Assessing the utility of coding and non-coding genomic regions for plant DNA barcoding

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Plant DNA barcoding

- CO1 – the basis of barcoding for animals
  - existing data indicates low substitution rates in plants
- Number of plastid regions proposed for plants
  - *rpoB*, *rpoC1*, *matK*, *rbcL*, *trnH-psbA* intergenic spacer, UPA (universal plastid amplicon)
- CPBG evaluation project
  - Goal: to objectively evaluate each region
    - Compare amount of variation
    - Identification success
    - Ease of amplification and sequencing

Experimental Design

- 3 samples/species
- 3 locations
- Minimum distance = 100 km

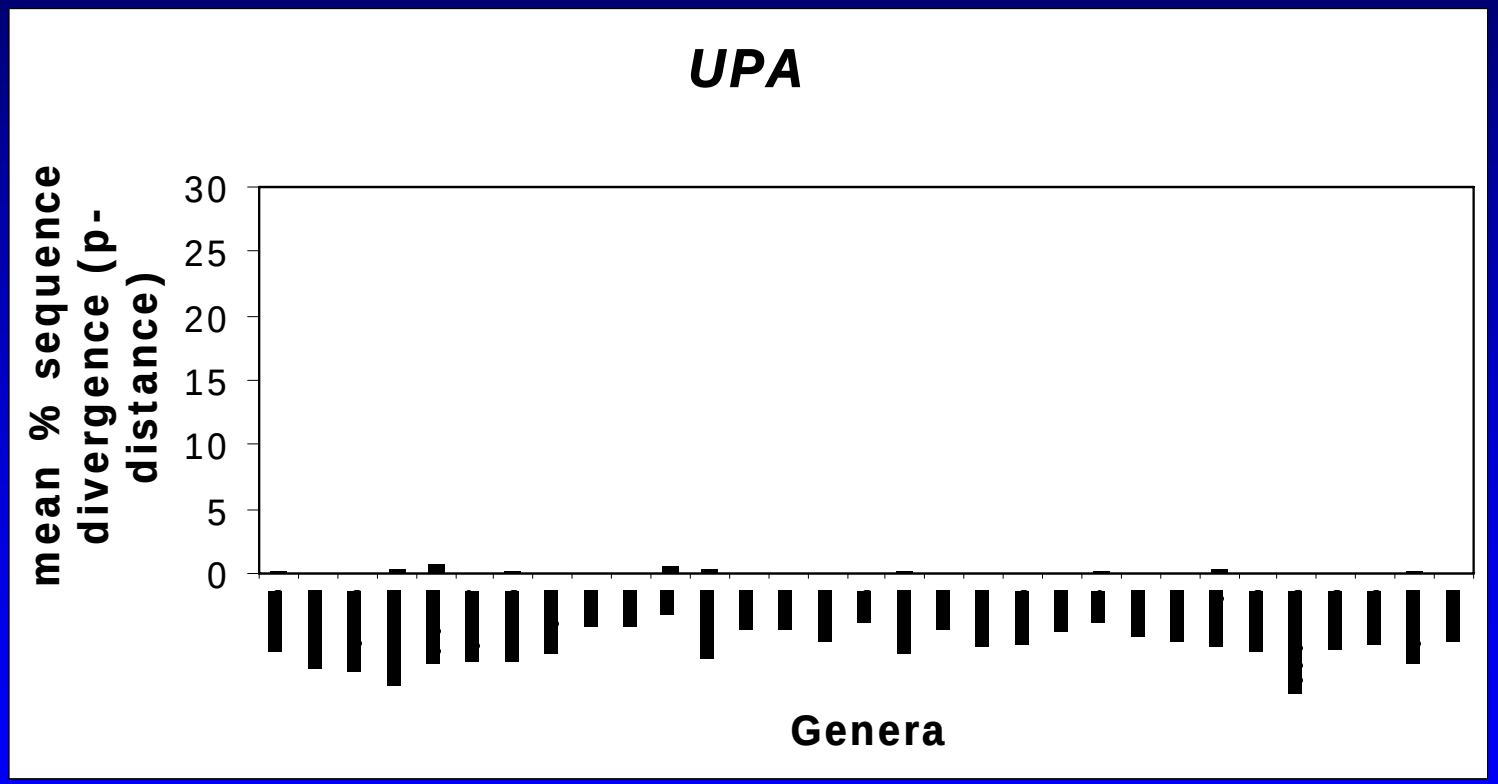
- Total of 240 samples
- 90 species in 33 genera

Analysis

- For each region:
  - Species pairwise distance within genera (minimum of all intraspecific distances)
  - Neighbor joining trees
  - Identification success (closest match is conspecific)
- Combined analysis
  - Neighbor joining trees
  - Identification success
- Summary
  - Compared resolution and PCR success
  - Effort (primer sets) to obtain data

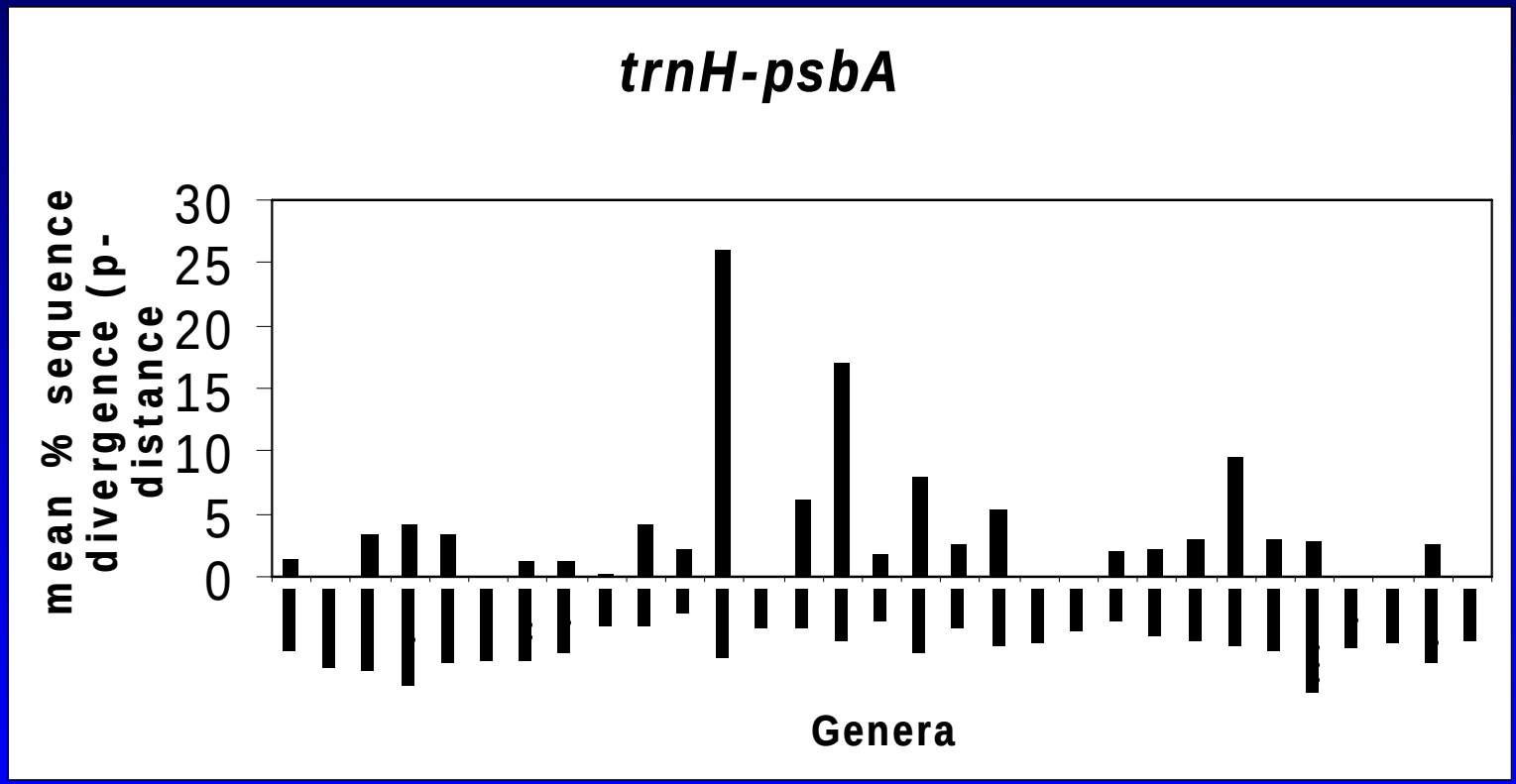
Results

pairwise distance



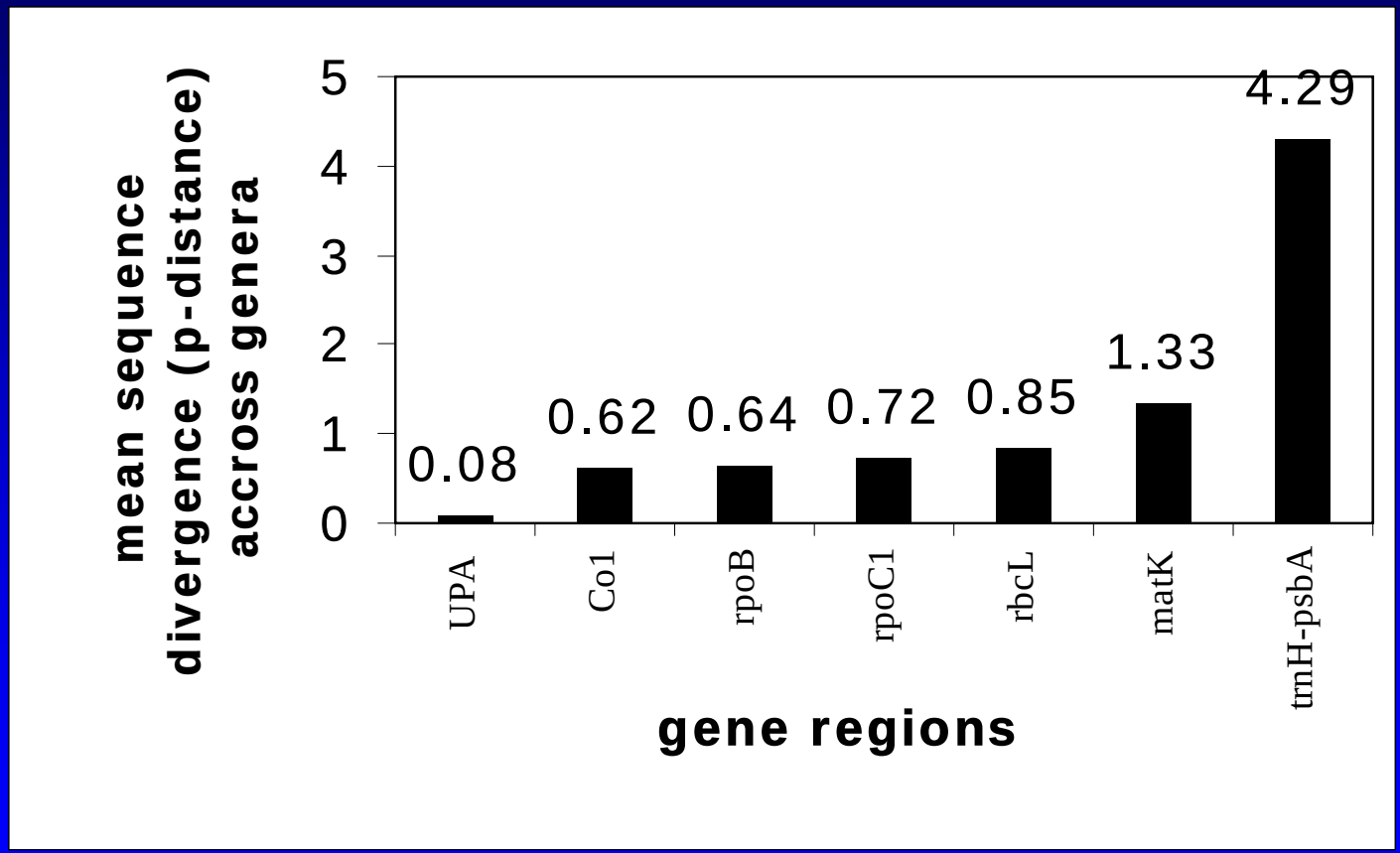
Results

pairwise distance

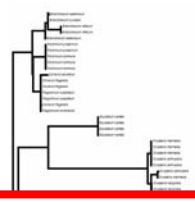


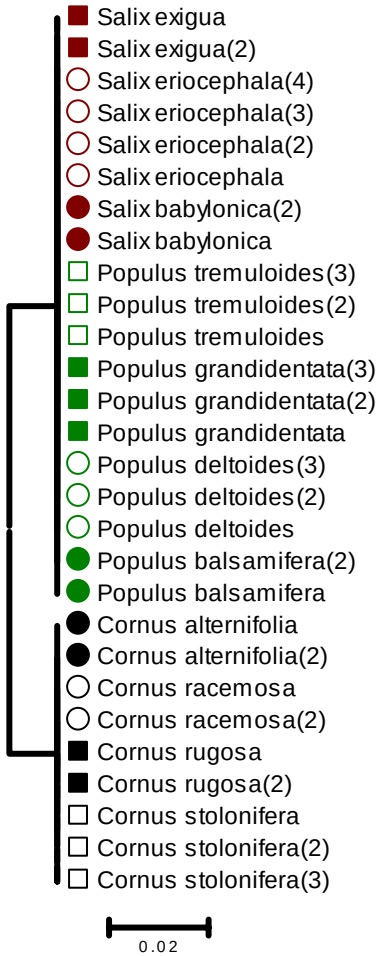
Results

pairwise distance



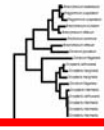
UPA

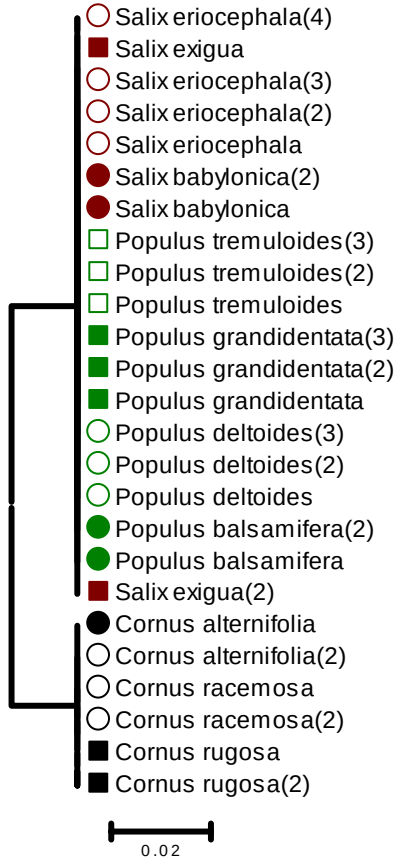




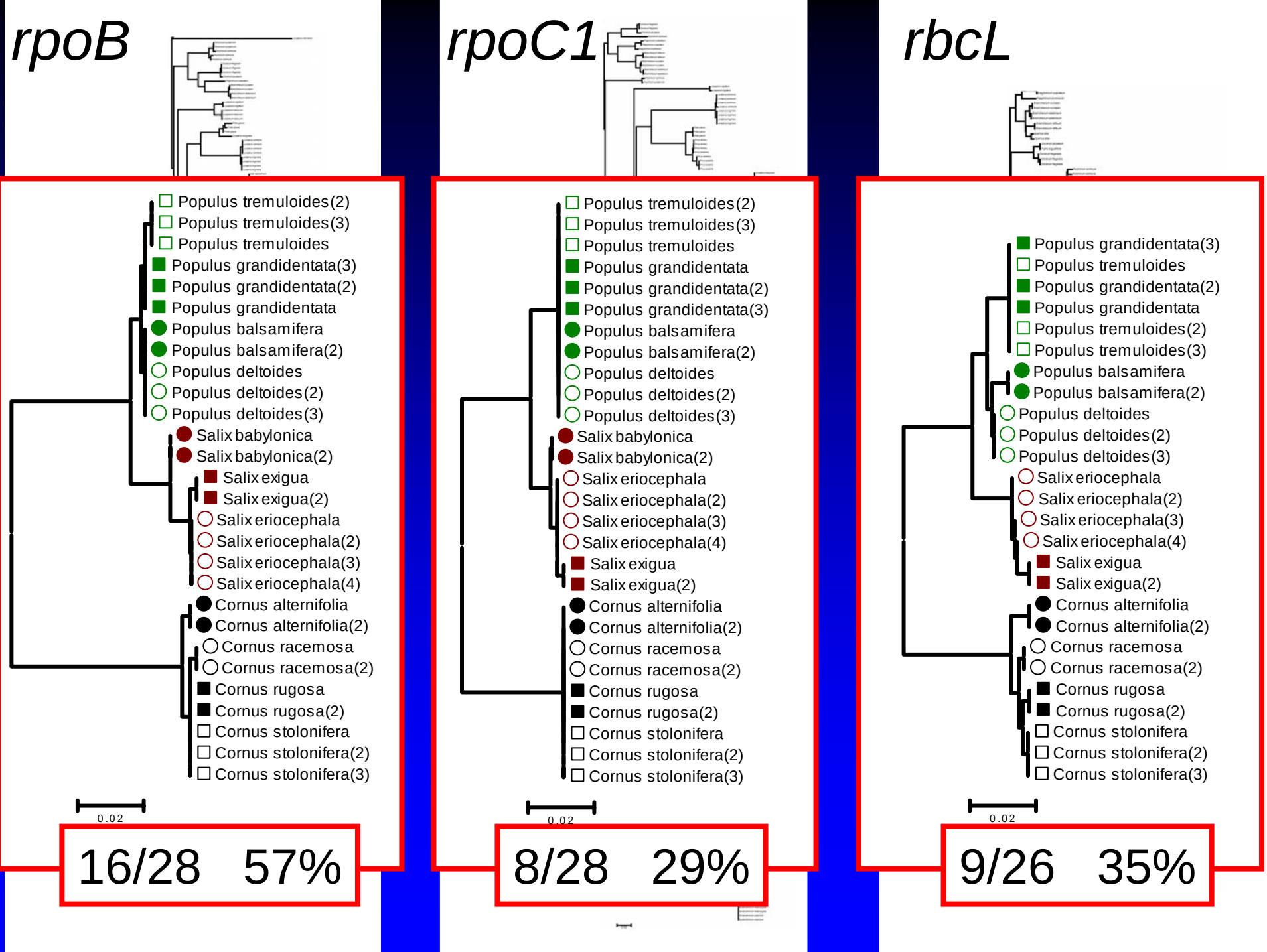
0/28 0%

CO1

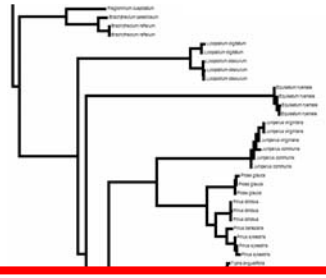


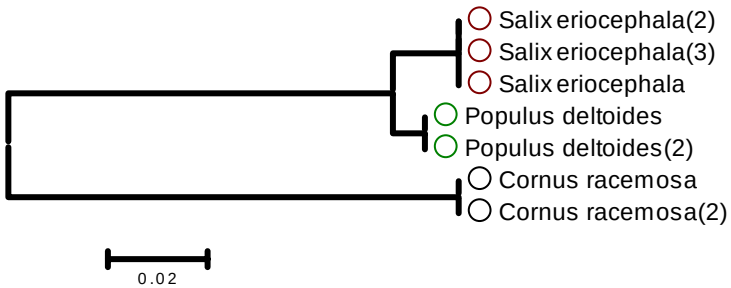


0/25 0%

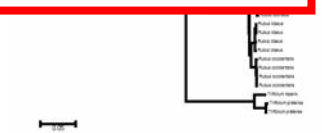

rpoB
Populus tremuloides(2)
Populus tremuloides(3)
Populus tremuloides
Populus grandidentata(3)
Populus grandidentata(2)
Populus grandidentata
Populus balsamifera
Populus balsamifera(2)
Populus deltoides
Populus deltoides(2)
Populus deltoides(3)
Salix babylonica
Salix babylonica(2)
Salix exigua
Salix exigua(2)
Salix eriocephala
Salix eriocephala(2)
Salix eriocephala(3)
Salix eriocephala(4)
Cornus alternifolia
Cornus alternifolia(2)
Cornus racemosa
Cornus racemosa(2)
Cornus rugosa
Cornus rugosa(2)
Cornus stolonifera
Cornus stolonifera(2)
Cornus stolonifera(3)
0.02
16/28 57%
rpoC1
Populus tremuloides(2)
Populus tremuloides(3)
Populus tremuloides
Populus grandidentata
Populus grandidentata(2)
Populus grandidentata(3)
Populus balsamifera
Populus balsamifera(2)
Populus deltoides
Populus deltoides(2)
Populus deltoides(3)
Salix babylonica
Salix babylonica(2)
Salix eriocephala
Salix eriocephala(2)
Salix eriocephala(3)
Salix eriocephala(4)
Salix exigua
Salix exigua(2)
Cornus alternifolia
Cornus alternifolia(2)
Cornus racemosa
Cornus racemosa(2)
Cornus rugosa
Cornus rugosa(2)
Cornus stolonifera
Cornus stolonifera(2)
Cornus stolonifera(3)
0.02
8/28 29%
rbcL
Populus grandidentata(3)
Populus tremuloides
Populus grandidentata(2)
Populus grandidentata
Populus tremuloides(2)
Populus tremuloides(3)
Populus balsamifera
Populus balsamifera(2)
Populus deltoides
Populus deltoides(2)
Populus deltoides(3)
Salix eriocephala
Salix eriocephala(2)
Salix eriocephala(3)
Salix eriocephala(4)
Salix exigua
Salix exigua(2)
Cornus alternifolia
Cornus alternifolia(2)
Cornus racemosa
Cornus racemosa(2)
Cornus rugosa
Cornus rugosa(2)
Cornus stolonifera
Cornus stolonifera(2)
Cornus stolonifera(3)
0.02
9/26 35%

matK

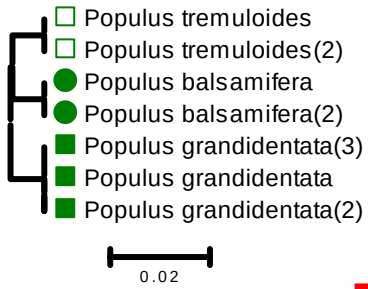




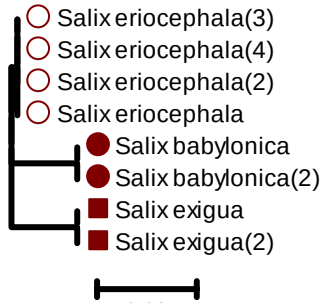
7/7 100%*



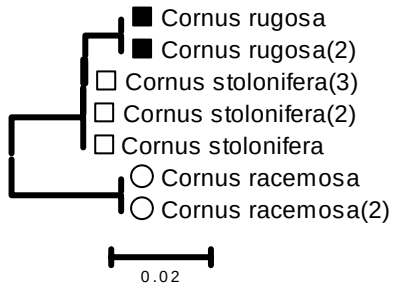
trnH-psbA



7/7 100%

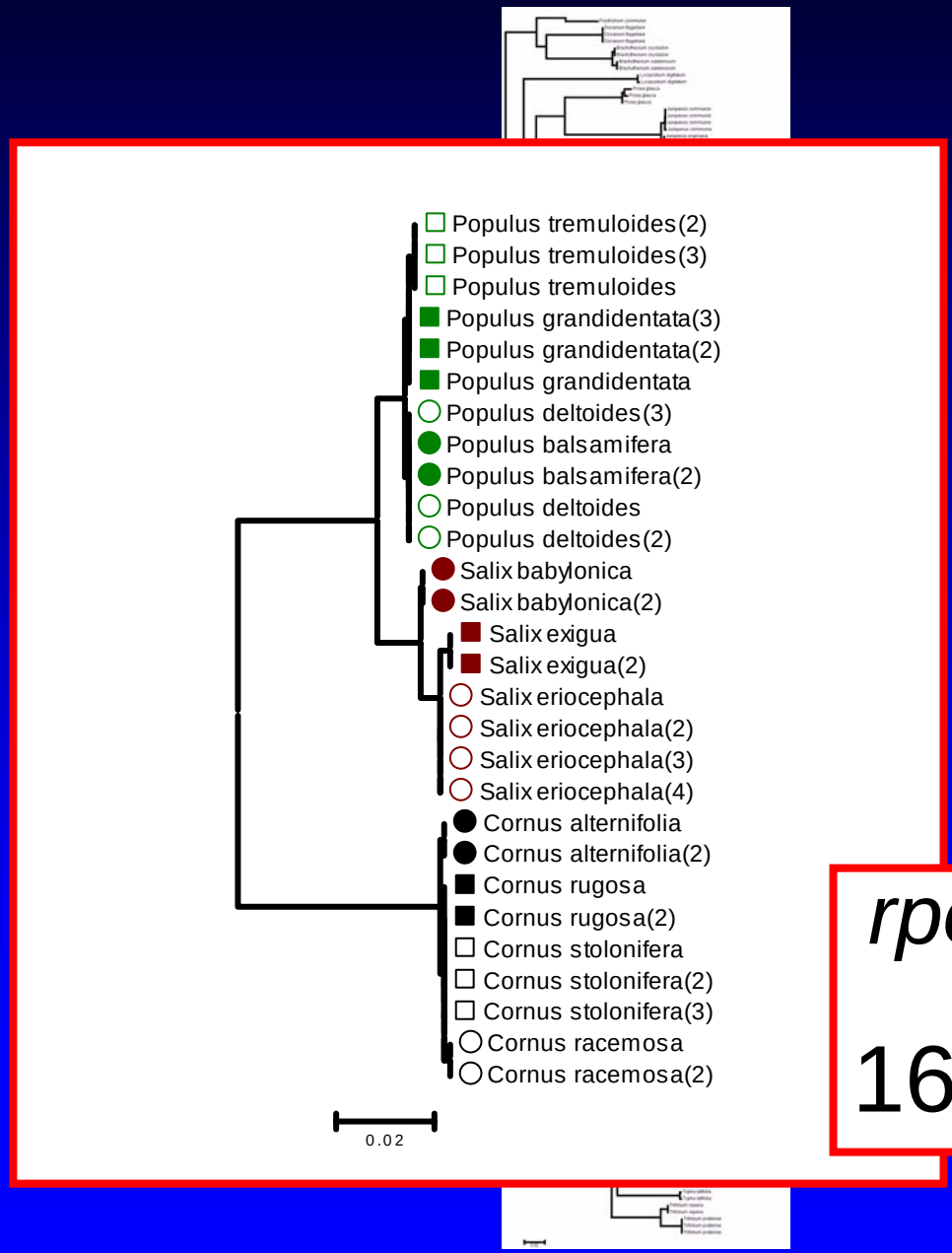


7/8 88%



7/7 100%

Multigene approach



Identification success: All samples

Single

rpoB (58%)

rpoC1 (50%)

Combined

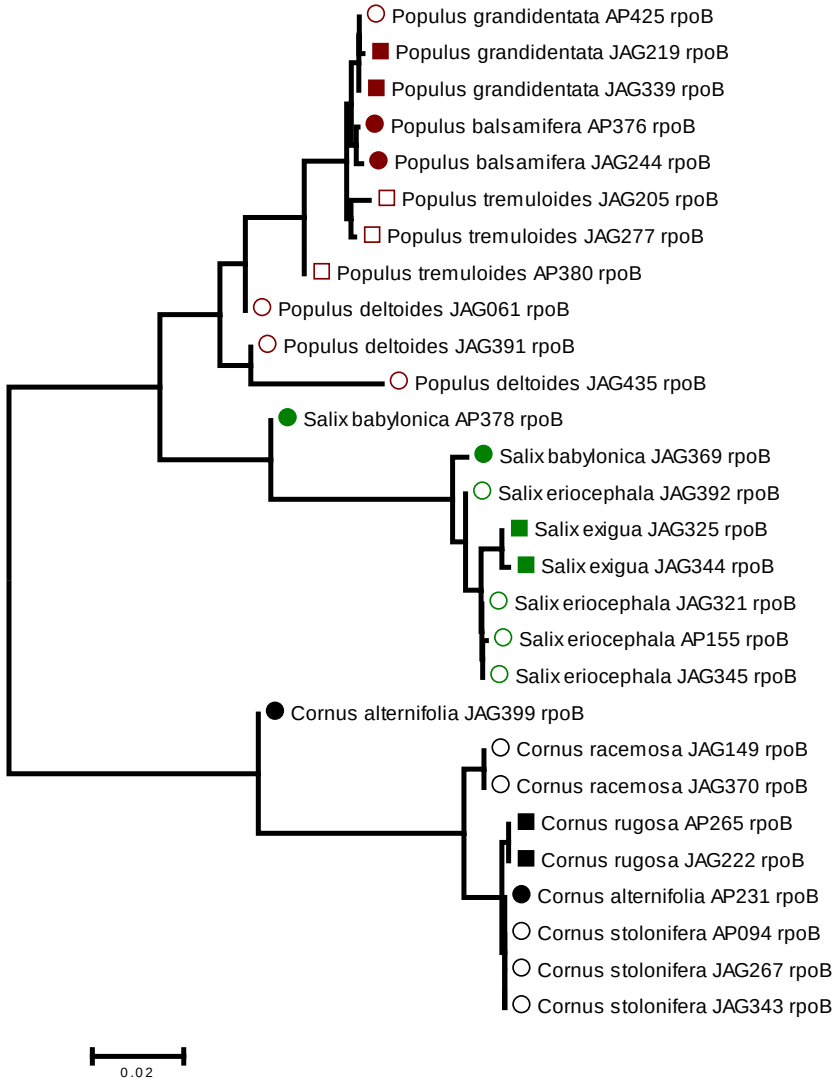
rpoB + *rpoC1*

119/181 65%

rpoB + *rpoC1*

16/28 57%

Multigene approach



rpoB,
rpoC1,
trnH-psbA

13/28 46%

Summary: Amplification success vs. effort for all samples

Region	Amplification success	Identification success	Effort Primer sets
UPA	94%	20%	1
CO1	79%	27%	5
rpoB	84%	58%	5
rpoC1	91%	50%	4
rbcL	65%*	66%	1
matK	56%	72%	10
trnH-psbA	91%	78%	1

* Recent addition to the dataset

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