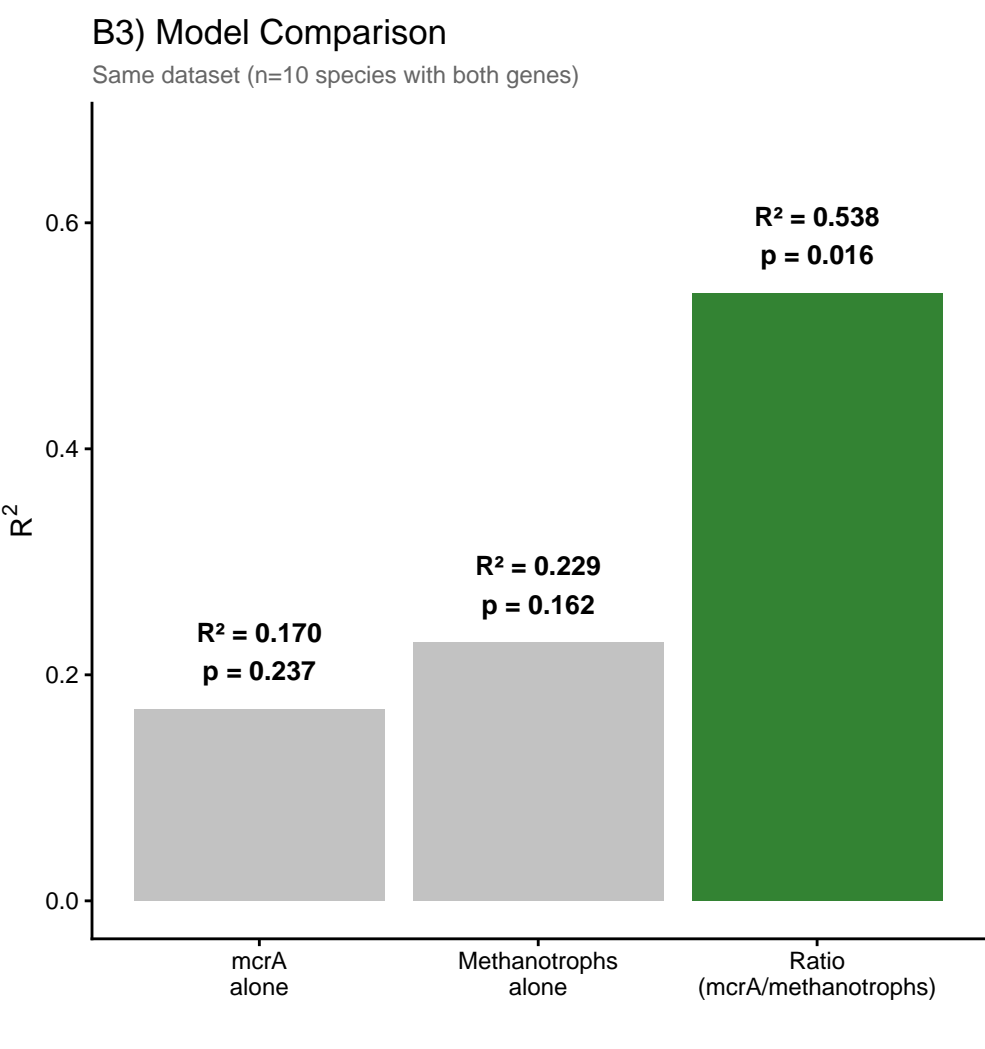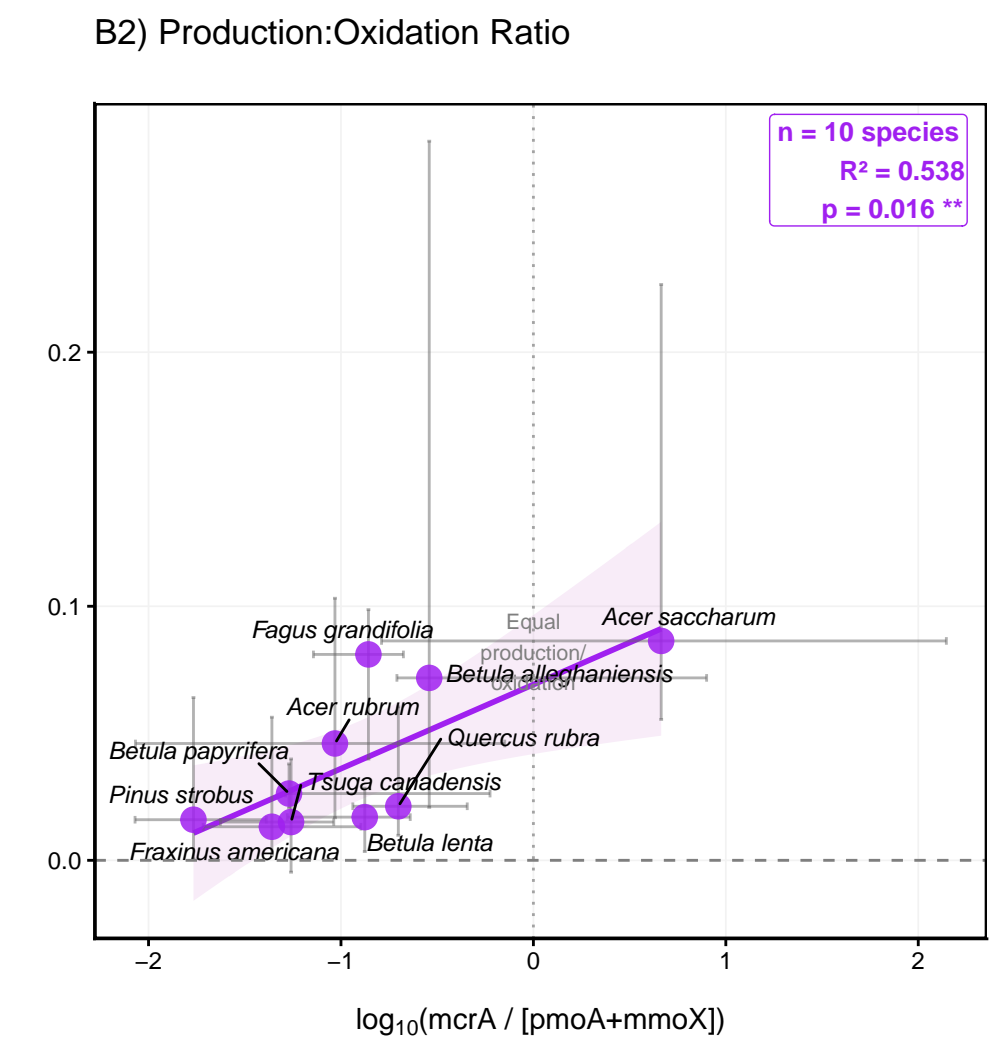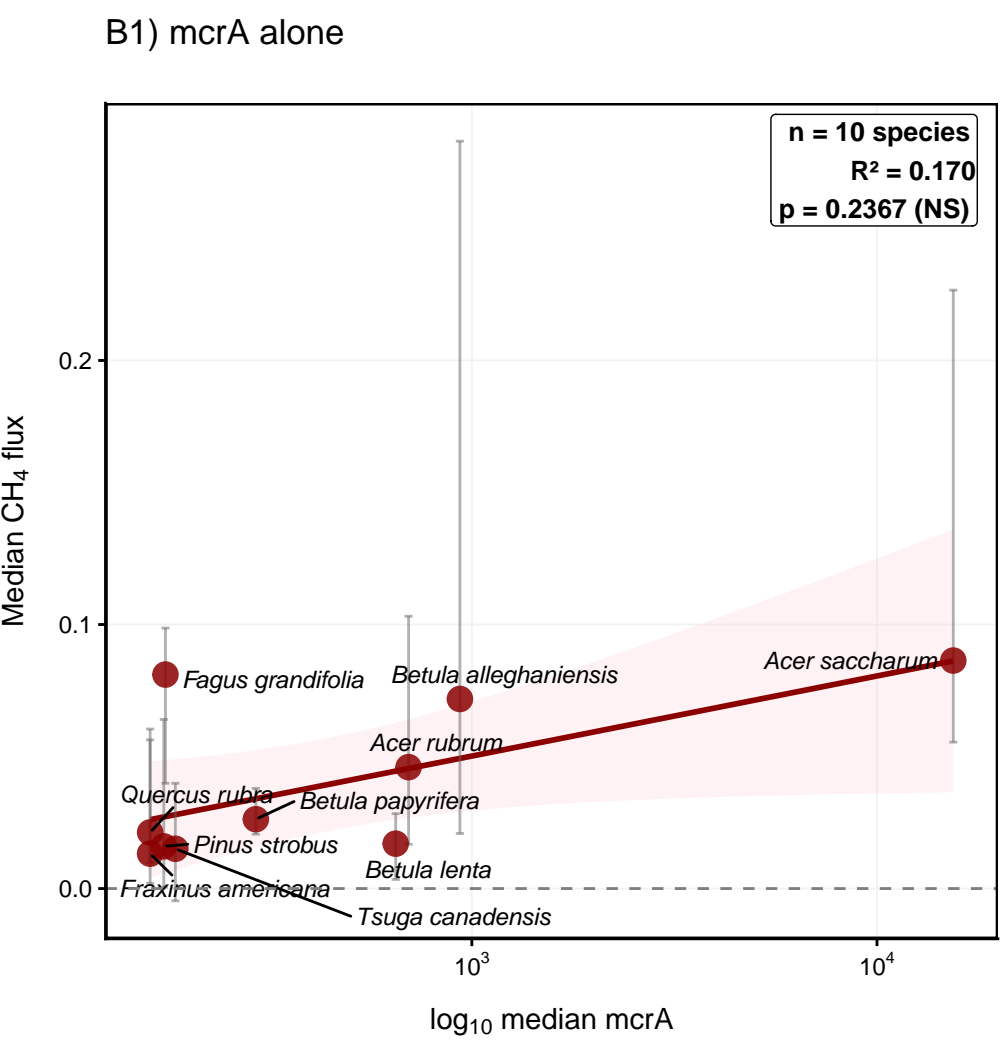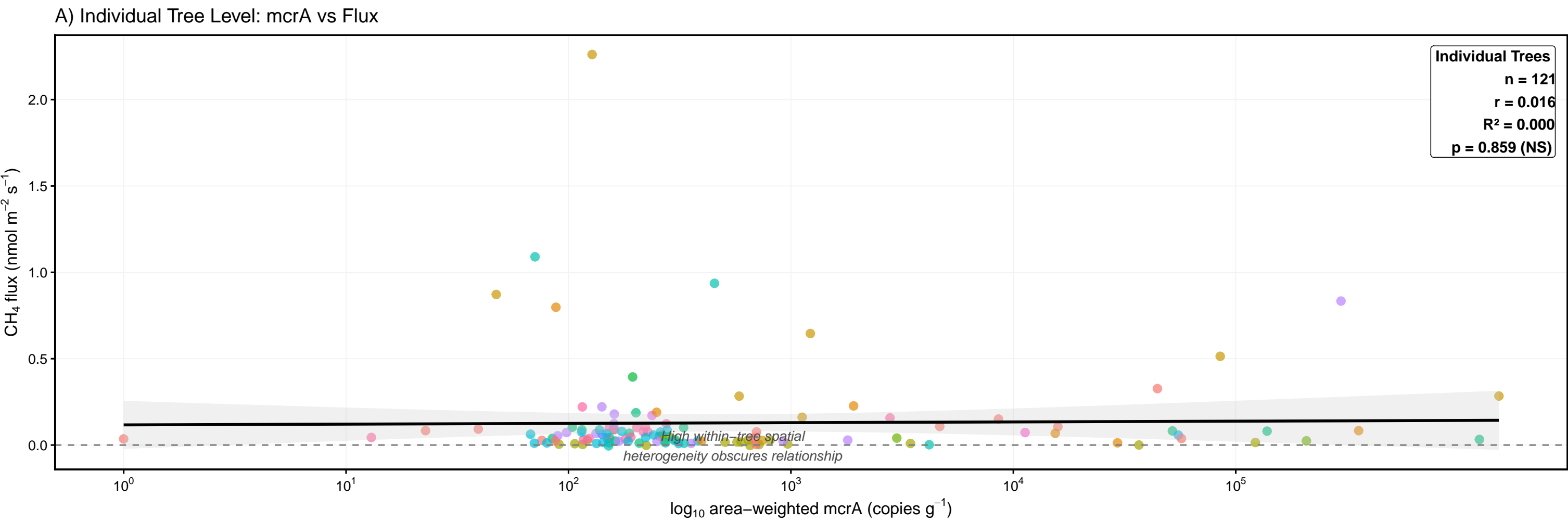# Scale−Dependent Gene−Flux Relationships

Individual trees (n=121) show weak correlation; Species aggregation (n=10) reveals strong production−oxidation balance

A) Individual Tree Level: mcrA vs Flux

Individual Trees
n = 121
r = 0.016
R² = 0.000
p = 0.859 (NS)

High within−tree spatial
heterogeneity obscures relationship

CH$_4$ flux (nmol m^{-2} s^{-1})

log$_{10}$ area−weighted mcrA (copies g^{-1})

B1) mcrA alone

n = 10 species
R² = 0.170
p = 0.2367 (NS)

Fagus grandifolia
Betula alleghaniensis
Acer saccharum
Acer rubrum
Quercus rubra
Betula papyrifera
Pinus strobus
Betula lenta
Fraxinus americana
Tsuga canadensis

Median CH$_4$ flux

log$_{10}$ median mcrA

B2) Production:Oxidation Ratio

n = 10 species
R² = 0.538
p = 0.016 *

Fagus grandifolia
Equal production/oxidation
Acer saccharum
Betula alleghaniensis
Acer rubrum
Quercus rubra
Betula papyrifera
Tsuga canadensis
Pinus strobus
Betula lenta
Fraxinus americana

log$_{10}$(mcrA / [pmoA+mmoX])

B3) Model Comparison

Same dataset (n=10 species with both genes)

R² = 0.538
p = 0.016

R² = 0.229
p = 0.162

R² = 0.170
p = 0.237

R²

mcrA alone | Methanotrophs alone | Ratio (mcrA/methanotrophs)

Significance   p >= 0.05   p < 0.05