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Mutations in Several Auxin Biosynthesis Genes and their Effects on Plant Phenotypes in Arabidopsis

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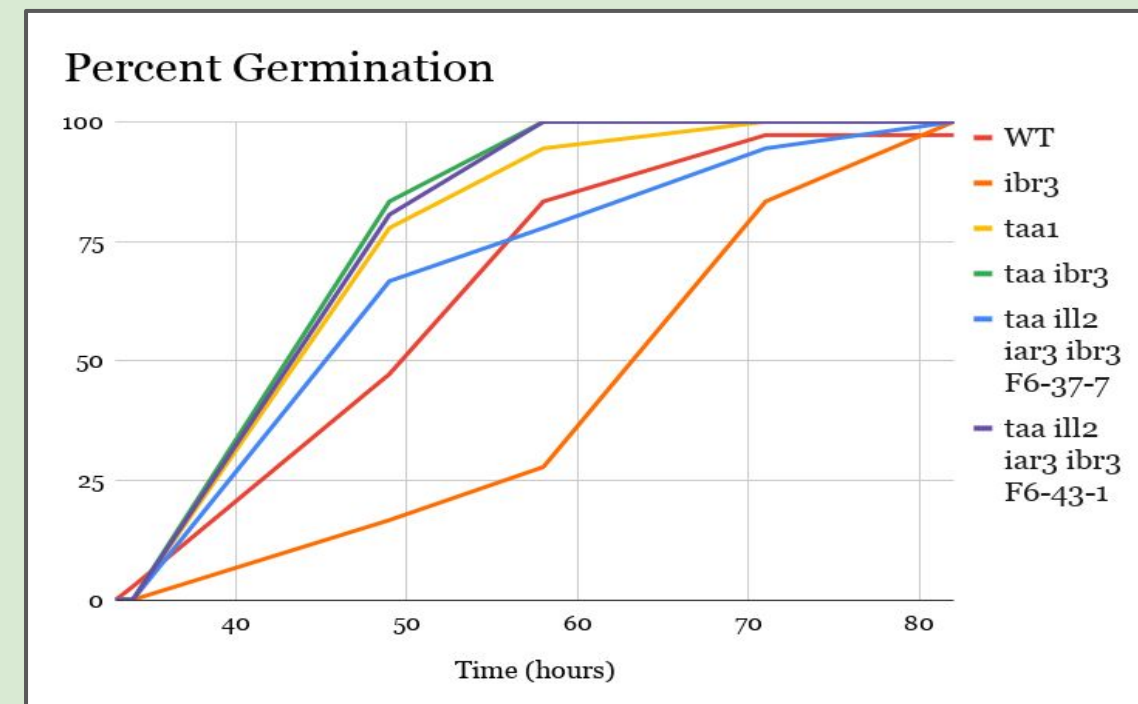
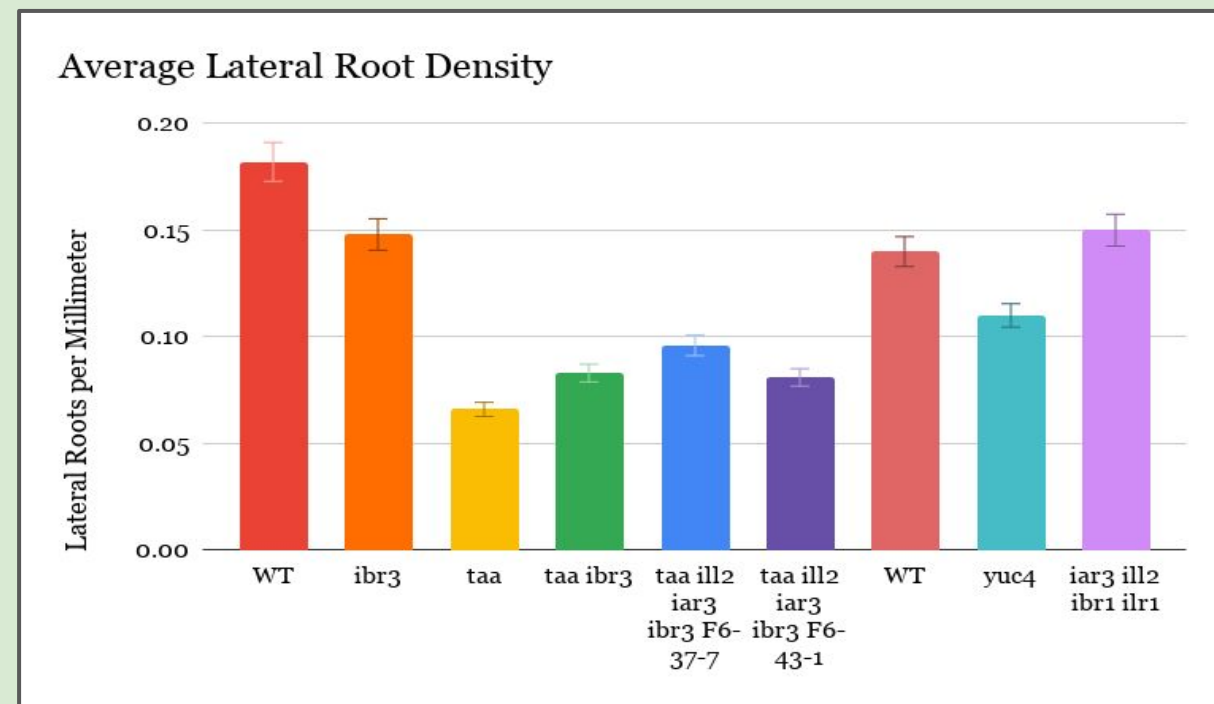
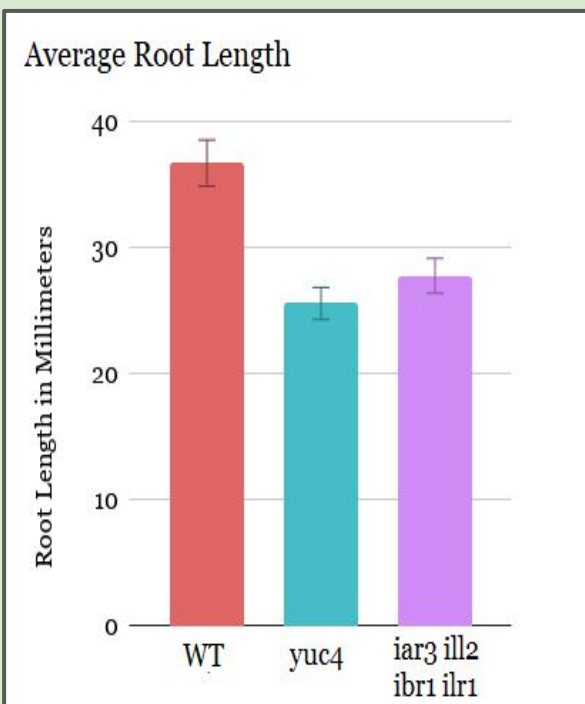
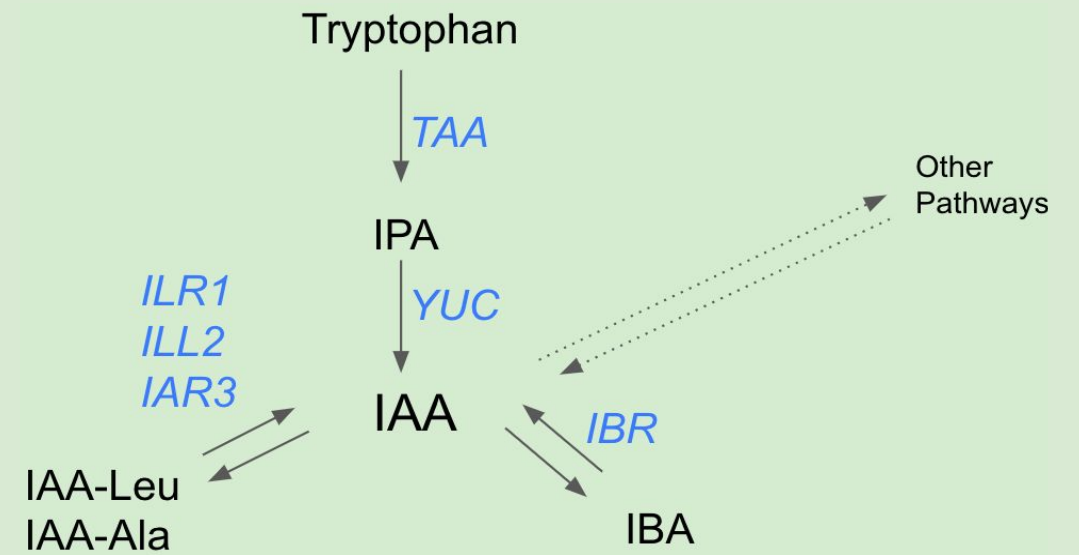
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Mutations in Several Auxin Biosynthesis Genes and their Effects on Plant Phenotypes in Arabidopsis

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*these authors had equal contributions to the project

- IAA is involved in plant growth and development
- *YUC4* and *TAA1* are genes involved in IAA synthesis
- *IBR1* and *IBR3* convert IBA → IAA
- *ILL2*, *IAR3*, and *ILR1* hydrolyze IAA-amino acid conjugates → IAA
- Genes in these IAA pathways may interact if one or more is disrupted, showing measurable changes in phenotype. Through these assays, we sought to better understand how these pathways and the genes involved in them interact to promote plant growth and development.



ROOT ELONGATION
All lines with mutations in biosynthesis or conjugation pathways had shorter roots than WT. The *yuc4* single mutant line showed the biggest difference. All genes studied appear to be involved in root elongation, and loss of a biosynthesis gene was particularly impactful.

LATERAL ROOTS:
All lines with mutations in biosynthesis or conversion genes showed decreased lateral rooting. The *iar3 ill2 ibr1 ilr1* conjugation mutant line showed slightly increased lateral rooting.

GERMINATION:
All *taa* biosynthesis single and combination mutants germinated more quickly than WT, and the *ibr3* single conversion mutant line germinated more slowly. This indicates that IBA metabolism may be more important to rapid germination than IAA biosynthesis.

FUTURE DIRECTIONS

- Confirm genotypes
- Repeat root elongation and germination assays and compare with past results
- Create new crosses, particularly of *taa1* and *yuc4*
- Follow plants to adulthood and note phenotypic differences in apical dominance and leaf size

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