

Distribution and populations of *Armillaria* in the region



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Armillaria Species and Relative Pathogenicity

NABS ^a	Species	Pathogenicity	Primary Host
I	<i>A. ostoyae</i>	High	Conifers
VI	<i>A. mellea</i>	High	Hardwoods
	<i>A. tabescens</i>	High?	Hardwoods
II	<i>A. gemina</i>	Moderate?	Hardwoods
IX	<i>A. nabsnona</i>	Moderate?	Hardwoods
III	<i>A. calvescens</i>	Low	Mixed
V	<i>A. sinapina</i>	Low	Mixed
VII	<i>A. gallica</i>	Low	Mixed
XI	<i>A. cepistipes</i>	Low	Mixed
X	Unnamed	Rarely pathogenic	Mixed

^aNABS = North American Biological Species

IFTNC *Armillaria* species summary

During the 1999 and 2000 field seasons over 8,500 trees were sampled for *Armillaria*, 1,310 isolates of *Armillaria* were collected from 23 IFTNC sites.

Based on over 8,000 somatic-incompatibility tests, these isolates were found to consist of 221 genets (individual clones).

Of the 10 North American Biological Species 6 were associated with the IFTNC sites.

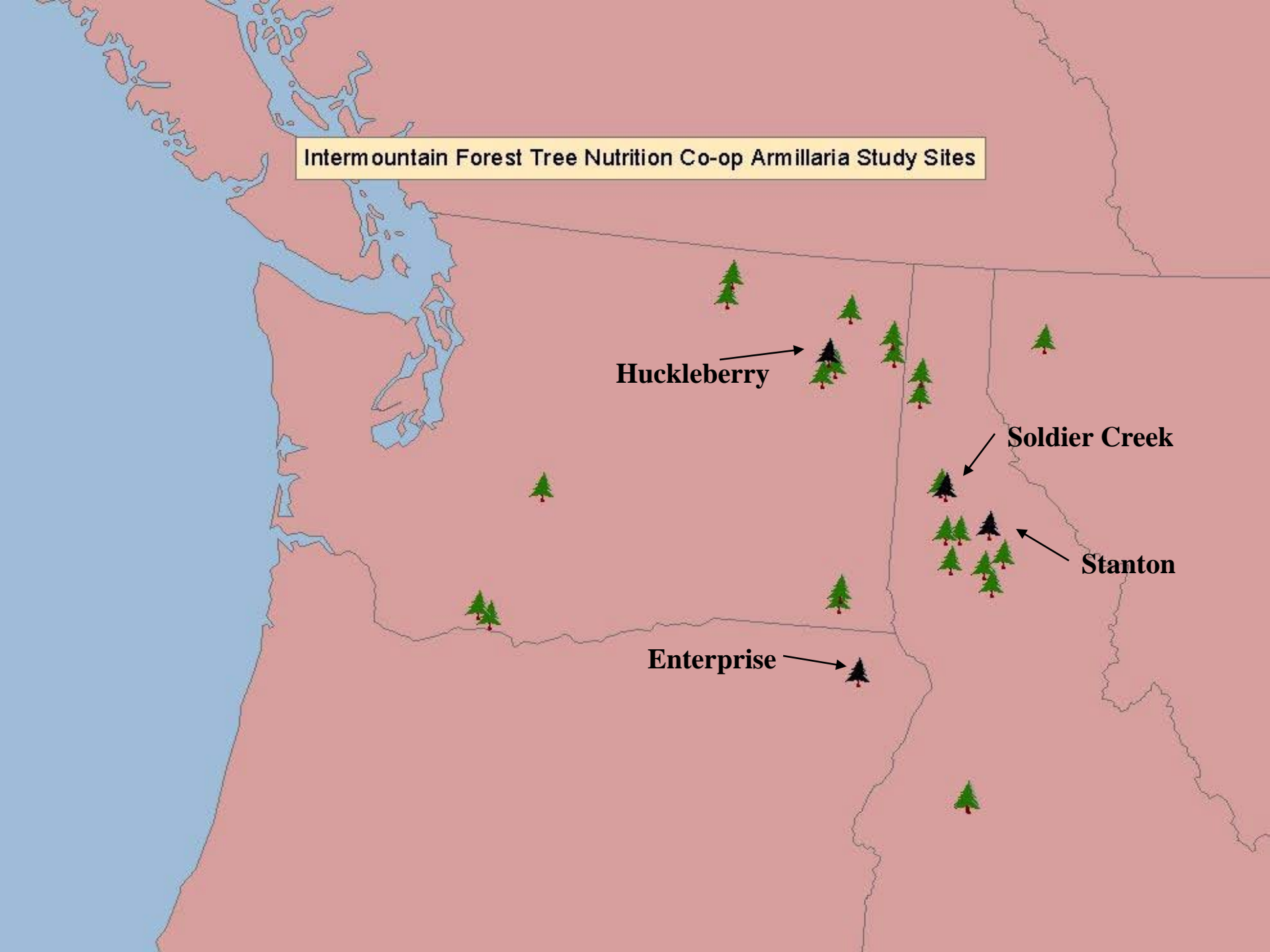
Intermountain Forest Tree Nutrition Co-op Armillaria Study Sites

Huckleberry

Soldier Creek

Stanton

Enterprise



NABS I – *Armillaria ostoyae*

62 genets collected from 17 IFTNC sites



- ❖ Serious plant pathogen found throughout the Northern Hemisphere that causes root and butt rot on diverse woody plant hosts.
- ❖ Adversely impacts commercial timber production by causing tree mortality and growth reduction.
- ❖ Genetically diverse and may be comprised of several races. Intraspecific hybrids are common.

NABS X – Unnamed *Armillaria* species

69 genets collected from 16 IFTNC sites

- ❖ Unnamed *Armillaria* species found in the northwestern United States.
- ❖ Mainly saprophytic, living on dead organic matter.



NABS III, V, VII complex –

A. calvescens, A. sinapina, A. gallica

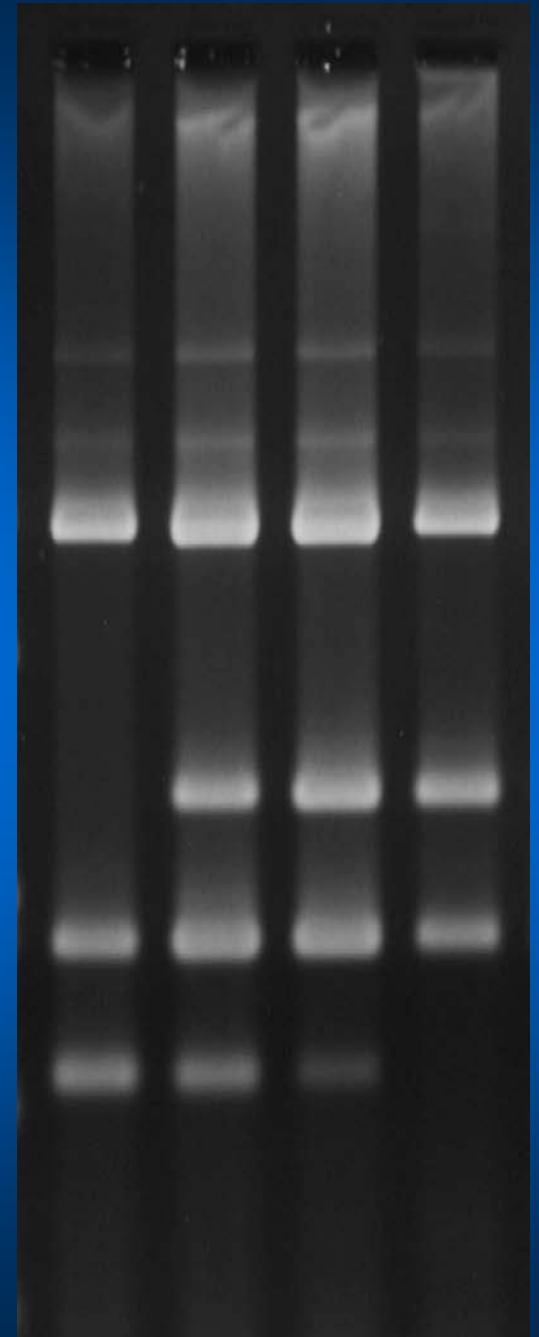
58 genets collected from 14 IFTNC sites

- ❖ Group of similar species of *Armillaria* found throughout North America.
- ❖ Primarily saprophytic with low pathogenicity (less than 5%).
- ❖ Hybridization is common between species.
- ❖ Hybrids are difficult to identify.

NABS X / NABS III, V, VII complex hybrids

31 genets collected from
12 IFTNC sites

- ❖ Common within the Inland Northwest.
- ❖ Previously grouped with NABS X until their discovery using molecular techniques.
- ❖ Mainly saprophytic (less than 5% pathogenic).



NABS IX – *Armillaria nabsnona*

1 genet collected from 1 IFTNC site

- ❖ A rare species found primarily on hardwoods, such as *Alnus* species, in riparian areas of western North America.
- ❖ IFTNC's isolation of this species from *Abies grandis* is one of the first reports of this species being isolated from a conifer.



Types of information collected from Nutrition Co-op sites

- ❖ Isolate ID
- ❖ Location
- ❖ Host Species
- ❖ Collection Type (Bark Fan, Rhizomorph, or Wood)
- ❖ Host Collection (Dead or Alive)
- ❖ Habitat Type
- ❖ Fertilization Treatment
- ❖ Species ID
- ❖ Rock Type

Bark fan collection type



UC Statewide IPM Project
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Bark fans from live trees indicate high pathogenicity of an *Armillaria* individual

Dead trees with bark fans and resinosus and or wound periderm may indicate pathogenicity

Dead trees with bark fans without resinosus indicate saprophytic behavior

Wood collection type

Robert L. Anderson, USDA Forest Service
forestryimages.com

Wood samples are usually taken from trees that have recently been killed or are infected with a pathogenic *Armillaria* individual.

Often dark lines known as zone lines can be seen in infected wood.

Rhizomorph collection type

Robert L. Anderson, USDA Forest Service
forestryimages.com

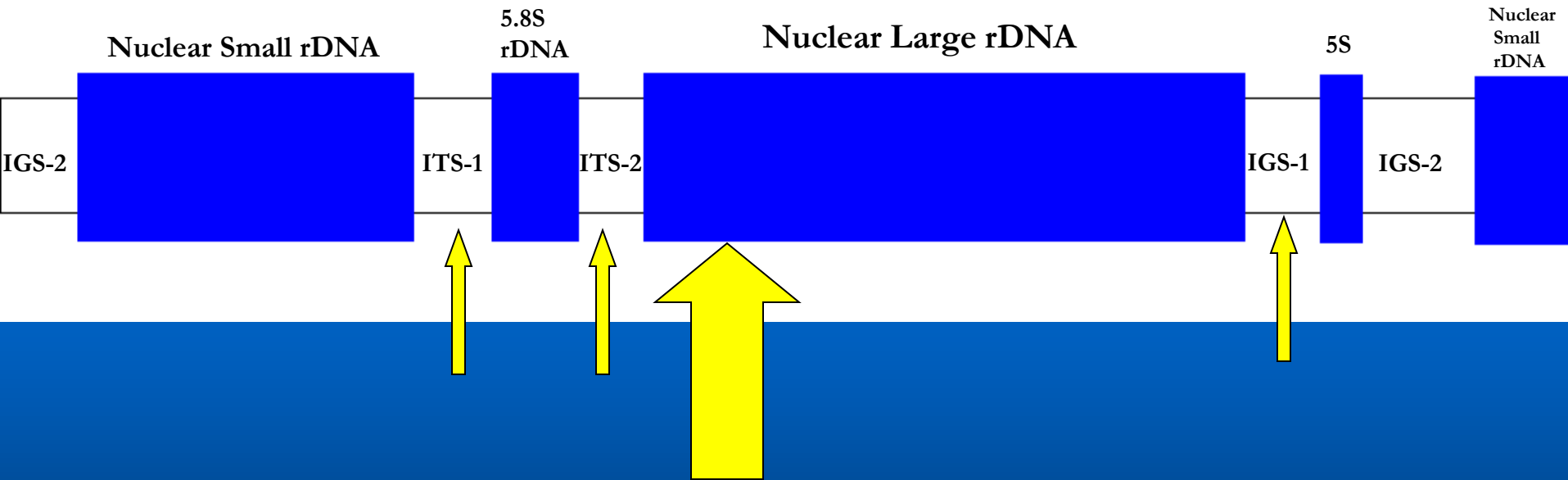


All species of *Armillaria* form rhizomorphs.

Most rhizomorphs are found on the surface of a root, some grow freely through the soil, and others can be found under the bark of a highly infected tree.

Presence of rhizomorphs does not necessarily indicate pathogenicity of an *Armillaria* individual.

DNA Sequencing

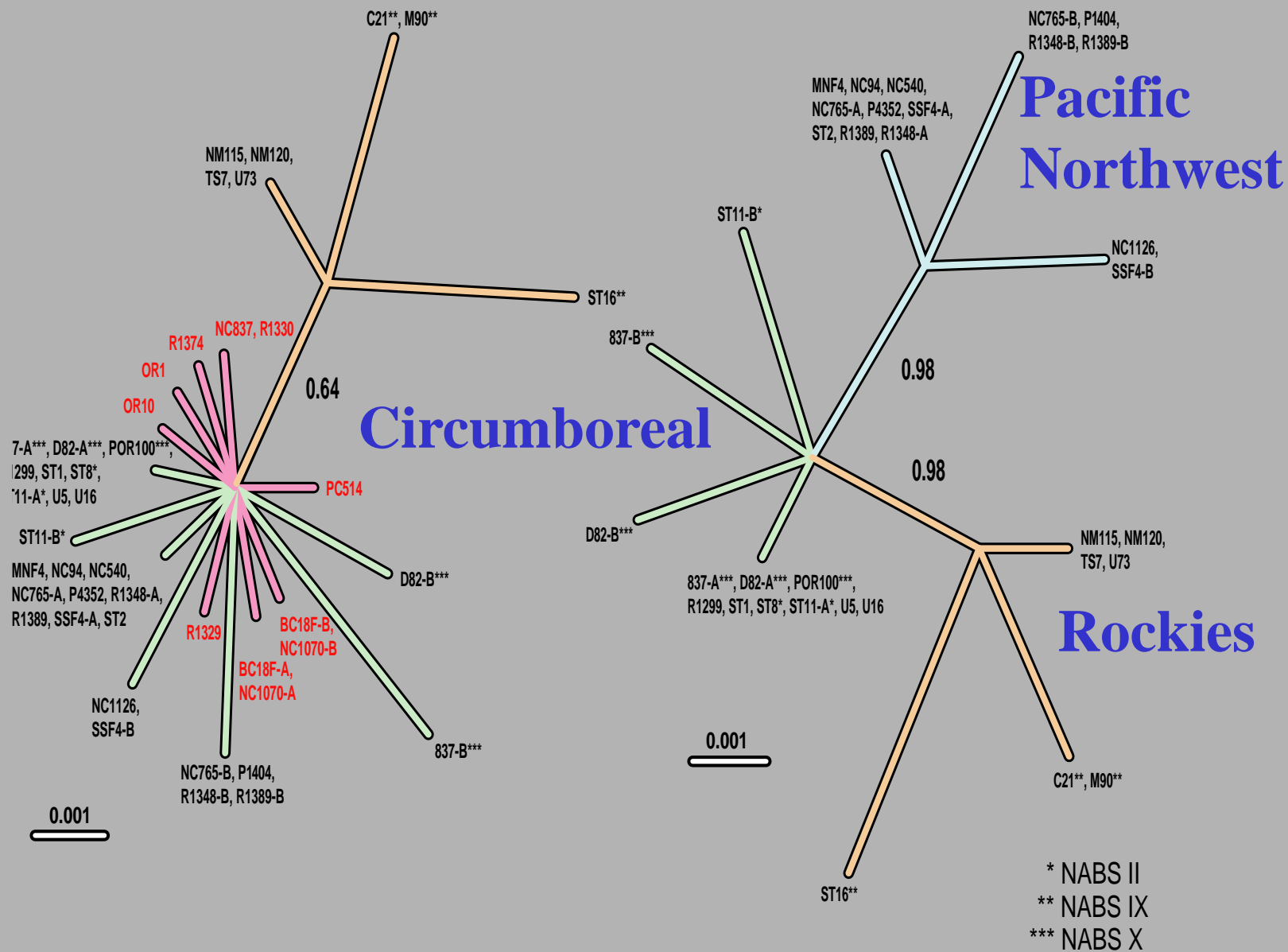


Ribosomal DNA regions currently being investigated for phylogenetic signal include IGS, ITS, and LSU.

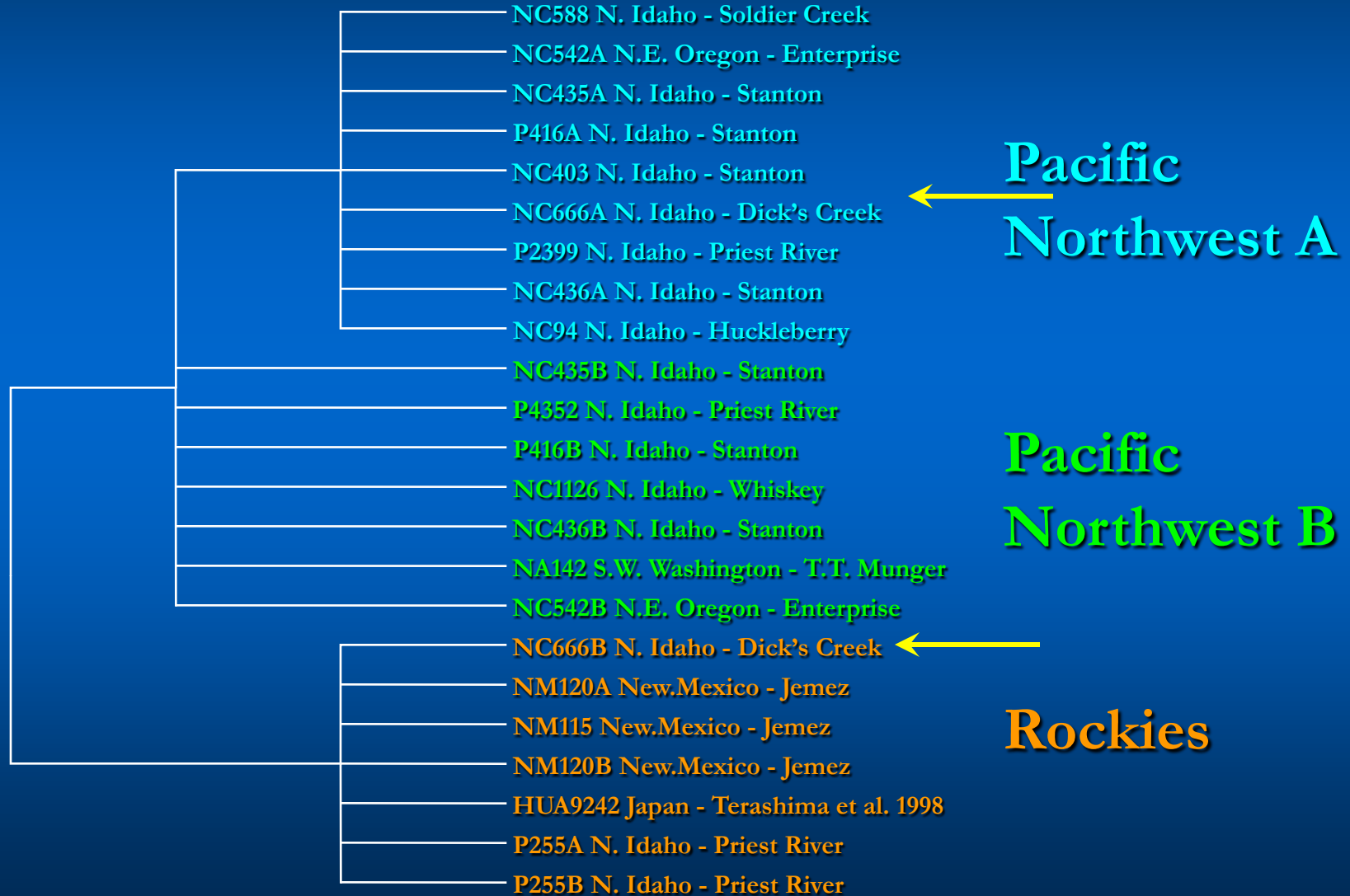
Variable nucleotide positions of aligned nLSU sequences.

GENET	126bp	129bp	165bp	172-173bp	227bp	407bp	470bp	477bp	481bp	500bp	514bp	518bp	524bp	602bp	656bp	750bp	787bp	812bp
837-A***, D82-A***, POR100***, R1299, ST1, ST8*, ST11-A*, U5, U16	A	T	C	GA	T	C	T	C	C	C	G	A	C	G	A	A	T	T
ST11-B*	A	T	C	GA	T	C	T	C	C	C	G	A	C	G	G	A	T	T
837-B***	A	C	C	GA	T	C	T	C	C	C	G	A	C	G	A	A	T	T
D82-B***	A	T	C	GA	T	C	T	C	C	C	G	G	C	G	A	A	T	T
MNF4, NC94, NC540, NC765-A, P4352, R1348-A, R1389, SSF4-A, ST2	A	T	C	GA	T	C	T	T	C	C	G	A	C	G	A	A	T	T
NC765-B, P1404, R1348-B, R1389-B	A	T	C	GA	T	C	T	T	C	A	G	A	C	G	A	A	T	T
NC1126, SSF4-B	A	T	C	GA	T	C	T	T	C	C	G	A	C	A	A	A	T	T
BC18F-A, NC1070-A	A	T	Y	GA	T	C	T	T	C	C	G	A	C	G	A	A	T	T
BC18F-B, NC1070-B	A	T	Y	~~	T	C	T	T	C	C	G	A	C	G	A	A	T	T
R1329	A	T	C	GA	Y	C	T	T	C	C	G	A	C	R	A	A	T	T
OR1	A	T	C	GA	T	C	T	Y	M	C	R	A	C	G	A	A	T	Y
OR10	A	T	C	GA	T	C	T	Y	M	C	R	A	C	G	A	A	T	T
PC514	A	T	C	GA	T	C	T	Y	C	C	G	A	Y	G	A	A	T	T
NC837, R1330	A	T	C	GA	T	Y	Y	Y	C	C	G	A	Y	G	A	A	T	T
R1374	A	T	C	GA	T	Y	Y	Y	C	M	G	A	Y	G	A	A	T	T
NM115, NM120, TS7, U73	A	T	C	GA	T	C	T	C	C	C	G	A	T	G	A	A	T	T
ST16**	G	T	C	GA	T	C	T	C	C	C	G	A	T	G	A	G	T	T
C21**, M90**	A	T	C	GA	T	C	T	C	C	C	G	A	T	G	A	A	C	T

analysis of 850 base-pairs in the nLSU rDNA region. Scale bar = 0.001 substitutions per site.



Phylogenetic tree showing genetic diversity of *Armillaria ostoyae* based on the IGS-1 DNA region



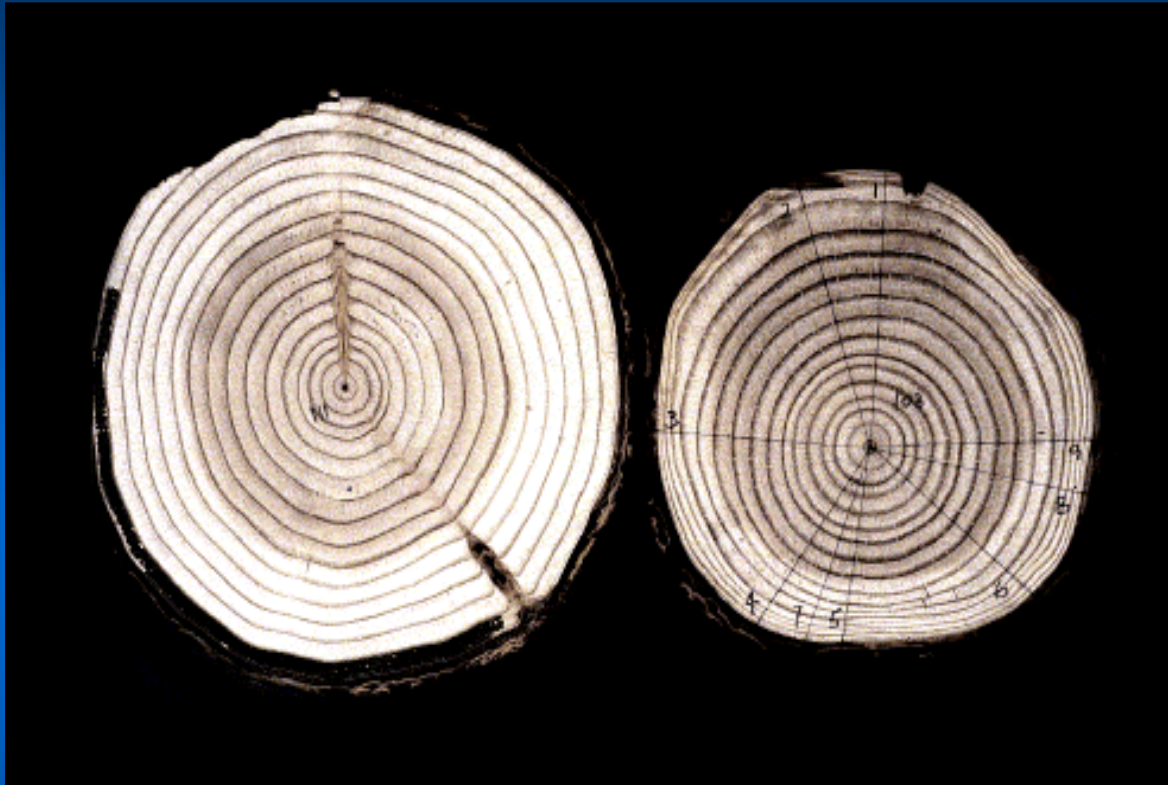
Factors associated with genetic races and intraspecific hybridization within *A. ostoyae*

- ❖ Adaptation to a variety of environments
- ❖ May be responsible for differing levels of pathogenicity and virulence
- ❖ “Hybrid vigor” may contribute to enhanced growth, survival, and/or pathogenicity
- ❖ Hybrids may adapt better to environmental change

Does *Armillaria* affect tree growth?



Impact of Armillaria Root Disease on Tree Growth



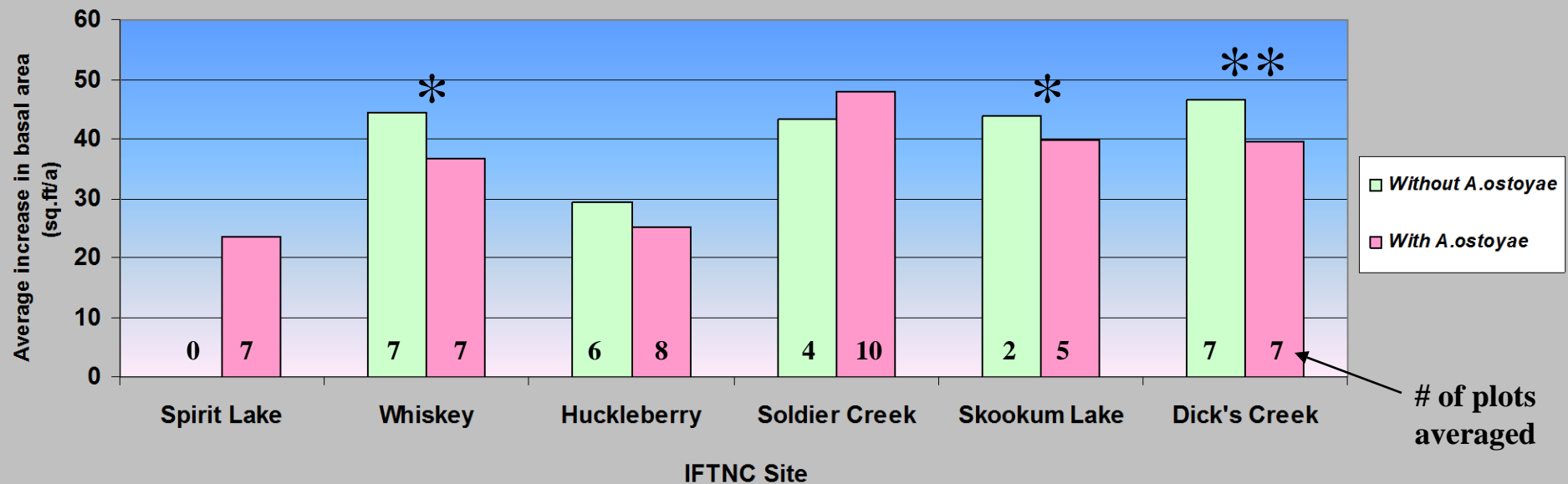
Volume loss has been shown as high as 40% over 4-8 years in eighteen-year-old Douglas-fir (Cruickshank, 2000).

Average mortality rates in a 10-year period for sites covering northern Idaho, northeastern Oregon, and eastern Washington vary from 8.8% for Douglas-fir, 4.2% for grand fir, and 1.5% for redcedar habitat types based on 8 sites (Moore et al., 2000).

Growth loss and mortality due to *Armillaria* in British Columbia have been cited as between 1.4 and 3.8 million m³ annually (White and Morrison, 1999).

Does *Armillaria* affect tree growth?

Influence of *Armillaria ostoyae* collected adjacent to growth plots on six-year gross-basal-area growth (sq.ft/a)



* $\alpha < .05$

** $\alpha < .10$

6-year Net- and Gross-Basal-Area Growth (sq.ft/a) in GREEN



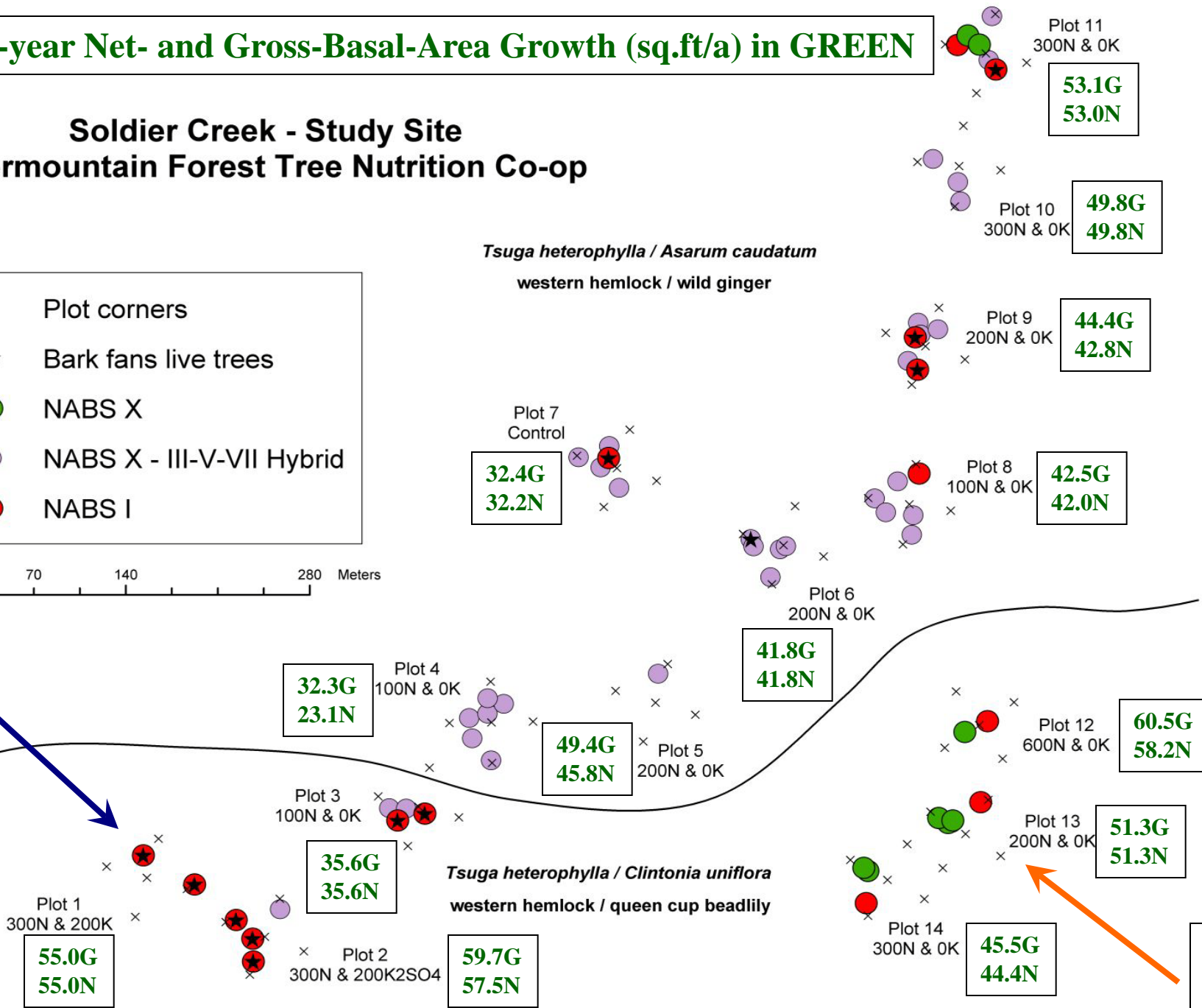
Soldier Creek - Study Site Intermountain Forest Tree Nutrition Co-op

Tsuga heterophylla / Asarum caudatum
western hemlock / wild ginger

- × Plot corners
- ★ Bark fans live trees
- NABS X
- NABS X - III-V-VII Hybrid
- NABS I

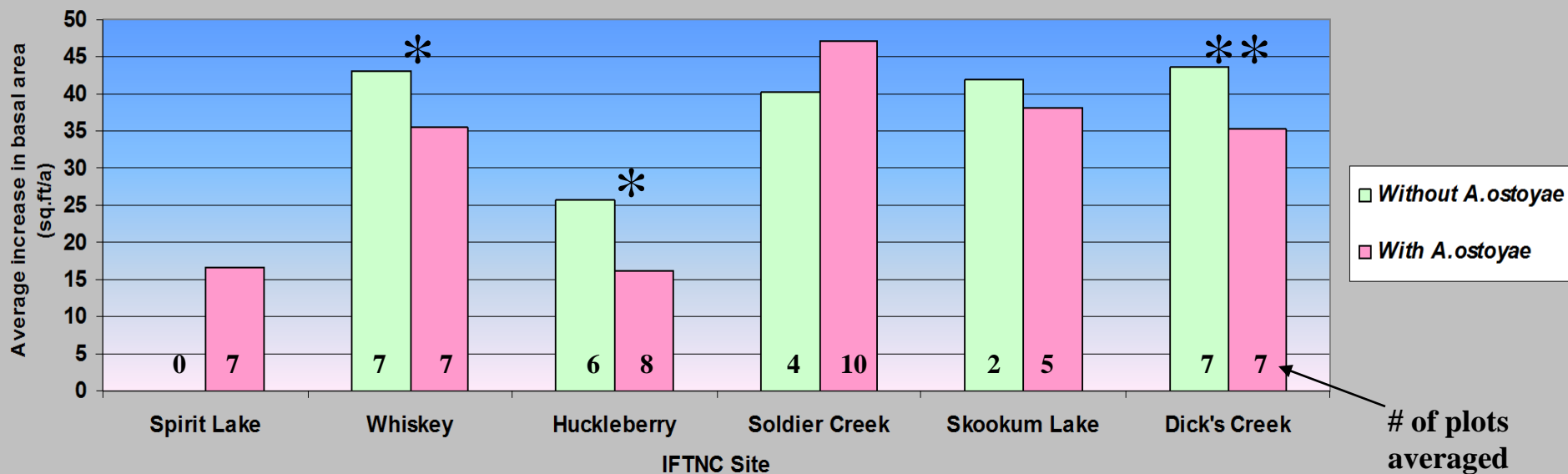
0 70 140 280 Meters

1



2

Influence of *Armillaria ostoyae* collected adjacent to growth plots on six-year net-basal-area growth (sq.ft/a)



* $\alpha < .05$

** $\alpha < .10$

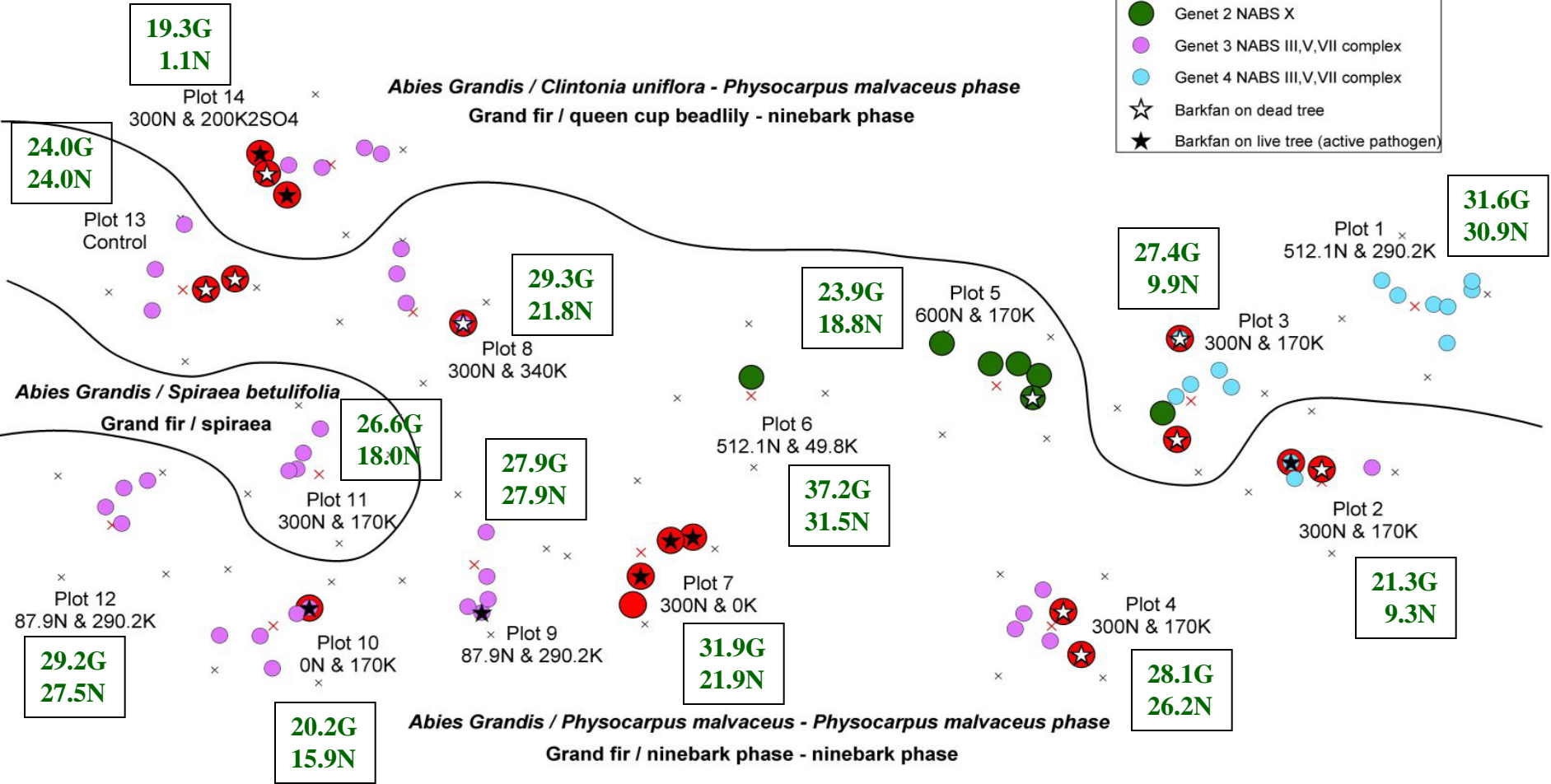
6-year Net- and Gross-Basal-Area Growth (sq.ft/a) in GREEN

Huckleberry Creek - Study Site Intermountain Forest Tree Nutrition Co-op



Legend

- × plot corners
- × plot centers
- Genet 1 NABS I A.ostoyae
- Genet 2 NABS X
- Genet 3 NABS III,V,VII complex
- Genet 4 NABS III,V,VII complex
- ☆ Barkfan on dead tree
- ★ Barkfan on live tree (active pathogen)



1 inch equals 61.886223 meters

6-year Net- and Gross-Basal-Area Growth (sq.ft/a) in GREEN

Spirit Lake - Study Site Intermountain Forest Tree Nutrition Co-op

Legend

- × plot corners
- × plot centers
- Genet 1 NABS | *A.ostoyae*
- Genet 2 NABS | *A.ostoyae*
- Genet 3 NABS | *A.ostoyae*
- Genet 4 NABS X
- ☆ Barkfan on dead tree
- ★ Barkfan on live tree (active pathogen)
- ★ Wood Sample (Note: from *Holodiscus discolor*)

Thuja plicata Series
western redcedar Series

1



Plot 1
600N & 0K

27.7G
24.2N

17.4G
-12.9N

Plot 2
0N & 170K

Tsuga heterophylla Series
western hemlock Series

2

Plot 3
200N & 0K

28.7G
24.7N

Thuja plicata Series
western redcedar Series

Plot 4
300N & 0K

31.4G
29.5N

Plot 5
300N & 170K

21.3G
20.7N

18.6G
16.4N

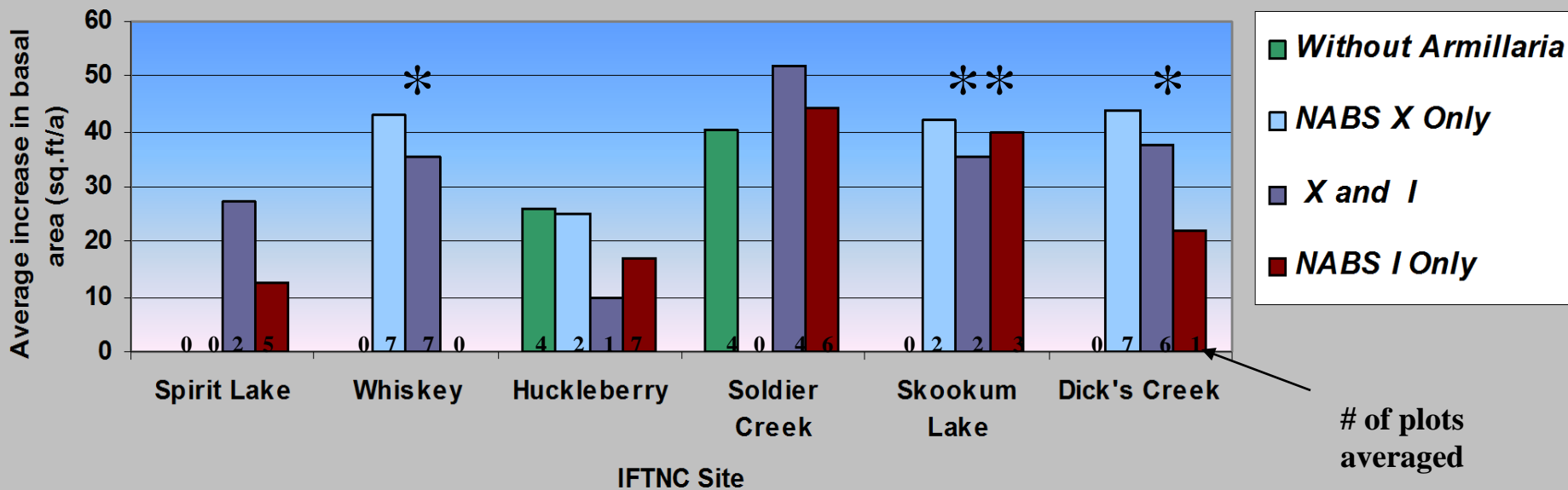
Plot 7
Control

Plot 6
100N & 0K

19.4G
14.7N



Influence of *Armillaria* species collected adjacent to growth plots on six-year net-basal-area growth (sq.ft/a)



* $\alpha < .05$

** $\alpha < .10$

Factors that interact with *Armillaria* to influence tree growth

Interacting Factors :

Habitat Type
Soil Characteristics
Parent Material
Fertilization
Other Pests



Future Studies

Better characterize *Armillaria* species with molecular genetic techniques to better understand pathogenicity and virulence

Assess direct effects of *Armillaria ostoyae* on tree growth

Evaluate effect of *Armillaria* species interactions on tree growth

Investigate saprophytic *Armillaria* species as a possible biological control of *Armillaria ostoyae*

Tree growth is affected by a multitude of interacting factors that include *Armillaria*.

It is difficult to assess how nutritional treatments affect *Armillaria* impacts on growth without knowledge of pre-existing *Armillaria* influences.

Pretreatment studies of *Armillaria* distribution and impacts across a range of environments are needed as baseline information. This baseline would help forest managers better understand how treatments affect *Armillaria* and overall growth of a stand.

Acknowledgements

**Intermountain Forest Tree
Nutrition Co-op
and the
University of Idaho**

**Mariann Garrison-Johnston
Mark Kimsey
Howard Jennings
Bob Atwood
Peter Mika
Leonard Johnson**

USDA Forest Service

**James B. Donley
Raini C. Rippy
Jane E. Stewart
Bryce A. Richardson
Troy Hensiek
Joanne Tirocke
Kwan-Soo Woo
Jonalea R. Tonn
Paul J. Zambino
Debbie S. Page-Dumroese**