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Canada

Systematics, Diagnostics and Genomics of Plant-related Ascomycetous Fungi

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Claviceps spp. research updates

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Research focuses

- Phylogenetics & Taxonomy
- Molecular identification
- Population structure & genotyping
- Genomics & Metabolomics
- Alkaloid gene evolution

Research results

- New Canadian lineages identified (Shoukouhi et al 2019)
- Molecular assay developed for differentiating *C. purpurea* s.s from other relatives (Shoukouhi et al 2019)
- Taxonomic descriptions of Canadian lineages
- 53 genomes sequenced

IMA Genome-F 10

Nine draft genome sequences of *Claviceps purpurea* s.lat., including *C. arundinis*, *C. humidiphila*, and *C.* cf. *spartinae*, pseudomolecules for the pitch canker pathogen *Fusarium circinatum*, draft genome of *Davidsoniella eucalypti*, *Grosmannia galeiformis*, *Quambalaria eucalypti*, and *Teratosphaeria destructans*

IMA Genome-F 10A

Nine draft genome sequences of *Claviceps purpurea* s.lat., including *C. arundinis*, *C. humidiphila* and *C.* cf. *spartinae*

INTRODUCTION

Taylor & Francis

Phylogeny of Canadian ergot fungi and a detection assay by real-time polymerase chain reaction

Parivash Shoukouhi, Carmen Hicks, Jim G. Menzies, Zlatko Popovic, Wen Chen, Keith A. Seifert, Rafik Assabgui, and Miao Liu

ARTICLE HISTORY

KEYWORDS

INTRODUCTION

Can. J. Plant Pathol., 2019
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Taylor & Francis

Fungi Canadenses No. 349

CLAVICEPS ZIZANIAE

Fig. 1-14. *Claviceps zizaniae*. **(1, 2)** Sclerotia and germinated sclerotia (bar = 10 mm). **(3)** cross sections of a sclerotium, upper showing the sections from tip, middle and base of the sclerotium from left to right (bar = 2 mm), bottom showing tissue types. **(4–5, 11)** Stromata and cross section (bar = 0.5 mm, 2 mm, 200 µm, the scale bar does not apply to the inset showing the moisture chamber for sclerotium germination). **(6)** Immature sclerotium showing the sphacelial (honeydew) state at the base. **(7)** Conidiogenous types (bar = 20 µm). **(8–9)** Asci and ascospores (bar = 20 µm). **(10)** Perithecium cross-section (bar = 20 µm). **(12)** Conidia from sclerotium surface and honeydew (bar = 20 µm). **(13)** Conidia from culture (bar = 20 µm). **(14)** Colonies on PDA after 21 days (bar = 10 mm). **(1, 4, 5, 8–11, 13–14)** National Mycological Herbarium DAOM 907677. **(2)** DAOM 56855(b) (epitype). **(3, 6, 7, 12)** DAOM 56855(a).

Ongoing research

- Population structure & genotyping
- Metabolomics
- Genome annotation
- Alkaloid gene evolution

Blumeria graminis research updates

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Allen Xue, SeaRa Lim (AAFC)

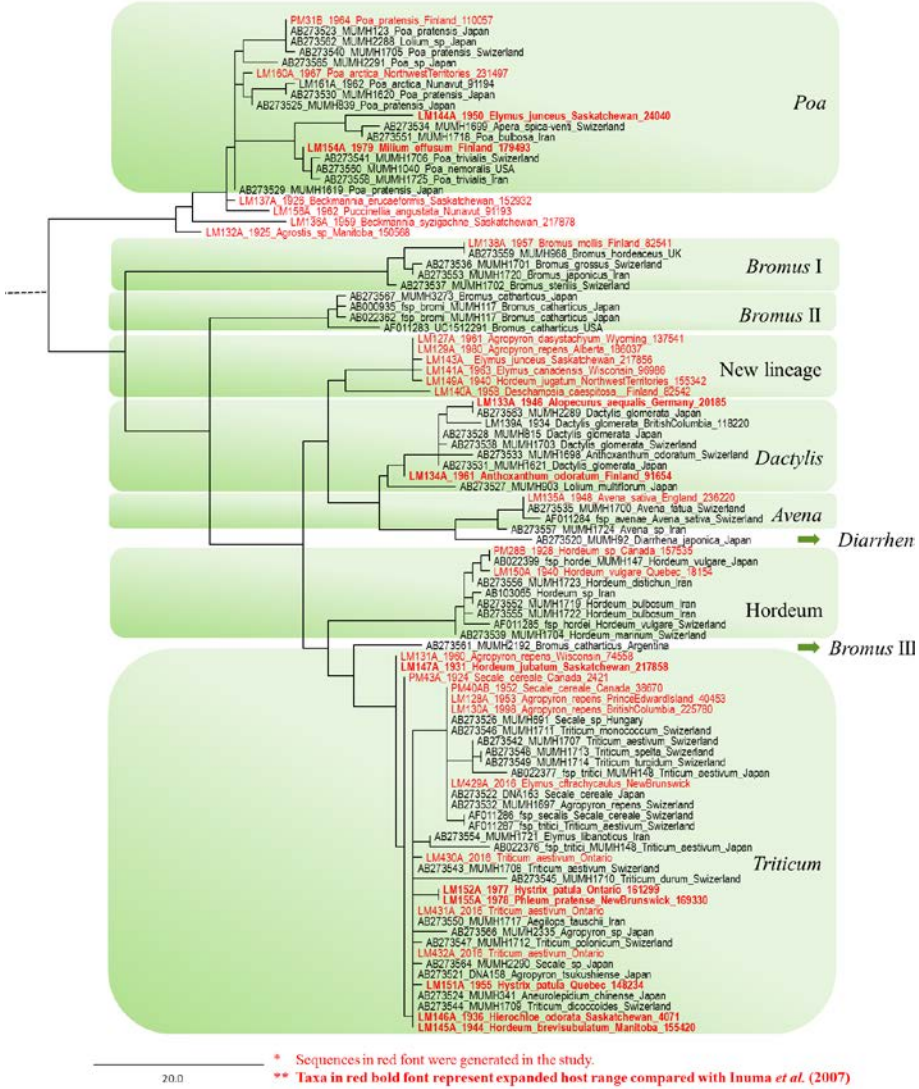
Research focuses

- Phylogenetics & Taxonomy
- Molecular identification
- Population structure & genotyping

Background, material, methods

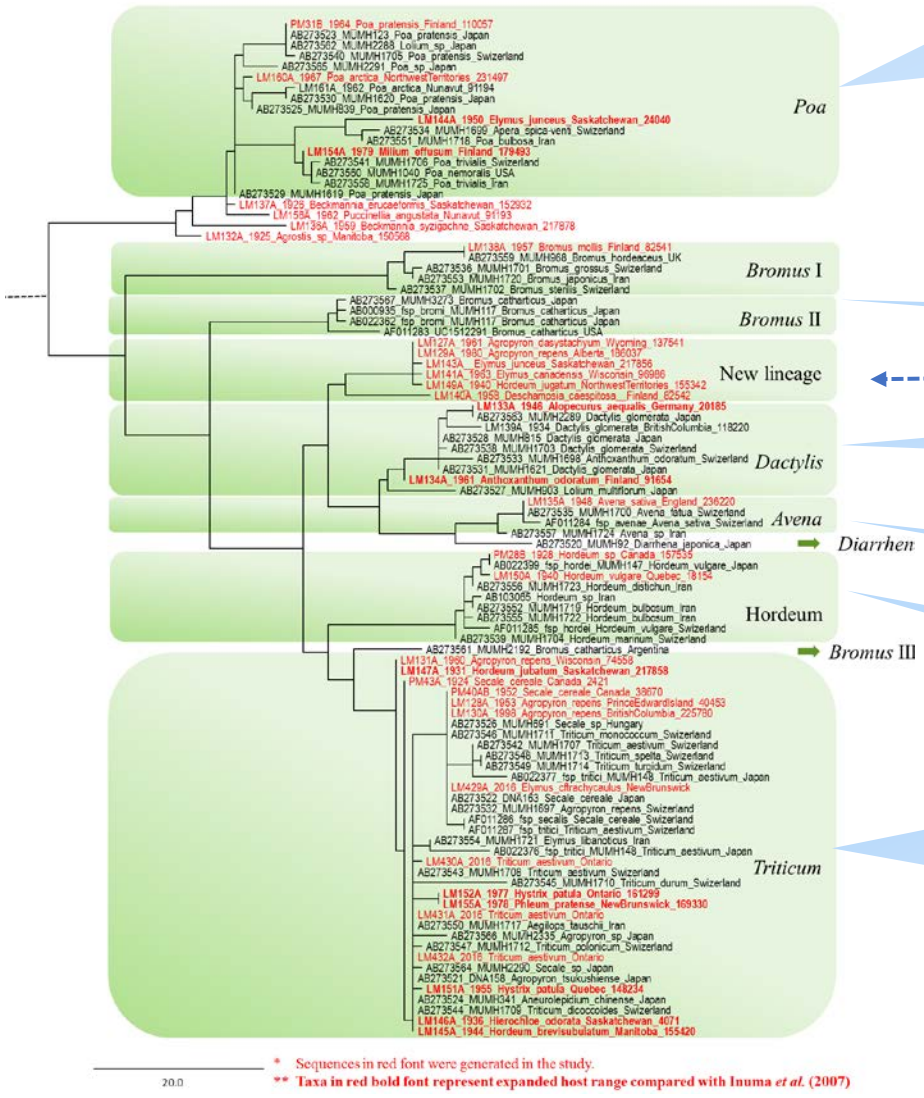
- Background
  - Obligate biotrophic
  - Host range: cereal crops and grasses in over 100 genera (Poaceae)
  - Inuma et al: nine lineages (ITS, 28S, CHS, TUB)
- Samples: 179 samples (DAOM, BPI) on 87 grass species
- Primers
  - From literature: ITS-28S (Various authors), CHS and TUB (Inuma et al 2007, Seko et al 2011); PPA, PCA, AOX and TUB (Parks et al 2009)
  - Designed using 31 genomes (Menardo et al 2017): five anonymous regions, TEF

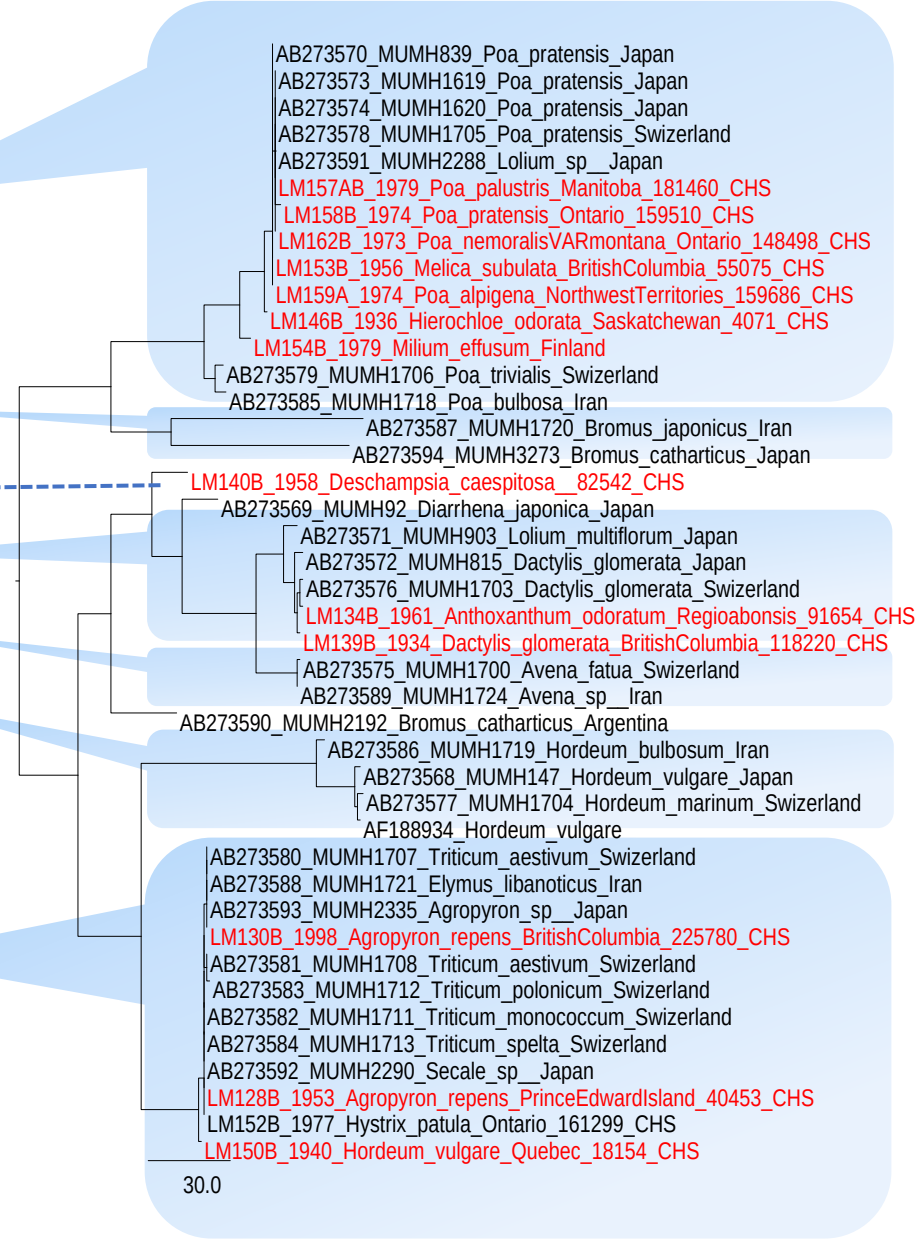
Results



ITS-28S tree

Results

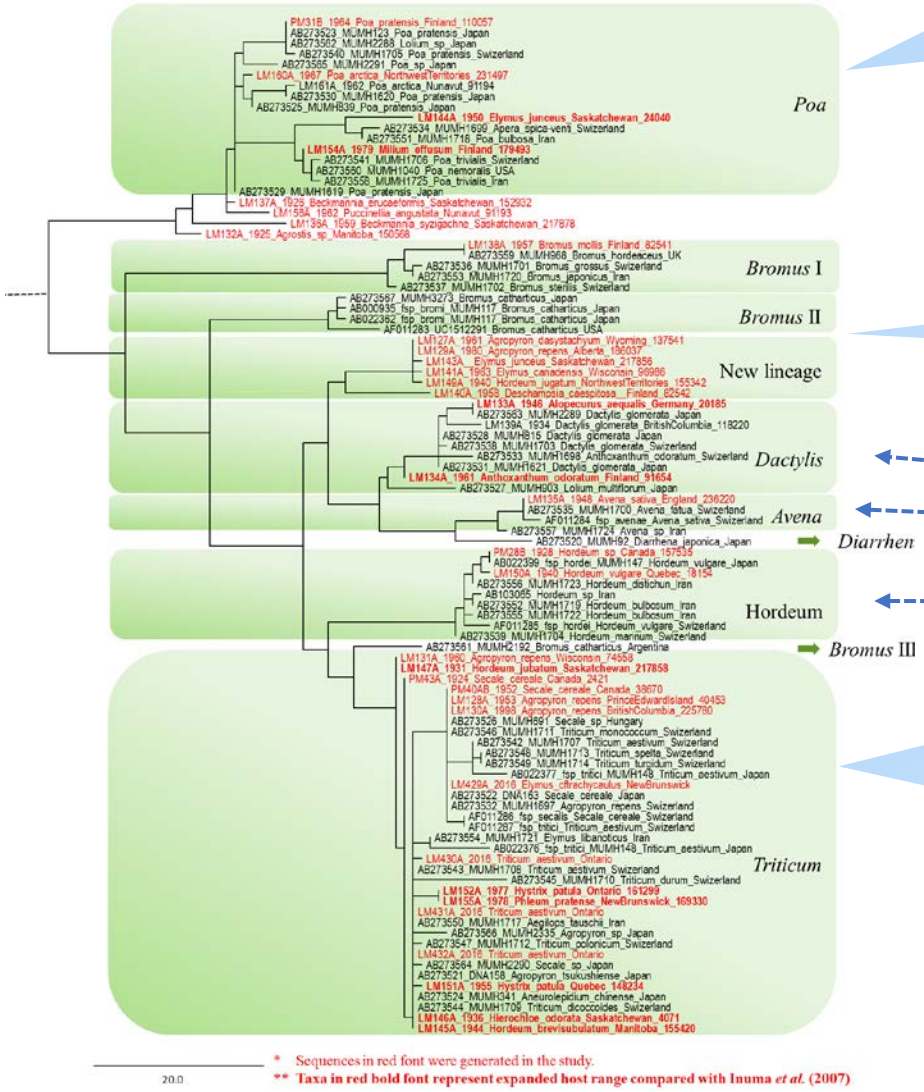


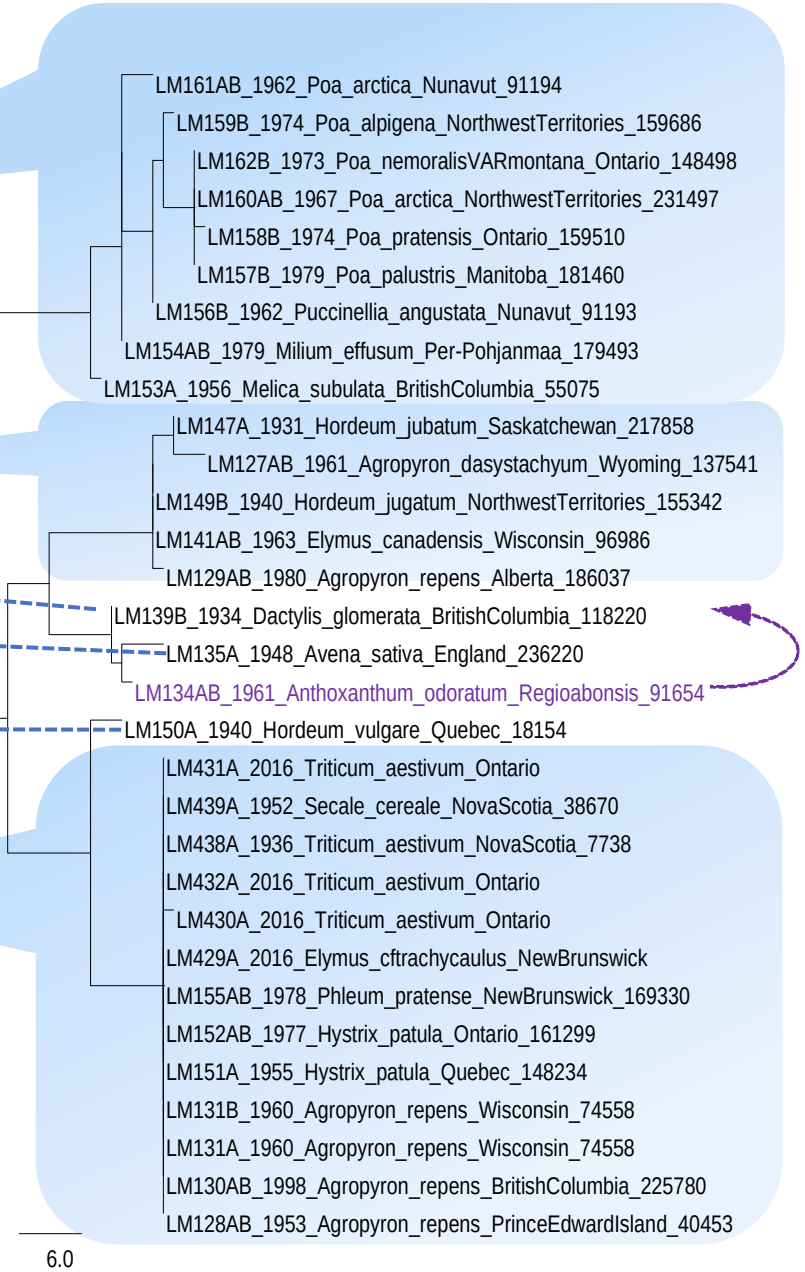


ITS-28S tree

CHS

Results



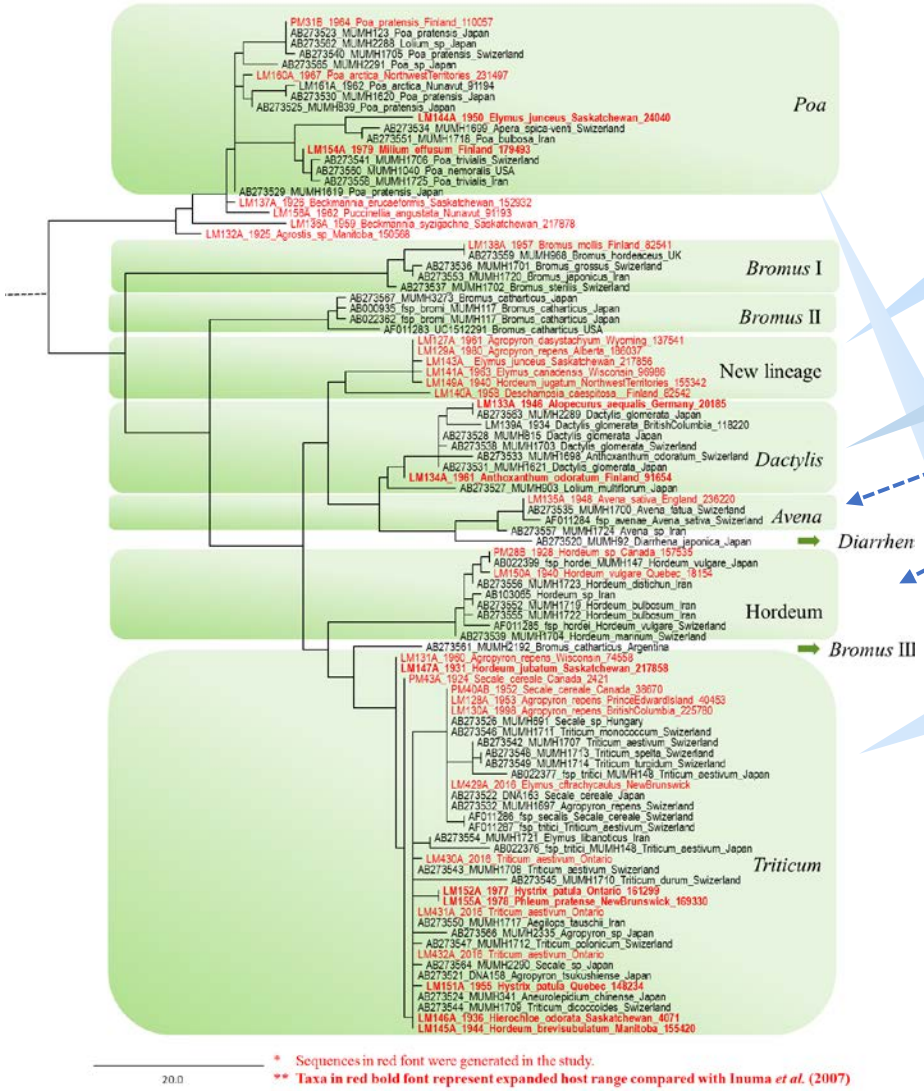


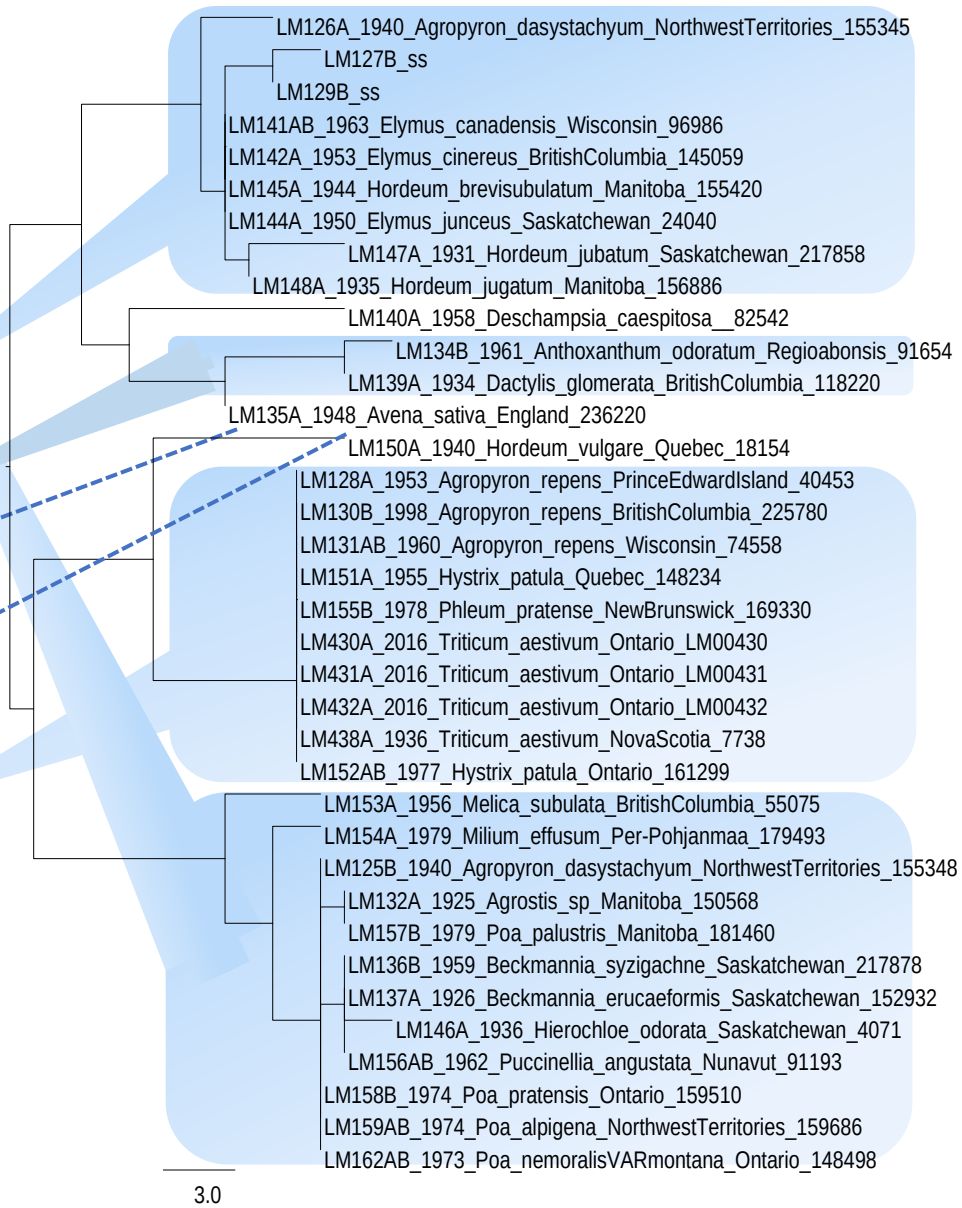
ITS-28S tree

FM27522: designed from 31 genomes

(F. Menardo et al 2017)

Results

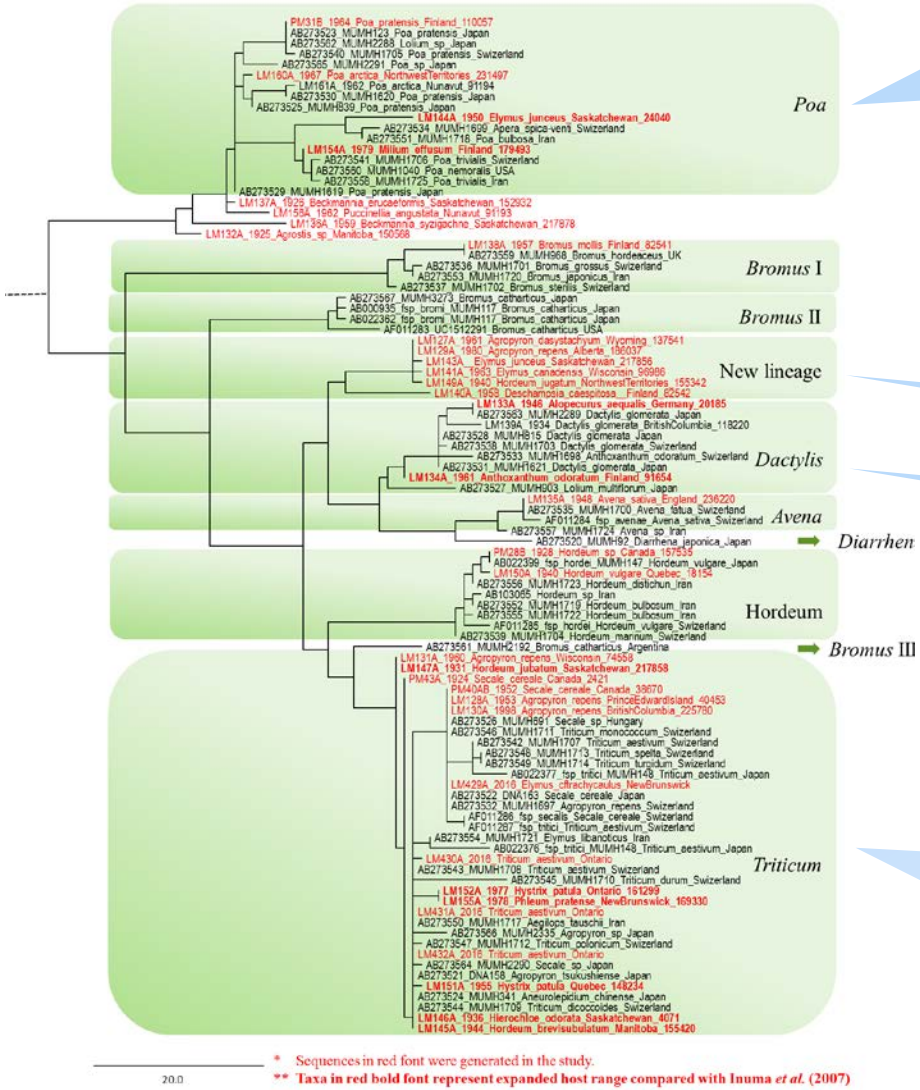


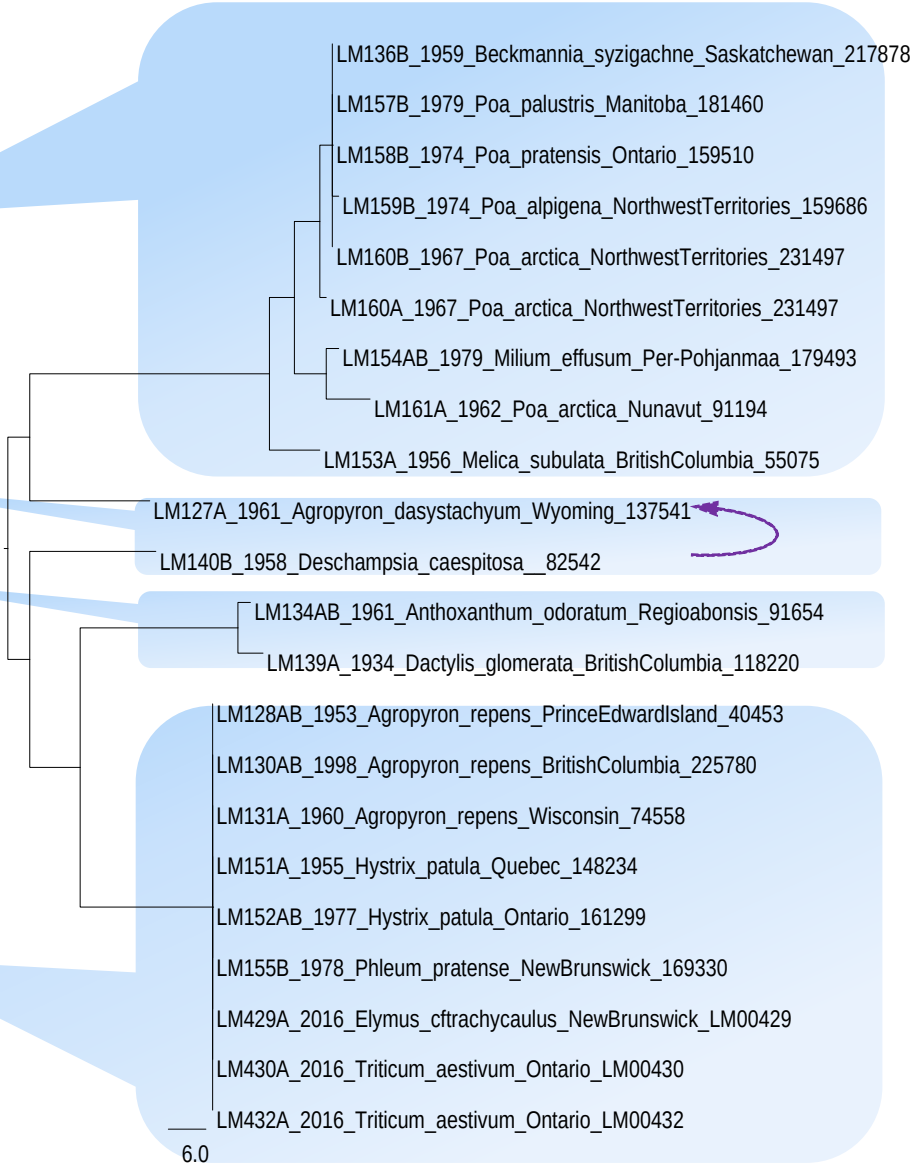


ITS-28S tree

FM110716

Results





ITS-28S tree

FM56044

Results

Statistics of the most parsimony trees

Column1	ITS-28S	CHS	FM27522	FM110716	FM56044
# of taxa	97	42	31	36	22
# of characters	1661	401	405	230	771
Informative	142	98	63	40	100
Tree	2568	484	45690	2360	7
Length	466	247	96	85	178
CI	0.730	0.704	0.802	0.694	0.882
RI	0.908	0.926	0.962	0.921	0.965
RC	0.662	0.652	0.772	0.64	0.851
HI	0.270	0.296	0.198	0.306	0.118
G-fit	-115.107	-81.779	-58.65	-35.029	-94.95

Results

Markers for population level variation (Parks et al 2009)

- For 16 samples (on wheat), PKA and TUB each had 1 polymorphic site, PPA 2 sites, AOX no polymorphic site.
- 3-gene genotyping: 5 haplotypes

	PKA	PPA		TUB
Haplotype (frequency)	492	104	366	112
H1 (1)	A	T	C	T
H2 (7)	A	C	T	T
H3 (6)	T	C	T	T
H4 (1)	T	T	C	T
H5 (1)	T	C	T	C
AOX: no polymorphic sites				

On going

- Continue developing multi-gene sequences for samples on various grasses
- Multi-gene sequence analyses
- Taxonomic revision
- Future: Canadian population genotyping