

Leaf architecture of *Pisum sativum* L. and *Dalbergia sissoo* Roxb. of family Fabaceae Lindl

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ABSTRACT

Plant taxonomy is based upon identification, classification and nomenclature of plants. There are various methods to achieve these three basic goals of plant taxonomy, leaf architecture being one of the most important ways. Plants usually have their reproductive phase for only a very short period of time but most keys require them to be in flowering or fruting state in order to be classified and identified. Leaf architecture may be an important breakthrough to help identify plants in any season and help pace up the related research works.

Key Words :- Leaf architecture, Pisum sativum L., Dalbergia sissoo Roxb., Fabaceae Lindl.

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INTRODUCTION

Pisum sativum is commonly known as Pea/Matar. Dalbergia sissoo is locally known as Shisham. Both taxa belong to Subfamily Faboideae in Family Fabaceae according to the APG IV classification and in Subfamily Papilionoideae of Family Fabaceae in the traditional classifications.

Family Fabaceae is the 3rd largest family of angiosperms. It has diverse members with cosmopolitan distribution and varied habits. It was earlier known as Family Leguminosae and was divided into three very well-known and widely accepted Sub-families; Caesalpinioideae DC, Mimosoideae DC and Papilionoideae DC. The widely accepted APG IV classification categorises the family into six sub-families namely Caesalpinioideae DC., Cercidoideae LPWG, Detarioideae LPWG and Papilionoideae DC.

Leaf architecture is the study of leaf morphology in detail. The characters may be grouped as qualitative or quantitative. In recent times, Leaf architecture has established itself as an important operational taxonomic unit and serves as an essential tool to help classify plants and differentiate a taxon from another.

MATERIALS & METHODS

Materials used in the study were leaves of *Pisum* sativum L. and *Dalbergia sissoo* Roxb. from different localities of Ranchi, Jharkhand. The quantitative and qualitative morphological characters were observed on fresh leaves while the micromorphological details were studied from cleared leaves. The leaves were cleared using Franklin's solution at room temperature for about 24 hours. After washing the cleared leaf with water, leaf samples were placed in a weak solution of sodium hypochlorite to study the details.

MEGA11 software was used to align the DNA of the species.

OBSERVATIONS



Figure 1. Leaflet of Pisum sativum L.

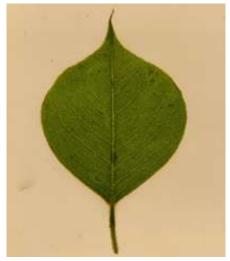


Figure 2. Leaflet of *Dalbergia sissoo* Roxb.

Table 1- Quantitative and qualitative morphological characters in <i>Pisum sativum</i> L. and <i>Dalbergia</i>
sissoo Roxb. leaves.

	Pisum sativum L.	Dalbergia sissoo Roxb.
Leaf organization	Paripinnate	Imparinnate
Phyllotaxy	Alternate	Alternate
Rachis	Straight	Zig-zag
Petiole	Present	Present
Petiolar attachment	Marginal	Marginal
Petiolule length	0.1 cm	0.4 cm
Leaf type	Paripinnate	Imparipinnate
Leaflet organization	Opposite	Alternate
Leaflet shape	Ovate	Oblong
Leaflet margin	Serrate	Entire
Leaflet base	Acute	Acute
Leaflet base angle	95°	95°
Leaflet apex	Obtuse	Acuminate
Leaflet apex angle	120 [°]	10 [°]
Lobation	Unlobed	Unlobed
Leaflet length	1.5-6cm	2.5-7.5 cm
Leaflet width	1-4cm	2-6 cm
Leaflet area	~100-1600mm ²	~333.34-3000mm ²
Blade class	Nanophyll – Microphyll	Microphyll- Notophyll
Vein category	Random reticulate	Regular polygonal reticulate
Leaflets per leaf	4 to 6	3 to 5
Tendril	Present (4 in number)	Absent
Stipule	Present	Present
Stipule type	Foliaceous	Free lateral stipule

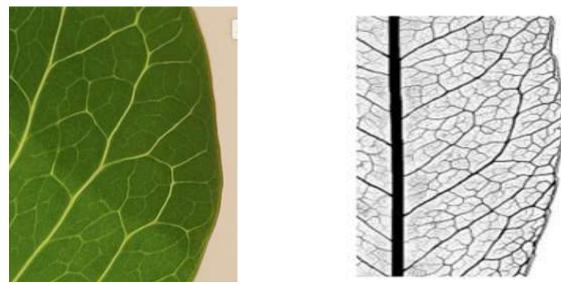


Figure 3: Leaflet of *Pisum sativum L.* showing random reticulate vein category



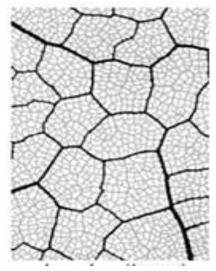


Figure 4: Leaflet of *Dalbergia sissoo* Roxb. showing regular polygonal reticulate vein category



Figure 5: Alignment of DNA of Pisum sativum L. and Dalbergia sissoo Roxb.

RESULT & DISCUSSIONS

The study successfully supported the taxonomic value of leaf architecture as an essential tool for identification of *Pisum sativum* L. and *Dalbergia sissoo* Roxb. in their vegetative state. This may further aid in identifying the plants in forensics when the identification is needed to be done using a fragment of leaf.

The two species belong to subfamily Faboideae which was earlier known as Papilionoideae. According to the molecular taxonomy data, *Pisum satium* L. belongs to IRLC (inverted repeat-lacking clade) whereas *Dalbergia sissoo* Roxb. belongs to Dalbergieae of the major clade Dalbergioids.

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