Verbascum is being reported. Figure 1A-U gives the embryogeny and structural details of proembryo till torpedo-stage. It is seen that embryogeny in Verbascum phlomoides conforms to the Crucifer type as is also the case in Celsia coromandeliana Vahl⁴. Based on the pattern of embryogeny, the two genera, Verbascum and Celsia may be merged into one.

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HETEROTIC POTENTIALS FOR SEED OIL IN GOSSYPIUM ARBOREUM L.

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Cotton seed is the second important source of edible oil in India. There are some reports on the variability of seed oil content in cotton¹⁻³. However, very little information is available on the heterosis in seed oil content in cotton and that too in the upland species (Gossypium hirsutum L.)⁴. Hence 51 crosses of G. arboreum L. were screened to find out the magnitude of heterosis and inbreeding depression in seed oil content.

The 51 F_1 s and their 20 parents were grown in randomized block design with 3 replications during 1987. Each entry had a single row of 10 plants spaced at 60×45 cm. The F_1 crossed seeds and the seeds obtained from F_1 plants (original) are geneti-

cally considered as F_2 . Oil was estimated in pooled seed samples of 5 crossed bolls in F_1 and 15 bolls (5/replication) in F_2 by a non-destructive nuclear magnetic resonance (NMR) technique using Newport analyser. The heterosis over mid parent, better parent and standard variety (AKH4), and the inbreeding depression were worked out.

The range of seed oil content was higher in F₁s (19.2-26.3%) than in parents (17-24.4%). Considerable positive heterosis for seed oil content was observed over mid parent, better parent and standard variety (table 1). Of the 51 crosses evaluated, 26 exhibited positive heterosis over the mid parent in the range 0.22-20.1%. The highest mid parent heterosis (20.1%) was observed in nakedseeded \times LS2, closely followed by NAS4 \times LS3 (16.3%) and AC $3063 \times LS2$ (15.4%). Heterobeltiosis was exhibited by 18 crosses with a range of 1.3–14.8%. The highest heterobeltiosis of 14.8% was recorded in naked-seeded × LS2, followed by LS1 \times LS2 (11.3%) and AC 3063 \times LS2 (11.1%). The standard heterosis was exhibited by 45 crosses ranging from 0.49-29.6%. The highest standard heterosis of 29.6% was observed in naked-seeded \times LS2, followed by AC 3063 \times LS2 (23.6%) and NAS2 × LS2 (22.7%). Thus 2 crosses, viz. nakedseeded \times LS2 and AC 3063 \times LS2, exhibited high heterosis on all the 3 levels. Dani4 reported heterosis of up to 7.3% over mid parent and 1.6% over better parent in 12 crosses and their reciprocals in upland cotton.

The 15 superior heterotic combinations selected in F_1 showed inbreeding depression in F_2 generation ranging from -11.1 to 23.3%. This suggests that expression of seed oil content is largely governed by non-additive gene action. Dani⁴, however, observed gain in a few crosses in F_2 ranging from 0.05 to 24.55%. This variation may be due to difference in species.

Thus in G. arboreum there was considerable heterosis in seed oil content. Expression of this trait is largely governed by non-additive gene action.

Table 1 Range and magnitude of heterosis in seed oil content in G. arboreum L.

Heterosis over	Range of positive heterosis (%)	Number of crosses with positive heterosis			
		0-10%	10-20%	20-30%	Total
Mid parent	0.22-20.1	16	9	1	26
Better parent	1.31 - 14.8	14	4	0	18
Standard variety	0.49 - 29.6	20	19	6	45

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BIOCHEMICAL CHARACTERIZATION OF ROOT REGION SOILS FROM ARECA-BASED CROPPING SYSTEMS

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Mixed cropping of banana (Musa sapientum L.), cacao (Theobroma cacao L.) and pepper (Piper nigrum L.) with areca (Areca catechu L.) is in practice. Root exudates from these plants may influence soil composition as the exudates have been shown to contain amino acids, sugars and organic acids'. Studies on root exudates from areca, banana, cacao and pepper growing under different areca-based cropping systems have revealed a significant reduction in exudation of amino acids by roots of arecafrom mixed and high density multispecies (HDMS) cropping systems compared to the exudation by roots of areca grown in a mono-cropping system¹. Hence studies were undertaken to characterize soils from root regions of areca, banana and cacao from areca-based cropping systems.

Soils from 0 to 25 cm depth (six samples) from each plot) were collected during the pre-monsoon season (February to May). The samples were collected around the roots of areca, banana and cacao growing under mono-, mixed and HDMS cropping systems. The spacing of these crops has been described earlier². All these crops received normal recommended doses of fertilizer and were irrigated in summer.

An ethanol extract of the soil sample was fractionated into amino acids, sugars and organic acids by ion exchange chromatography using Dowex 50 (H⁺) and Dowex 1 (formate form) resins. Total sugars³, amino acids⁴ and phenols⁵ were estimated. Individual amino acids, sugars, organic acids and phenols were separated by descending paper

chromatography using different solvent systems⁶. Amino acids were detected by spraying the chromatogram with 0.3% ninhydrin. Sugars were detected using different spray reagents⁷⁻⁹. Organic acids were visualized by dipping the chromatogram in 0.04% bromophenolblue in 95% ethanol. The organic acid fraction was extracted with an equal volume of ethyl acetate and the organic phase was used for chromatography of phenols. Phenols were detected by dipping the chromatogram in ferric chloride—potassium ferricyanide reagent¹⁰.

The results of the analysis are shown in table 1. A significant reduction was noticed in the phenol content of soils from root regions of areca, banana and cacao growing under HDMS cropping system compared to that of soils from mono-cropping systems. Sugar content of soils from areca, banana and cacao under HDMS cropping system was higher than that of soils from the respective mono-cropping systems. Amino acid content of soils from cacao under HDMS and under areca-cacao mixed plot systems was significantly lower than that of soil from cacao under the mono-cropping system.

The present studies revealed the presence of the sugars fructose, glucose, sucrose, maltose, lactose, raffinose; and the amino acids lysine, serine/glycine, glutamic acid, alanine, tyrosine, trypto-

Table 1 Biochemical composition of soils from different areca-based cropping systems

Crop	Cropping system ^a	Total sugars ^b	Amino acids ^c	Phenols ^b
Агеса	A	5.03	20.1	0.63
	В	5.46	22.0	0.52
	C	4.73	36.1	0.67
	D	11.89	35.1	0.11
CD 5%		2.59	NS	0.22
Banana	Α	3.47	32.1	0.75
	В	5.66	15.7	0.84
	D	8.06	24.0	0.061
CD 5%		1.79	8.97	0.224
Cacao	Α	2.83	25.9	0.87
	C	4.61	15.3	0.13
	D	6.87	15.2	0.057
CD 5%		1.79	6.0	0.092

^{*}A, mono crop; B, areca + banana mixed plot; C, areca + cacao mixed plot; D, areca + banana + cacao + pepper + cosfee + clove + pineapple HDMS.

^bExpressed as mg/100g dried soil.

Expressed as μg amino nitrogen/100 g dried soil. Each value is the mean of estimations from six soil samples.