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Network pharmacology and *in vitro* validation of anti-adipogenic property of *Ipomoea mauritiana* Jacq.

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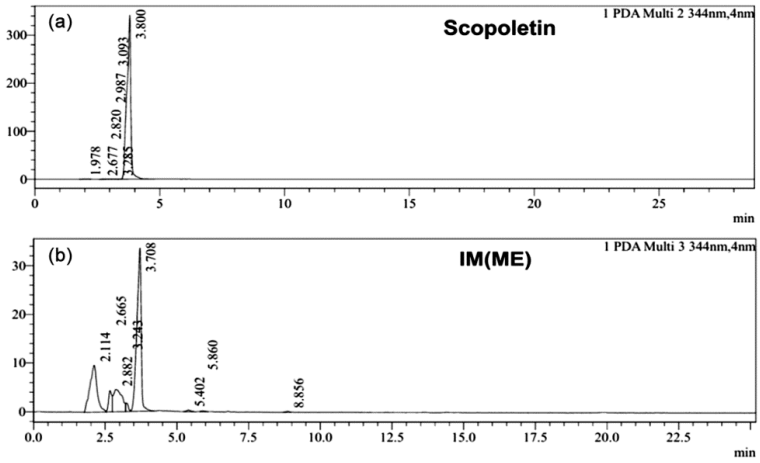
Supplemenatary data



Suppl. Fig. S1 — HPLC Chromatogram of standard (scopoletin-100 µg/mL) and IM (1 mg/mL). Retention time of scopoletin was 3.8 min and one of the peaks in IM extract was 3.7 min

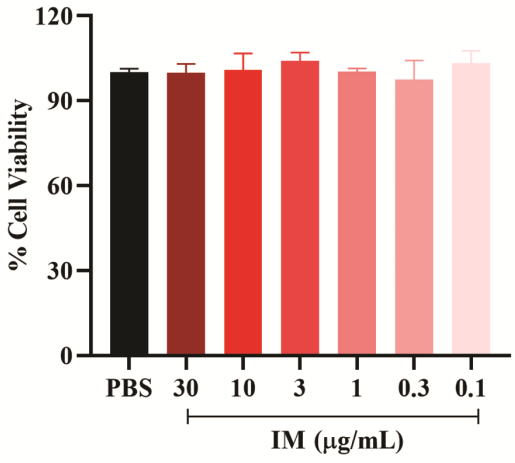


Fig. S2 — Safety profile of IM methanolic extract on 3T3L1 cells. Cell viability after 24 h of treatment with different concentrations of IM extract

Suppl. Table S1 — Sequence of primers used in the study

S. No.	Gene	Sequence (5′-3′)
1.	β-Actin	Forward- GCAGGAGTACGATGAGTCCG
		Reverse- ACGCAGCTCAGTAACAGTCC
2.	CD36	Forward- TCAATGGCTGTCAGGCGTC
		Reverse- TTGGCTTCAGGGAGACTGTTG
3.	PLIN	Forward- GGTGAGTGGCCTGTGTTAGTC
		Reverse- CACACGCCTTGAGAGAAACAG
4.	FAS	Forward- TTGGAGGGTGTGCCATTCTG
		Reverse- GCTATTCTCTACCGCTGGGG
5.	PPARγ	Forward- GAGGGACGCGGAAGAAGAG
		Reverse-CACAGGCTCCTGTCAGAGTG
6.	AdipoQ	Forward- TGACGACACCAAAAGGGCTC
		Reverse- ACCTGCACAAGTTCCCTTGG
7.	CEPBα	Forward- CCCTTGCTTTTTGCACCTCC
		Reverse-GCTTTCTGGTTCTGACTGGGG
8.	RBP4	Forward-AATGGTTACTGTCAAAGCAG
		Reverse-AATAGAGATGAAGACCGGATG
9	FATP1	Forward- GCCAGGGATCTCTCTCTCCA
		Reverse-GTGCTGGAGCTTGCCTGAT

Suppl. Table S2 — List of phytochemicals identified from IM

Fatty Acids	Isobutyric Acid
	(S)-2-Methylbutyric Acid
	Tiglic Acid
	N-Decanoic Acid
	N-Dodecanoic Acid
	Palmitic Acid
	Stearic Acid
	Oleic Acid
	Linoleic Acid
	Linolenic Acid
	Myristic Acid
Coumarins	Umbelliferone
	Scopoletin
	Scoparone
	Scopolin
Sterols	β-Sitosterol
	Taraxerol
	Taraxerol Acetate
Polyesters/Resin Glycosides	Jalapin
	Quamoclinic Acid A
	Operculinic Acid A
	Digitatajalapin I
	Convolvulin
	Murucoidin XI
	Murucoidin IV
	Quamoclin IV
Aromatic Acids and Derivatives	Cinnamic Acid
	Chloroacetic Acid
Glycosides	3-O-β-D-Glucoside
	1-O-Ethyl-β-D-Glycopyranoside
	Caffeoyl Glucose
Alcohols	Octadecan-1-ol

Alkanes	Octacosane
	Nonacosane
	Tetracosane
Aldehydes	Myristaldehyde
Methyl Esters	Methyl N-Dodecanoate
Miscellaneous	Jalapinolic Acid
	Paniculatin

Suppl. Table S3 — Major Hub genes identified

Gene	Involvement in Malnourishment
HMGCR	Key enzyme in cholesterol biosynthesis[1]
ESR1	Mediates estrogen signaling, influencing metabolism and adiposity[2]
PPARA	Regulates lipid metabolism and energy homeostasis[3]
CYP19A1	Converts androgens to estrogens[4]
NR1I2	Regulates genes involved in drug metabolism and lipid homeostasis[5]
CYP17A1	Involved in steroid hormone biosynthesis[6]
CYP11A1	Initiates steroidogenesis by converting cholesterol to pregnenolone[7]
LSS	Catalyzes a key step in cholesterol biosynthesis[8]
EPHX2	Metabolizes epoxides to diols, affecting lipid signaling[9]
ESR2	Mediates estrogen signaling, influencing various physiological processes[2]
CYP51A1	Involved in cholesterol biosynthesis[10]
CYP4A11	Metabolizes fatty acids and eicosanoids[11]
HSD17B3	Converts androstenedione to testosterone[12]
AKR1C3	Involved in steroid metabolism and prostaglandin synthesis[13]
AR	Mediates the effects of androgens like testosterone[14,15]

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