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Extension of oil biosynthesis during the mid-phase of seed maturation increases seed oil in *Arabidopsis thaliana*

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Regulation of oil biosynthesis in plant seeds has been studied, and transgenic approaches have been designed to enhance seed oil content. Oil and protein synthesis is negatively correlated in seeds, but the mechanisms controlling interactions between these two pathways are unknown. To understand the molecular mechanism controlling oil and protein content in seeds, we utilized transgenic *Arabidopsis* plants overexpressing *WRINKLED1* (*WRI1*), a master transcription factor controlling seed oil biosynthesis, and knockout mutants of major seed storage proteins. Oil and protein synthesis in wild-type plants was sequentially activated during early and late seed maturation, respectively. The negative correlation between oil and protein contents in seeds arises from competition between the pathways. Extension of *WRI1* expression during mid-phase of seed maturation significantly increased seed oil content. This study demonstrates that temporal activation of genes involved in oil biosynthesis enhances the seed oil content in *Arabidopsis thaliana*. These results provide novel insights into potential breeding strategies to generate crops with high oil contents in seeds.

References

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Factors affecting seed yield in selected *Festuca* species

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An experiment has been performed in four locations in Poland (Radzików, Leszno, Szelejewo and Nieznance). Fifteen genotypes from three species (*Festuca arundinacea*, *F. pratensis* and *F. rubra*) were measured and observed during two consecutive years. Despite of phenological observations (heading and flowering start dates), biometrical measurements (plant height, leaf dimension, number of generative stems etc.) and some physiological traits (chlorophyll contents index, nitrogen contents) seed yield of single panicle, seed yield of plant and seed yield per plot (i.e. 50 plants) were determined. Temperature and precipitation averages specific for each location were also used for calculations.

Multiple linear regression analysis with a forward stepwise variable selection procedure was used to estimate major factors affecting seed yield. It resulted in different predictors for different species.

For meadow fescue almost all traits (18 from all 19) used were selected and 16 were statistically significant. For tall fescue it was 12 with 4 statistically significant, but for red fescue only 6 with 3 statistically significant. Significant predictors had different weights in different species. Specific genotype features were significant only in meadow fescue, also with precipitation averages and many other traits. For tall fescue, location thermal characteristic (normal value for growing season) were negatively related to seed yield. Conclusion is that for each species different measures should be applied to predict seed yield.