

International Oaks

The Journal of the International Oak Society

Proceedings

8th International Oak Society Conference October 18-21, 2015



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Photos. p. 9: James MacEwen (Michael Heathcoat Amory); p. 10: Guy Sternberg (8th International Oak Society Conference participants); p. 11: Charles Snyers d'Attenhoven (Quercus stellata); p. 13: Béatrice Chassé (Q. ×fernowii).

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First International Oak Society Silent Auction



Quercus bicolor at Starhill Forest Arboretum (Charles Snyers d'Attenhoven).

Best Under Stress: Does An Episodic Hybrid Advantage Suppress Reproductive Barriers in Oaks?

Warren B. Chatwin¹, Chris R. Heim², Mark V. Coggeshall², and Jeanne Romero-Severson¹

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The effects of hybridization in oaks (*Quercus*) are poorly understood. Even among allopatric species, intrinsic reproductive barriers appear weak. Why have these barriers not arisen despite millions of years of separation? We hypothesize that, under episodic climate stress, hybrids have a periodic advantage that suppresses the development of intrinsic reproductive barriers, resulting in a highly conserved genomic architecture among interacting species. This conservation preserves a general oak "lineage pool" which allows species to emerge, split, and fuse according to changes in long-term climate trends.

Given that selection is most intense in seedlings, we will determine the relative fitness of hybrid and parental seedlings under drought, flooding, and permissive conditions. We will also use genetic mapping with ddRADtags to infer their genomic architecture. We have used 18 EST-SSR markers (mapped in $Q.\ robur\ L.$) to identify the parentage of the progeny of two F_1 hybrids. We have genotyped 256 germinated progeny, 70 progeny that failed to germinate, and all potential pollen parents within 500 m (including $Q.\ varei$ Green & Hess, $Q.\ vschuettei$ Trel., $Q.\ robur$, $Q.\ bicolor$ Willd., and five other species). We inferred parentage using CERVUS. Parentage assignment was successful with positive LOD scores for 167 progeny. Our analysis indicates that most progeny are backcrosses to $Q.\ robur$. Starting fresh in Fall 2015, we have collected thousands of acorns to be used in a four-year study to test our hypothesis of a periodic hybrid advantage under climate stress. We expect these data to help us understand why oaks, and other forest trees, have not developed strong reproductive barriers over millions of years of ecological speciation.

Advantage Suppress Reproductive Barriers in Oaks? Best Under Stress: Does An Episodic Hybrid

NOTRE DAME

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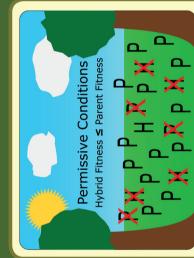
Results & Conclusions:

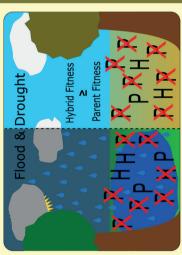
- the Q. × warei with the highest seed set
- leverage the Q. robur genome sequence and will generate enough progeny for phenotypic testing These backcrossed progeny enable us to
- tors, but a low seed set (likely due to its geograph- The other Q. × warei has a variety of pollinaic placement between two tall buildings)
- in pollinator for acorns that germinate and acorns There does not appear to be any difference that fail to germinate
- enough statistical power to study the mechanisms Our parentage analysis shows that we have that sustain weak species boundaries in oaks.

ntroduction:

ly separated species, intrinsic reproductive barriers brids have a periodic advantage which suppresses The effects of hybridization in oaks (Quercus) are poorly understood. Even among geographicalture among interacting species. This conservation the development of intrinsic reproductive barriers, appear weak. Why have these barriers not arisen ows species to emerge, split, and fuse according resulting in a highly conserved genomic architecpothesize that, under episodic climate stress, hypreserves a general oak "lineage pool" which aldespite millions of years of separation? We hyto changes in long term climate trends.

of two F, hybrid crosses, Q. × warei (Q. bicolor × Q. expect these data to help us understand why oaks and permissive conditions. Many of the F, hybrids Our study focuses on examining the progeny pus. We will evaluate the relative fitness of hybrid ture and search for novel gene combinations. We carpa) located on the University of Missouri camrobur) and Q. *schuettei (Q. bicolor * Q. macrocies. We will also analyze their genetic architecare more stress tolerant than either parent speand parental seedlings under drought, flooding,

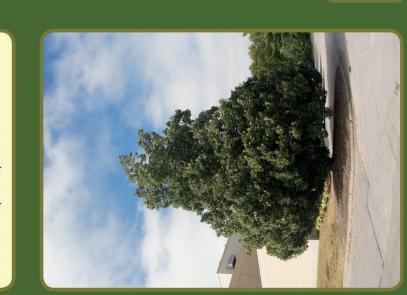




oped strong reproductive barriers over millions of and many other torest tree taxa have not develyears of ecological speciation.

Hypotheses:

- 1. F, hybrid seedlings will survive severe abiotic stress better than parental species.
- 2. Under permissive conditions hybrid seedlings will have little or no survival advantage.
 - 3. Genomic architecture will be highly conserved across sympatric species pools.
- 4. Conserved genomic architecture will persist even under allopatric speciation.



P = Parent Species Seedlings H = Hybrid Seedlings X = Deceased

Materials and Methods:

Collect Acorns from Hybrid Trees

18 EST-SSR markers from Q. robur

Detect the pollen parent using

seedlings to stress tests (drought, flooding) Subject groups of hybrid and parent species

Survival, growth metrics) Collect Phenotypic data

Use high throughput sequencing of genetic markers (ddRADtags) for parents and progeny

Construct genetic maps

Assess genomic architecture in both hybrid and parent species pecies

arei

The distribution of pollen parents for two different Q. × warei for acorns that either germinated or failed to germinate in 2014. Table 1: Pollen Parentage Assignment

Putative Species	Q. robur fastigiata	Q. robur fastigiata	Q. ×warei	Q. bicolor	Q. robur fastigiata	Q. robur fastigiata	Q. × warei	Q. robur fastigiata	Q. robur fastigiata	Q. bicolor
Number Pollinated	132	15	1	-	98	10	1	46	5	-
Pollen Parent	22082	22080	22133	22091	22082	22080	22133	22082	22080	22091
Q. ×warei#3	TOTAL			GERMINATED			FAILED TO GERMINATE			

Putative S	Q. ×W	Q. lyrë	Q. rot	Q. bicc	Q. × jack	Q. bicc	Q. macro		
Number Pollinated	7	က	8	2	1	-	1		
Pollen Parent	22133	22127	22112	22098	22100	22104	22122		
Q. ×warei#2		GERMINATED							
Locate novel combinations of stress resistant/folerant genes using QTL analysis and the <i>Q. robur</i> genome				Acknowledgements: The authors would like to thank Arpita Konar, Andi Noakes, and Lauren Fiedler for	their sacrifices of time and supplies to support this project. WC acknowledges support from the National Science Foundation through a Graduate Research Fellowship (DGE-	1313583). WC thanks his advisor JRS for her time and constant mentoring to help him become a better scientist and human citizen. He also thanks his wife for her patience	with not seeing him much recently, as well as his mother for instilling in him a love for the outdoors and encouraging him to reach his lofty goals.		

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