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## Short Communication

# Oil content and fatty acid composition variability in wild peanut species

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**Abstract**

Wild peanut species are useful genetic resources for improving the levels of disease/pest resistance and for enhancing the quality of seed composition by interspecific hybridization. The variation in oil content and fatty acid composition of wild peanut species in the United States Department of Agriculture germplasm collection is unknown. Seeds available from 39 wild species (plus a cultivated peanut) were requested from the U.S. peanut germplasm collection. Oil content was measured using nuclear magnetic resonance, fatty acid composition was analysed using gas chromatography, and the D150N functional mutation of the *FAD2A* gene was screened by real-time PCR. Significant variability in oil content (41.7–61.3%) was identified among the wild peanut species. *Arachis magna* contained significantly more oil (61%) than cultivated peanut (56%). There was no functional mutation identified within the *FAD2A* gene target, and no wild species were identified with a high ratio of oleic acid to linoleic acid. The results from gas chromatography and real-time PCR analyses were consistent. However, *Arachis sylvestris* contained a significantly higher amount (22%) of long-chain fatty acid (LCFA) than the cultivated peanut (4%). Thus, *A. magna* and *A. sylvestris* may be good breeding materials to use for increasing oil content or LCFA composition of cultivated peanuts in breeding programs.

**Keywords:** fatty acid composition; oil content; peanut germplasm; real-time PCR genotyping; wild species

## Experimental procedure

The genus *Arachis* contains about 80 species divided into nine sections (Krapovickas and Gregory, 1994; Valls and Simpson, 2005). Unique and useful traits exist in these wild peanut species. Therefore, these wild species can be used as a secondary pool for improvement of cultivated peanut. Successful examples relate to improvement in resistances to root-knot nematode, leaf spot and rust by interspecific introgression from wild species to cultivated peanut. Within the U.S. *Arachis* germplasm collection, there are 70 wild peanut species, and these wild species have not been well characterized. Because oil content and fatty acid composition are important seed quality traits for peanut breeding programs, the objective of this study was to determine the oil content and fatty acid composition variability among the wild peanut species.

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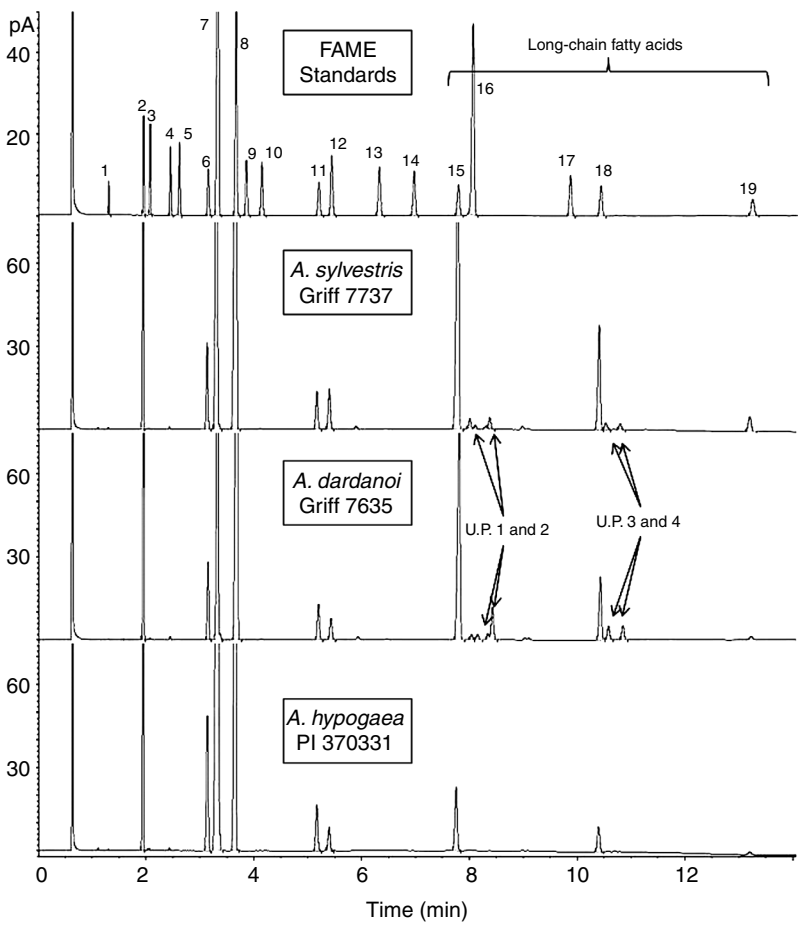
Available seeds from 49 accessions (representing 39 *Arachis* species plus one cultivated line, PI 370331) were requested from the Plant Genetic Resources Conservation Unit, Griffin, GA, USA (Supplementary Table S1, available online only at http://journals.cambridge.org). Prior to oil content and fatty acid composition analyses, the seed-coat colour was scanned and recorded using Hewlett-Packard Scanjet 7400C. The procedures for the determination of oil content and fatty acid composition and the functional mutation screening for *FAD2A* by real-time PCR were based on the methods described by Wang *et al.* (2009) and Barkley *et al.* (2010), respectively. An analysis of variance was performed on the data, and means were separated using Tukey's multiple comparison procedure.

The seed size of the wild peanut species was very different from the cultivated peanut (Supplementary Fig. S1, available online only at http://journals.cambridge.org). The variability in oil content among the wild peanut species ranged from 41.7 to 61.3%, with an average of 52.8%. There were four *Arachis* species accessions (PI 468328, PI 210554, Griff 7635 and PI 468337) that contained over 59% oil, which is much higher than the cultivated peanut (Supplementary Table S1, available online only at http://journals.cambridge.org). On an average, the wild peanut species contained a much lower amount of oleic acid (35.76%) and much higher amount of linoleic acid (36.25%) than the cultivated peanut (58.5 and 21.5%, respectively). Furthermore, no functional mutation in the *FAD2A* gene (for high oleic acid) was




1 = C14:0, 2 = C16:0, 3 = C16:1, 4 = C17:0, 5 = C17:1, 6 = C18:0, 7 = C18:1,
8 = C18:2, 9 = C18:3γ, 10 = C18:3α, 11 = C20:0, 12 = C20:1, 13 = C20:4, 14 = C20:5,
15 = C22:0, 16 = C22:1, 17 = C22:6, 18 = C24:0, 19 = C26:0, U.P. = unidendified peaks.

**Fig. 1.** Comparison of fatty acid profiles in wild peanut species with cultivated peanut on gas chromatograms. The top of several peaks (7, 8, 15 and 16) cannot be seen because of image enlargement. The peaks within the bracket indicate the long-chain fatty acid, and the unidentified peaks are indicated by arrows. FAME, fatty acid methyl esters; *A. sylvestris, Arachis sylvestris*; *A. dardanoi, Arachis dardanoi*; *A. hypogaea, Arachis hypogaea*.

identified in the wild peanut species (Supplementary Table S2, available online only at http://journals.cambridge.org), and no species was found with a high oleic acid to linoleic acid ratio. However, several species contained significantly higher amounts of long-chain fatty acid (LCFA, C ≥ 22) than *Arachis hypogaea*. For example, *Arachis sylvestris* (Griff 7737) and *Arachis dardanoi* (Griff 7635) contained 22.3 and 19.0% LCFA, respectively, much higher than the cultivated peanut (4.2%, Supplementary Table S1, available online only at http://journals.cambridge.org and Fig. 1). Fatty acid analysis revealed that some wild species contained unidentified fatty acid peaks. For example, both *A. sylvestris* and *Arachis dardanoi* contained four unidentified peaks (U.P. 1–4 on Fig. 1).

## Discussion

Significant variability in the oil content and fatty acid composition has been detected among the wild peanut relatives. Our results were consistent with a previously published report (Stalker *et al.*, 1989). The diploid species *Arachis magna* contains 61% oil, and *A. sylvestris* contains 22% LCFA, which may be useful for developing high oil content or LCFA peanut cultivars. The unidentified peaks from gas chromatography analysis may be from long-time temporal seed storage. Confirmation of the origin of unidentified peaks will require the comparison between the chromatograms generated from stored seeds and freshly harvested seeds of the same species.

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