N 95.7 W	MOR 175238	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	P. Berrang		USA: North Carolina	35.2535 N 82.1970 W		USDA Forest Service, Milwaukee, W	HiSeq_2000_100PE
	S. Forry		USA: Pennsylvania	41.5073 N 79.2442 W		USDA Forest Service, Allegheny Natl	HiSeq_2000_100PE
	B. Degen	2013	Russia	54.416667 N 56.666667 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2008	Russia	52.674197 N 58.742517 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
MOR392			Russia	55.8 N 37.6 E		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	B. Degen	20. July 2009	France	44.737028 N -0.776389 W		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	20. July 2009	France	44.737028 N -0.776389 W		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2013	Ukraine	49.052833 N 37.9295 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2013	Ukraine	49.052833 N 37.9295 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	03. June 2008	Finland	59.974439 N 23.435525 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	03. June 2008	Finland	59.974439 N 23.435525 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2013	Belarus	53.685833 N 23.792833 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
	B. Degen	2013	Belarus	53.685833 N 23.792833 E		Thuenen Institute of Forest Genetic	HiSeq_2000_100PE
MOR388	P. J. van der Linden		USA: Iowa	40.6123 N 91.6857 W		Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
	P. Berrang		USA: Wisconsin	33.9025 N 83.3824 W		USDA Forest Service, Milwaukee, W	HiSeq_2000_100PE
MOR133	R. Gankin	9/8/1968	USA: California	34.0 N, 119.6 W	MOR 174688	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR377	unknown		USA: California	38.8 N 120.1 W	MOR 174684	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE
MOR397	D. Cavagnaro	10/7/1963	USA: Texas	30.0 N, 101.2 W	MOR 174580	Morton Arboretum, Lisle, IL	HiSeq_2000_100PE

sample ID	index	yield (Mb)	sequence reads	Mean Q Score (PF)	mapped cp reads	% cp	coverage depth, mean	assembly ACGT_count	assembly N_count	assembly length
lane1-index703-D508-CGCTCATT-GTACTGAC-QUAL_MN_1	CGCTCATT-	595	6,373,964	34.87	249664	3.92%	170.6	135303	77	135380
lane1-index704-D501-GAGATTCC-TATAGCCT-QUAL_NC_2	GTACTGAC GAGATTCC-	1,399	14,782,704	35.47	369454	2.50%	245.0	135312	78	135390
lane1-index704-D505-GAGATTCC-AGGCGAAG-QUAL_PN_1	TATAGCCT- GAGATTCC-	586	6,322,916	33.56	124491	1.97%	78.8	135291	100	135391
lane1-index704-D508-GAGATTCC-GTACTGAC-QUAL_VT_4	AGGCGAAG GAGATTCC-	501	5,488,628	32.54	106476	1.94%	69.7	135291	94	135385
lane1-index701-D502-ATTACTCG-ATAGAGGC-AZ-HU-15	GTACTGAC ATTACTCG-	849	9,084,856	35.02	404289	4.45%	289.2	135315	78	135393
lane1-index701-D505-ATTACTCG-AGGCGAAG-CA-DAV-MH047	ATAGAGGC ATTACTCG-	933	10,140,768	33.99	696427	6.87%	500.9	135258	77	135335
lane1-index705-D503-ATTCAGAA-CCTATCCT-QUBI_KS_1	AGGCGAAG ATTCAGAA-	639	6,817,672	34.82	222426	3.26%	150.3	135309	80	135389
lane1-index705-D502-ATTCAGAA-ATAGAGGC-QUBI_IL_1	CCTATCCT- ATTCAGAA-	663	7,108,492	34.33	304107	4.28%	210.1	135325	73	135398
lane1-index703-D504-CGCTCATT-GGCTCTGA-IL-SH-24	ATAGAGGC CGCTCATT-	590	6,366,160	34.41	197645	3.10%	140.3	135293	94	135387
lane1-index701-D503-ATTACTCG-CCTATCCT-AZ-HU-17	GGCTCTGA ATTACTCG-	1,165	12,559,072	34.85	633634	5.05%	454.0	135073	110	135183
lane1-index702-D505-TCCGGAGA-AGGCGAAG-CA-MH070	CCTATCCT- TCCGGAGA-	728	7,821,994	34.71	290406	3.71%	206.5	135165	120	135285
lane1-index07-CAGATC-Qd1	AGGCGAAG CAGATC	826	8,837,518	35.79	241152	2.73%	173.5	135155	197	135352
lane1-index03-TTAGGC-Qd3	TAGATC	684	7,255,918	36.09	129861	1.79%	92.4	135215	147	135362
lane1-index04-TGACCA-Qd4	TGACCA	671	7,082,146	36.2	98189	1.39%	69.4	135166	190	135356
lane1-index05-ACAGTG-Qd5	ACAGTG	803	8,590,947	36.02	157466	1.83%	111.3	135166	190	135356
lane1-index08-ACTTGA-Qd6	ACTTGA	803	8,506,833	36.08	206509	2.43%	149.1	135113	246	135359
lane1-index06-GCCAAT-Qd9	GCCAAT	855	8,990,739	36.3	222537	2.48%	160.0	135154	197	135351
lane1-index01-ATCACG-Qd10	ATCACG	613	6,450,784	36.26	103182	1.60%	73.4	135192	167	135359
lane1-index702-D506-TCCGGAGA-TAATCTTA-CA-MH-073	TCCGGAGA- TAATCTTA	723	7,741,604	34.87	535794	6.92%	385.7	135240	78	135318
lane1-index701-D507-ATTACTCG-CAGGACGT-CA-DAV-MH035	ATTACTCG- CAGGACGT	581	6,202,948	34.89	282616	4.56%	201.8	134991	179	135170
lane1-index702-D507-TCCGGAGA-CAGGACGT-IL-MOR-MH092	TCCGGAGA- CAGGACGT	825	8,766,240	35.02	450494	5.14%	323.2	135315	77	135392
lane1-index701-D501-ATTACTCG-TATAGCCT-AZ-CH-11	ATTACTCG- TATAGCCT	635	6,784,452	35.13	365201	5.38%	262.7	135319	77	135396
lane1-index705-D507-ATTCAGAA-CAGGACGT-QUGA4_CA_1	ATTCAGAA- CAGGACGT	806	8,492,498	35.23	624694	7.36%	438.5	135273	77	135350
lane1-index705-D508-ATTCAGAA-GTACTGAC-QUGA4_OR_1	ATTCAGAA- GTACTGAC	713	7,594,074	35.02	97511	1.28%	57.6	135244	85	135329
lane1-index702-D503-TCCGGAGA-CCTATCCT-CA-DAV-MH53	TCCGGAGA- CCTATCCT	836	8,975,916	34.69	272176	3.03%	193.1	135244	137	135381
lane1-index706-D506-GAATTCGT-TAATCTTA-QULY_MO_1	GAATTCGT- TAATCTTA	859	9,182,292	34.08	226311	2.46%	159.9	135315	72	135387
lane1-index706-D504-GAATTCGT-GGCTCTGA-QULY_GA_1	TAATCTTA GAATTCGT-	782	8,374,828	33.84	445477	5.32%	311.2	135316	72	135388
lane1-index703-D503-CGCTCATT-CCTATCCT-IL-SH-187	GGCTCTGA CGCTCATT-	856	9,352,144	33.94	229705	2.46%	161.9	135316	79	135395
lane1-index703-D502-CGCTCATT-ATAGAGGC-IL-SH-186	CCTATCCT- CGCTCATT-	845	9,059,634	34.85	279190	3.08%	198.7	135305	92	135397
lane1-index708-D503-TAATGCGC-CCTATCCT-QUMA2_QU_1	ATAGAGGC TAATGCGC-	1,089	11,585,406	35.34	303174	2.62%	202.9	135299	91	135390
lane1-index707-D501-CTGAAGCT-TATAGCCT-QUMA2_KS_1	CCTATCCT- CTGAAGCT-	339	3,863,516	29.22	101898	2.64%	70.1	135302	87	135389
lane1-index708-D505-TAATGCGC-AGGCGAAG-QUMA2_WI_3	TATAGCCT- TAATGCGC-	1,126	11,974,486	35.43	371944	3.11%	254.5	135319	77	135396
lane1-index702-D502-TCCGGAGA-ATAGAGGC-CA-DAV-MH50	AGGCGAAG TCCGGAGA-	1,004	10,683,146	35.12	472335	4.42%	336.8	135302	84	135386
	ATAGAGGC									

lane1-index709-D503-CGGCTATG-CCTATCCT-QUMI_MO_1	CGGCIAIG- CCTATCCT	484	5,195,530	34.92	280918	5.41%	196.1	135334	71	135405
lane1-index709-D502-CGGCTATG-ATAGAGGC-QUMI_IN_1	CGGCIAIG- ATAGAGGC	782	8,368,284	35.17	336682	4.02%	232.1	135312	77	135389
lane1-index709-D501-CGGCTATG-TATAGCCT-QUMI_IL_1	CGGCIAIG- TATAGCCT	886	9,457,046	35.32	372635	3.94%	256.2	135330	73	135403
lane1-index701-D506-ATTACTCG-TAATCTTA-CA-DAV-MH051	ATTACTCG- TAATCTTA	808	8,604,404	35.42	367184	4.27%	263.5	135305	77	135382
lane1-index709-D504-CGGCTATG-GGCTCTGA-QUM05_CH_1	CGGCIAIG- GGCTCTGA	1,147	12,336,068	34.64	911239	7.39%	645.2	135258	69	135327
lane1-index09-GATCAG-Opb_13	GATCAG	437	4,588,607	36.18	359604	7.84%	263.3	135167	198	135365
lane1-index10-TAGCTT-Opb_21	TAGCTT	510	5,439,434	35.84	395156	7.26%	288.6	135190	170	135360
lane1-index11-GGCTAC-Opb_26	GGCTAC	1,097	11,586,375	36.11	458704	3.96%	332.8	135256	109	135365
lane1-index12-CTTGTA-Opl_19	CTTGTA	548	6,060,445	34.78	147333	2.43%	105.8	135351	25	135376
lane1-index13-AGTCAA-Opl_20	AGTCAA	1,067	11,235,782	36.19	244356	2.17%	175.4	135363	17	135380
lane1-index14-AGTTCC-Opl_21	AGTTCC	362	4,067,301	34.17	85682	2.11%	61.0	135350	25	135375
lane1-index15-ATGTCA-Oto_14	ATGTCA	532	5,876,125	35.02	68037	1.16%	47.6	135341	20	135361
lane1-index16-CCGTCC-Oto_3	CCGTCC	501	5,366,529	35.29	72884	1.36%	51.8	135341	22	135363
lane1-index19-GTGAAA-Ovl_2	GTGAAA	632	6,650,148	36.22	113363	1.70%	81.3	135189	164	135353
lane1-index20-GTGGCC-Ovl_4	GTGGCC	1,330	14,000,378	36.25	295851	2.11%	212.4	135330	23	135353
lane1-index18-GTCCGC-Ovl_14	GTCCGC	453	4,778,643	36.21	111867	2.34%	80.8	135342	21	135363
lane1-index21-GTTTCG-Qkor_2	GTTTCG	343	3,747,744	35.72	122680	3.27%	88.4	135322	25	135347
lane1-index22-CGTACG-Qkor_7	CGTACG	584	6,320,652	35.5	106471	1.68%	75.5	135320	24	135344
lane2-index19-GTGAAA-Qkor_8	GTGAAA	618	6,579,237	35.77	239676	3.64%	174.6	135342	28	135370
lane1-index25-ACTGAT-Qm_14	ACTGAT	1,445	15,243,269	36.3	87766	0.58%	59.0	135344	22	135366
lane1-index27-ATTCTT-Qm_18	ATTCTT	986	10,380,621	36.21	206516	1.99%	148.4	135343	32	135375
lane2-index01-ATCACG-Qm_20	ATCACG	793	8,320,777	36.27	116218	1.40%	82.8	135353	10	135363
lane2-index15-ATGTCA-Qm_42	ATGTCA	660	6,926,209	36.26	228592	3.30%	166.1	135353	10	135363
lane2-index16-CCGTCC-Qm_44	CCGTCC	725	7,604,072	36.21	154351	2.03%	110.8	135340	22	135362
lane2-index18-GTCCGC-Qm_49	GTCCGC	778	8,149,115	36.22	147999	1.82%	106.4	135348	12	135360
lane2-index02-CGATGT-Qm_65	CGATGT	481	5,143,973	35.79	95571	1.86%	68.0	135140	212	135352
lane2-index03-TTAGGC-Qm_68	TTAGGC	432	4,712,797	35.52	120385	2.55%	86.1	135311	24	135335
lane2-index04-TGACCA-Qm_71	TGACCA	370	4,306,265	33.52	113799	2.64%	81.3	135125	233	135358
lane1-index23-GAGTGG-Qm_SUW_4	GAGTGG	605	6,315,482	36.24	501129	7.93%	366.2	135369	2	135371
lane1-index702-D508-TCCGGAGA-GTACTGAC-IL-MOR-MH103	TCCGGAGA- GTACTGAC	454	4,868,858	34.83	133092	2.73%	94.0	135274	112	135386
lane1-index703-D505-CGCTCATT-AGGCGAAG-IL-SH-57	CGCTCATT- AGGCGAAG	825	8,855,086	34.87	225532	2.55%	158.6	135324	77	135401
lane1-index702-D501-TCCGGAGA-TATAGCCT-CA-DAV-MH49	TCCGGAGA- TATAGCCT	570	6,102,298	34.9	271728	4.45%	194.4	135308	78	135386
lane2-index05-ACAGTG-HB_175	ACAGTG	505	5,282,756	35.99	113388	2.15%	81.5	135354	15	135369
lane2-index06-GCCAAT-HB_181	GCCAAT	1,203	12,628,934	35.98	303839	2.41%	218.5	135358	14	135372
lane1-index709-D505-CGGCTATG-AGGCGAAG-QUPE2_PO_1	CGGCIAIG- AGGCGAAG	1,561	16,719,416	34.87	648087	3.88%	445.5	135256	72	135328
lane2-index07-CAGATC-MST_29	CAGATC	815	8,500,932	36.29	646991	7.61%	472.7	135366	11	135377
lane2-index08-ACTTGA-MST_30	ACTTGA	785	8,199,460	36.24	583314	7.11%	426.4	135367	11	135378
lane2-index09-GATCAG-MST_31	GATCAG	368	3,850,987	36.06	359410	9.33%	263.1	135359	13	135372
lane1-index710-D503-TCCGGGAA-CCTATCCT-QUPR2_VA_1	TCCGGGAA- CCTATCCT	863	9,251,870	34.83	343156	3.71%	235.0	135312	77	135389

lane1-index703-D501-CGCTCATT-TATAGCCT-IL-SH-096	CGCTCATT- TATAGCCT	817	8,751,196	34.92	226311	2.59%	159.9	135310	78	135388
lane1-index709-D506-CGGCTATG-TAATCTTA-QUPR2_NC_1	CGGCTATG- TAATCTTA	890	9,499,730	35.33	151100	1.59%	95.8	135313	79	135392
lane1-index710-D502-TCCGCGAA-ATAGAGGC-QUPR2_PN_1	TCCGCGAA- ATAGAGGC	1,171	12,484,692	35.17	303079	2.43%	203.1	135328	74	135402
lane2-index27-ATTCCT-ARK_15	ATTCCT	1,064	11,915,961	34.94	403126	3.38%	290.4	135340	28	135368
lane2-index10-TAGCTT-B2_1	TAGCTT	997	10,376,834	36.38	357705	3.45%	258.5	135378	12	135390
lane1-index710-D505-TCCGCGAA-AGGCGAAG-QURO2_RU_1	TCCGCGAA- AGGCGAAG	1,632	17,470,594	35	818393	4.68%	567.7	135285	72	135357
lane2-index12-CTTGTA-PIE_6	CTTGTA	611	6,366,688	36.37	303781	4.77%	220.5	135360	11	135371
lane2-index11-GGCTAC-PIE_10	GGCTAC	1,765	18,332,609	36.41	950637	5.19%	690.9	135374	5	135379
lane2-index23-GAGTGG-SVT_6	GAGTGG	977	10,224,657	36.21	287688	2.81%	211.4	135384	9	135393
lane2-index25-ACTGAT-SVT_11	ACTGAT	544	6,371,705	34.4	162957	2.56%	115.8	135368	18	135386
lane2-index13-AGTCAA-TAM_1	AGTCAA	641	6,702,004	36.21	269096	4.02%	195.3	135350	13	135363
lane2-index14-AGTTCC-TAM_10	AGTTCC	739	7,760,332	36.02	331159	4.27%	240.8	135350	11	135361
lane2-index21-GTTTCG-WR4_1	GTTTCG	190	2,851,967	28.17	18161	0.64%	11.5	135071	311	135382
lane2-index22-CGTACG-WR4_7	CGTACG	351	4,913,182	27.47	17859	0.36%	10.7	135079	349	135428
lane1-index711-D502-TCTCGCGC-ATAGAGGC-QUST_IA_1	TCTCGCGC- ATAGAGGC	545	5,810,094	35.2	203778	3.51%	138.4	135302	76	135378
lane1-index711-D501-TCTCGCGC-TATAGCCT-QUST_GA_2	TCTCGCGC- TATAGCCT	756	8,106,672	34.65	98394	1.21%	60.1	135280	105	135385
lane1-index701-D508-ATTACTCG-GTACTGAC-CA-DAV-MH14	ATTACTCG- GTACTGAC	744	7,957,296	34.84	240512	3.02%	170.8	135002	136	135138
lane1-index702-D504-TCCGGAGA-GGCTCTGA-CA-MH068	TCCGGAGA- GGCTCTGA	682	7,347,776	34.31	410357	5.58%	294.5	135036	151	135187
lane1-index701-D504-ATTACTCG-GGCTCTGA-CA-DAV-MH039	ATTACTCG- GGCTCTGA	639	6,877,046	34.74	309340	4.50%	221.1	135291	79	135370

Sheet1

<u>species</u>	<u>clade and region</u>	<u>all oaks</u>	<u>North American oaks</u>
chrysolepis	Protobalanus	x	x
tomentella	Protobalanus	x	x
vacciniifolia	Protobalanus	x	x
robur	White oaks - Eurasia	x	
petraea	White oaks - Eurasia	x	
mongolica	White oaks - Eurasia	x	
garryana	White oaks - California	x	x
berberidifolia	White oaks - California	x	x
douglasii	White oaks - California	x	x
lobata	White oaks - California	x	x
montana	White oaks - Eastern North America	x	x
michauxii	White oaks - Eastern North America	x	x
alba	White oaks - Eastern North America	x	x
lyrata	White oaks - Eastern North America	x	x
bicolor	White oaks - Eastern North America	x	x
macrocarpa	White oaks - Eastern North America	x	x
muehlenbergii	White oaks - Eastern North America	x	x
prinoides	White oaks - Eastern North America	x	x
boyntonii	White oaks - Eastern North America	x	x
margarettae	White oaks - Eastern North America	x	x
stellata	White oaks - Eastern North America	x	x
engelmannii	White oaks - Western North America	x	x
arizonica	White oaks - Western North America	x	x
mohriana	White oaks - Western North America	x	x
vaseyana	White oaks - Western North America	x	x

North American white oaks North American oaks without California eastern North American white oaks

[illegible]

All oaks

North American oaks only

North American white oaks without California, *Quercus engelmannii* excluded

North American white oaks without California