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RAFFLESIA - THE WORLD´S LARGEST FLOWER: A CENTENNIAL ANNIVERSARY

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The genus *Rafflesia* is both iconic and mysterious in terms of its floral morphology and phylogenetics. There are more than 39 species, mostly centred in Sumatera and the Philippines. While its morphology, host-parasitic relationship are quite well-known, evolution and molecular biology remain mysterious and conservation efforts are uncertain. It is an enigmatic flower with the gigantic size, unique features but unpleasant smell has enthralled the botanical world. The genus is distributed only in tropical rainforests of Southeast Asia and Malaysia. A total of 13 species have been reported from Malaysia; 8 from Peninsular Malaysia and 5 from Sabah and Sarawak. Unlike any other parasitic plants, although recognized as parasitic flower, Rafflesia was conserved and protected by laws and acts, even was used as flagship species to conserve the tropical rainforest from destruction and as symbol in plant kingdom.

Keywords: *Rafflesia*, parasitic flower, Southeast Asia, tropical rainforests

INTRODUCTION

The *Rafflesiaceae* members are leafless, stemless, and rootless nonphotosynthetic parasites living initially embedded in host plants and later blooming on the stems of host plant. This family is recognised to comprise of 3 genera, *Rafflesia, Rhizanthes* and *Sapria* [Takhtajan et al., 1985; Meijer, 1997; Nais, 2001; Barkman et al., 2004; Twyford, 2017], only found to grow in South-east Asia and about 39 species have been described. The phylogenetic analyses of mitochondrial, nuclear, and plastid data show that the members from this family have arisen from within *Euphorbiaceae*, the spurge family. Most euphorbs produce minute flowers, suggesting that the enormous flowers of *Rafflesiaceae* evolved from ancestors with tiny flowers. Given the inferred phylogeny, it was estimated that there was a circa 79-fold increase in flower diameter on the stem lineage of *Rafflesiaceae*, making this one of the most dramatic cases of size evolution reported for eukaryotes.

The most common and known genus is Rafflesia; likened to a 'giant panda of Plant Kingdom' in terms of its scientific value and conservation importance [Latiff, 2025]. It is the official state flower of Indonesia, the Sabah state in Malaysia, and of the Surat Thani Province, Thailand and classified as; Kingdom Plantae, Angiosperms, Eudicots, Rosids, Order: Malpighiales, Family: *Rafflesiaceae*, Genus: *Rafflesia*. The genus includes parasitic flowering plants, composed of nearly 39 species with 4 incompletely characterized ones, all found in southeastern Asia, in Peninsular Malaysia, Borneo, Sumatra, Java, Peninsular Thailand and the Philippines. It was found in the Sumatran rainforest by an Indonesian guide working for Dr. Joseph Arnold in 1818, and named after Sir Thomas Stamford Raffles, the leader of the expedition. However, it has been reported earlier by Louis Deschamps from Java in 1791 and 1794. His notes and illustrations were seized by the British in 1803. These were not available to the scientists until 1861. The plant is a holoparasite of vines in the genus Tetrastigma (*Vitaceae*), spreading its absorptive organ, the haustorium, inside the tissue of the vine. The only part of the plant that can be seen outside the host vine is the 5-petaled (perigones) flower [Latiff, 2025].

It is an endophytic holoparasite flowering plant, growing with the single flower, lacking chlorophyll, the flower parasitizes host plant species of Tetrastigma [Latiff, 1983; 2025]. The haustorium (thread-like structures) act as root-like appendages to link the flowers to the host plant. Each one of its species parasitizes a specific host plant. In all 32 species of Tetrastigma are found which include *T. hookeri, T. rafflesiae, T. diepenhorstii, T. curtisii, T. scortechinii, T. glabratum, T. papillosum, T. harmandii, T. scariosum, T. loheri, T. pisicarpum and T. magnum* [Wan Zakaria et al., 2016; Nasihah et al., 2016; Ahmad Puad et al., 2020; Latiff, 2021]. However, only *T. hookeri, T. rafflesiae, T. diepenhorstii* are proven host vines.

In *R. arnoldii*, the flower may be over 100 cm in diameter [Ozturk and Secmen, 1991] and weigh up to 11 kg [Latiff, 2025]; even the smallest species *R. consueloae* and *R. baletei* have ca. 9 cm and 12 cm diameter flowers, respectively. The flowers smell (when ready for pollination) like rotten body, hence its local name as "corpse flower" or "meat flower”. The foul odour attracts flies, which transport pollen from male to female flowers. All species have separate male and female flowers but little is known about seed dispersal. The tree shrews and other forest mammals eat the fruits and disperse the seeds.

Historical data. Rafflesia in the Philippines is reported to have existed as early as 5.2 to 9.3 mya [Bendiksby et al., 2010]. The flower was found distributed only in 5 larger islands, namely Luzon, Samar, Panay, Negros and Mindanao islands. Although it is significantly known with the enormous flower size, the smallest species are also found in the Philippines e.g., *R. consueloae* is just 9.73 cm in diameter [Galindon et al., 2016]. A significant study has been carried out by Barkman et al. [2008] on floral gigantism in *Rafflesiaceae*, where *Rafflesia* flower is believed to have evolved from the smaller flower species such as *R. consueloae* in the Philippines and *R. tengku-adlinii* in Borneo as possible ancestors to the larger-flowered species. In Thailand, since the first discovery by Kerr, only one species was discovered and studied, *R. kerri* described by Meijer in 1984. The subsequent discoveries of the species in South-east Asia, in particular on the islands of Java, Sumatera, Borneo and the Philippines are listed in Table [Latiff, 2025].

The name "corpse flower" is applied to Rafflesia , a little confusing because this name also refers to the titan arum (*Amorphophallus titanum*) of the family *Araceae*, which has the world's largest unbranched inflorescence and sometimes mistakenly credited as having the world's largest flower. Both *Rafflesia* and *Amorphophallus* are flowering plants, but they are only distantly related. *Rafflesia arnoldii* has the largest "single" flower of any flowering plant, at least in terms of weight and width. *A. titanum* has the largest "unbranched" inflorescence, while the monocarpic talipot palm (*Corypha umbraculifera*) forms the largest "branched" inflorescence, containing thousands of flowers. *Rafflesia* causes economic benefit through ecotourism: thousands of people go to Sabah (Malaysian, Borneo) and other parts of Malaysia annually hoping to see *Rafflesia* blooms [Nais and Wilcock, 1998].

Life cycle. According to Mursyidah et al. [2023], the species of this genus maintain a long embryonic state that can abruptly transition to the flowering stage without forming an elaborate vegetative body. The vegetative phase begins with the seed germination that exists in the host plant as a filament that resembles a substance called endophyte [Latiff, 2025]. *Rafflesia* endophyte forms a clonal network of vegetative meristematic cells, separated by the dividing host tissue where each meristematic cell cluster ultimately develops into primordial floral bud or protocorm. The exact information on the period of *Rafflesia* in the vegetative phase is unknown. However, the continuous flowering in the rainforest possibly on the same host plant suggests that the holoparasite spends an extensive time in the vegetative phase before continuing to the reproductive phase, which is indicated by the occurrence of the bud [Latiff, 2025].

Table. The data on the subsequent discovery of *Rafflesia* in Southeast Asia [modified from Latiff, 2025].

Year Described	Species	Where discovered	Remarks
1821	*R. arnoldii* R. Br.	Sumatera	Discovered by Sir Stamford Raffles and Dr. Joseph Arnold and described by Robert Brown in 1821.
1825	*R. patma* Blume	Sumatera, Java	Initially discovered by Louis Auguste Deschamps in 1797 and described by Blume in 1825.
1841	*R. manillana* Teschermacher	Leyte, the Philippines	J. E. Teschemacher described the unopened male bud in 1844.
1845	*R. lagascae* Blanco	Luzon, the Philippines	Discovered on Mt. Banahaw, Luzon.
1845	*R. philippensis* Blanco	Luzon, the Philippines	Discovered on Mt. Banahaw, Laguna and Quezon Province, Luzon.
1850	*R. rochussenii* Teijs. & Binn.	Sumatera, Java	Described based on specimen found at Mt. Gedeh-Pangerango near Cibodas in Java.
1868	*R. tuan-mudae* Beccari	Borneo	Specimen collected from Mt. Pueh and described by Beccari.
1879	*R. hasseltii* Suring.	Sumatera	Discovered in Central Sumatera and described by Suringar in 1879.
1884	*R. schadenbergiana* Goeppert	Mindanao, the Philippines	Discovered in Mindanao by Hieronymus and described by Goeppert.
1910	*R. cantleyi* Solms-Laubach	Peninsular Malaysia	Discovered by M. Cantley in 1881 and described by H. Graft Solms-Laubach.
1918	*R. borneensis* Koorders	Borneo	Specimen collected from G. Raya in Kalimantan.
1918	*R. ciliata* Koorders	Borneo	Specimen collected from G. Raya in Kalimantan.
1918	*R. witkampii* Koorders	Borneo	Specimen collected from G. Raya in Kalimantan.
1918	*R. atjehensis* Koorders	Aceh, Sumatera	Discovered in Lokop, Aceh, Sumatera.
1984	*R. gadutensis* Meijer	Sumatera	Described by W. Meijer in 1984.
1984	*R. keithii* Meijer	Sabah, Borneo	Described by W. Meijer in 1984.
1984	*R. kerri* Meijer	Peninsular Malaysia and Peninsular Thailand	Described by W. Meijer in 1984.
1984	*R. micropylora* Meijer	Sumatera	Described by W. Meijer in 1984.
1984	*R. pricei* Meijer	Borneo	Described by W. Meijer in 1984.
1989	*R. tengku-adlinii* Mat-Salleh & Latiff	Sabah, Borneo	Specimen collected from Mt.Trus Madi, Sabah
1902	*R. zollingeriana* Koorders	Eastern part of Java	Koorders discovered the species at Puger (Jember, East Java).
2002	*R. speciosa* Barcelona & Fernando	Panay and Negros	Specimen described from Mt. Poras, Antique Province, Panay.
2003	*R. azlanii* Latiff & Wong	Perak, Peninsular Malaysia	Species described based on specimen from Sg. Halong, Perak.
2005	*R. bengkuluensis* Susatya, Arianto & Mat-Salleh	South Sumatera	Species described based on specimen collected from Talang Tais, Bengkulu, Sumatera.
2005	*R. mira* Fernando & Ong	Mindanao, the Philippines	Discovered in Mt. Candalaga, in Maragusan Municipality, Compostela Valley Province.
2006	*R. lobata* Galang & Madulid	Panay Island, the Philippines	Species discovered on Mt. Igtuog & Mt. Sakpaw, Antique Province, North-Westren part, Panay.
2006	*R. baletei* Barcelona & Cajano	Luzon, the Philippines	Discovered on Mt. Isarog and Mt. Asog.

2008	*R. leonardii* Barcelona & Pelser	Luzon, the Philippines	Species discovered from Kalinga, Cagayan Province of Northern Luzon.
2009	*R. aurantia* Barcelona, Co & Balete	Luzon, the Philippines	Discovered from Quirino Province, Luzon.
2009	*R. su-meiae* Wong, Nais & Gan	Kelantan-Perak border, Peninsular Malaysia	Species discovered in 2008, and described in 2009.
2010	*R. meijeri* Wiriadinata & Sari	North Sumatera	Species distributed at Mt. Leuser, Brastagi, Tapanuli, Batang Gadis.
2010	*R. lawangensis* Mat-Salleh, Mahyuni & Susatya	North Sumatera	Species discovered from Bukit Lawang, Mt. Leuser National Park.
2010	*R. verrucosa* Balete, Pelser, Nickrent & Barcelona	Mindanao, the Philippines	Discovered from Mt. Kampalili, eastern Mindanao.
2013	*R. sharifah-hapsahiae* Adam, Mohamed, Aizat-Juhari & Wan	Peninsular Malaysia	Specimen collected from Mt. Benom FR, Ulu Dong, Raub, Pahang.
2014	*R. mixta* Barcelona, Manting, Arbolonio, Caballero & Pelser	Mindanao, the Philippines	Discovered from Caraga region of north-eastern Mindanao.
2016	*R. consueloae* Galindon, Ong & Fernando	Luzon, the Philippines	Distributed in Mt. Balukbok and Mt. Pantaburon, Pantabangan Municipality, Luzon.
2016	*R. parvimaculata* Sofiyanti, Mat-Salleh, Khairil, Zuhailah, Mohd. Ros & Burslem	Pahang, Peninsular Malaysia	Species described based on specimen collected from Lata Jarum, Pahang, Peninsular Malaysia.
2016	*R. tuanku-halimii* Adam, Aizat-Juhari, Azilah & Wan	Pahang, Peninsular Malaysia	Distributed in Sungai Kenau, Sungai Yol and Matau, Raub, Pahang.
2017	*R. kemumu* Susatya, Hidayati & Riki	Northern Bengkulu, Sumatera	Specimen was monitored since 2016 from Palak Siring FR Reserve, Northern Bengkulu, Sumatera.
2021	*R. tiomanensis*	Tioman Island, Peninsular Malaysia	Discovered in 2020

Rafflesia buds are commonly found on trailing stems mostly and frequently on the hanging stems and developmental phase can be divided into 3 stages; emergence stage from the host plant, 2nd and 3rd stages show medium growth with moderate size bud and nearly flowering bud with rapid growth [Mursyidah et al., 2023]. The bud growth has been recorded to take about 12-16 months followed by the flowering phase [Nais and Wilcock, 1998]. Mohamed and Mohd. Noor [2016] have reported *R. azlanii* as a fast-growing plant where the species only takes about 40 to 50 days from being a newly emerged bud to a full bloomed flower. In *R. patma* buds there are several differences between the early and the late stages of development [Latiff, 2025]. The early-stage bud has 3 types of cells - densely packed and meristematic distal region, non-elongated parenchyma in the middle region and elongated parenchyma in the proximal region. The late-stage bud develops the primordial central disc first, followed by the primordial bract and perigone lobes. *Rafflesia* only blooms for a short time and about a week before the flower dies. Nais and Wilcock [1998] report that blooming flowers can be found all year round and are not seasonal. It is noteworthy that seasonality has been observed in *Rafflesia* species with northerly distribution (Philippines and Thailand) compared to the documented equatorial species [Nais, 2001]. The more distinct periods in day-length and seasonal differences in the higher latitudes may be responsible for this mild seasonality. Its development, life cycle and anatomy have been recently described by Sharifah Haneira et al. [2021].

Due to their parasitic lifestyle, *Rafflesia* can tap into the reserves of its host and does not need to maintain a functional photosynthetic body. The evidence from RNA-seq analysis has demonstrated the lack of photosynthetic capacity in parasitic plants [Latiff, 2025]. Latiff [2025] has suggested that *Rafflesia* may be the 1st plant group where the chloroplast genome is entirely absent. Regardless of the plastid genome reduction in the plant, some nucleus-encoded proteins are transported back to the plastid to conduct biological functions which are not related to photosynthesis [Ng et al., 2019]. The genes expressed by *Rafflesia* are targeted for supporting plant growth and regulatory processes [Ng et al., 2019]. In about 9 months, the bud bursts, revealing an enormous, five-petaled flower. The reddish-brown flowers give off a pungent odor similar to rotting flesh, which attracts insects for pollination. These plants are unisexual and most often produce either male or female flowers at a single site. To succeed at pollinating the plant, insects must visit both male and female flowers, which are usually not in close proximity to one another. The fruit has smooth flesh that contains numerous tiny seeds. Once fruit and flower have both reached maturity, which takes 5-7 days, this marks the end of the plant's life cycle. The smell of the fruit's dead flesh attracts indigenous animals, distributing the seeds and continuing the plant's life cycle.

Pollination. *Rafflesia* requires pollinators as agents to pollinate the flower, male and female flowers need to bloom synchronizely, so the pollen from the male flower can be transferred to the female reproductive organ at the right time; a sapromyophilous flower providing primary attractants (yellow sticky mush of pollen and brooding site) and secondary attractants (odour and visual appearance) to locate and visit the gigantic flower [Latiff, 2025]. It is believed to be pollinated by the carrion flies [Beaman et al., 1988; Banzinger, 1991; Zuhud et al., 1998; Nais, 2001]. Adlan Ali et al. [2015] have listed several other visitors which frequently visited the flowers of *R. patma*, such as *Sarcophaga haemorrhoidalis, Drosophila colorata, Chrysomya megacephala, Paederus littoralis* and *Euprenolepsis procera*. Hor et al. [2021] have identified the possible pollinators for *R. kerri* in Lojing Highlands, Kelantan, Malaysia as calliphorid flies from the genera C*hrysomya, Lucilia* and *Hypopygiopsis*, whereas diptera and hymenoptera act as visitors.

A succesful pollination in *Rafflesia* results in the fruit setting, normally after about 4 days of bloom, the colour of the flower gradually changes to dark and almost black, entering the senescence stage, the lobes and perigone tube disintegrate and the reproductive organ hardens and becomes swollen, forming a fruit bearing thousand miniscule seeds. Several insects have been observed on decayed flower which probably act as decomposers [Adlan Ali et al., 2015]. The fruit maturation process takes several months, being 6 months in *R. arnoldii* [Bouman and Meijer, 1994], 8 months in *R. gadutensis* [Meijer, 1997], 6-8 months in *R. keithii* [Nais, 2001], after this period the seeds get dispersed, zoochory seems as the method of dispersal [Adlan Ali et al., 2015]. The mammals like treeshrews, squirrels and others such as wild pigs, elephants are accepted as the potential seed dispersal agents. In *R. patma* several mammal species (*Varanus salvator, Sus scrofa, Rusa* sp.) have been observed to visit the fruits and potentialy act as dispersal agents [Adlan Ali et al., 2015]. The animals with claws are potential dispersal agents as the tiny seeds might get attached on the claws and dispersed on the host plant [Syahbuddin, 1989]. The tiny seeds are also believed to be dispersed by ants (*Anoplolepis gracilipes, Ponera* sp., *Odontomachus simillimus*) and termites (*Macrotermes* sp.) [Zuhud, 1989; Pelser et al., 2013].

An evaluation of genus *Rafflesia* depicts that Malaysia has a total of 13 species (*R. hasseltii, R. keithii, R. tengku-adlini, R. azlanii, R. pricei, R.*

tuan-mudae, R. cantleyi, R. kerri, R. su-meiae, R. sharifah-hapsahiae, R. parvimaculata, R. tuanku-halimii and R. tiomanensis); Brunei has 1 species *R. pricei*, Thailand 1 species *R. kerri*, the Philippines (13 species) *R. lagascae, R. philippensis, R. consueloae, R. speciosa, R. schadenbergiana, R. mira, R. verrucosa, R. mixta, R. lobata, R. manillana, R. baletei, R. aurantia, R. leonardii* and Indonesia (17 species) *R. bengkuluensis, R. micropylora, R. meijeri, R. kemumu, R. gadutensis, R. lawangensis, R. arnoldii, R. rochussenii, R. patma, R. zollingeriana, R. pricei, R. tuan-mudae, R. hasseltii, R. atjehensis, R. witkampii, R. ciliata, R. borneensis,* including the incompletely known *R. witkampii, R. ciliata, R. borneensis*) [Sofiyanti et al., 2016; Hidayati and Walck, 2016; Adam et al., 2013, 2016; Susatya et al., 2017; Bascos et al., 2019; Ahmad Puad et al., 2020].

Peninsular Malayssian species. Rafflesia azlanii Latiff & Wong: The latest data has been published by Siti Munirah who discovered a ten-perigone lobes of *R. azlanii* from RBSP [Latiff, 2025]. This species is endemic to Peninsular Malaysia and only found in Perak and Pahang (Fig.).

R. cantleyi Solms-Laubach: First discovered at Bukit Berapit, Perak in 1881 by Cantley from Singapore Botanical Garden [Nais, 2001], but misidentified earlier as *R. hasseltii* [Ridley, 1910, 1924]. Latiff [2025] has provided details of the species and *R. cantleyi* is recognized as a different and distinct species from *R. hasseltii* from Sumatera. The species is endemic to Peninsular Malaysia, distributed in Kelantan, Pahang (include Pulau Tioman), Perak and Terengganu [Latiff and Mat-Salleh, 2001; Wong and Latiff, 2001; Nais, 2001]. It emits sweet fragrance instead of putrid smell [Wong and Latiff, 2001]. Wee et al. [2018] found that the floral scent of *R. cantleyi* was due to dimethyl disulfid and dimethyl trisulfide, responsible as chemical attractants to attract the carrion flies *Chrysomya chani* to visit the flower. This has filled the gap on pollination biology of *Rafflesia*, where *R. cantleyi* emits scent mimicking carrion and the ratio of chemical released (oligosulfides) play a key role in sex-biased pollinator specialization. Though the species is found in 4 states in Peninsular Malaysia its survival is still critical because outside RBSP the buds are collected by the Orang Asli and sold as a traditional medicine for post-partum. Hence, the species is greatly vulnerable to over-harvesting and threatened. In RBSP it is well-protected.

Figure. *R. azlanii* at Royal Belum State Park, Perak, Malaysia with 3 authors.

R. kerri Meijer: The only species discovered in the Malay Peninsula (which includes southern Thailand and Peninsular Malaysia); found in Perak, Kelantan and Pahang and named after A. F. G Kerr, a Scottish physician who also worked as botanist in Thailand. The first specimen was collected from Khao Pho Ta Luang Kaeo near Renong Province on February 3, 1929 [Nais, 2001]. In 1935, the species was discovered at Bukit Tepuh (Kelantan-Thailand border) and later the species was found in Gunung Stong State Park and Gunung Chamah, Kelantan, Peninsular Malaysia on February 12, 1992. It is easily distinguished from other species in Peninsular Malaysia by its numerous small white-pinkish warts scattered on the surface of the perigone lobes and large diameter of aperture [Wong et al., 2009].

R. su-meiae Wong, Nais & Gan: *Rafflesia lima-lidah* or *R. five-tongue* was discovered at the border of Kelantan and Perak, Peninsular Malaysia. The blooming female flower by chance was discovered by a group of hikers during their camping trip on August 2008. Wong and Gan [2002] separately had a follow-up visits on September, October, November and December 2008 to check on the species biology, population set up, and its habitat. *R. su-meiae* has been observed to resemble *R. kerri* from Kelantan by having the similar colour of the flower, big size, shape and numerous smallest white-pinkish warts scattered on perigone lobes. However, obvious 'tounge-like' appendages protruding from the rim of diaphragm differentiated the species, the large aperture allowing the inside structures to be viewed clearly and easily. The species was observed to have big size of flower where the opening of the blooming flower was reported to have 80-92 cm in diameter. It was also reported to have highest number of processes on the disc surface compared to other species reported from Peninsular Malaysia. The species was described as new in 2009 and named as *R. su-meiae*, after Cynthia Su-Mei Wong-Yau [Wong and Gan, 2003; Wong et al., 2009].

R. sharifah-hapsahiae Adam, Mohamed, Aizat-Juhari & Wan: It was discovered from Peninsular Malaysia by Jumaat Haji Adam and his research team [2013] and named after the VC of Universiti Kebangsaan Malaysia, Professor Tan Sri Dato' Seri Dr. Sharifah Hapsah Syed Hassan Shahabudin. The flower was found distributed in Mount Benom Forest Reserve, Ulu Dong, Raub, Pahang, on gentle hill slopes of after-logged primary lowland dipterocarp forest. It was found to be similar to *R. azlanii* and *R. hasseltii*, where perigone lobes were covered by rows of large coalesced white warts. However, through several floral characteristic observations, the species was found to differ from *R. azlanii* and *R. hasseltii* by the absence of marginal rings of white warts on the periphery of the window, the presence of high concentric rings of white warts on the window, the diaphragm has more high number of rings of circular dots, the number of processes is high, and high number of anthers. Formerly, this species had been named as *R. pahangensis* by the late Prof. Kamarudin Mat-Salleh, unfortunately the report was not published.

R. parvimaculata Sofiyanti, Mat-Salleh, Khairil, Zuhailah, Mohd. Ros & Burslem: This species was given the name to reflect the characters by having the numerous small warts on the lobes, where the term parvi refers to the small and maculata refers to the spots or warts. It has distinct characteristics from other species reported in Peninsular Malaysia (*R. azlanii* and *R. cantleyi*). The numerous small warts on perigone lobes and well-spaced arrangement of window distinguishes it from *R. azlanii*, coalesced and larger unit of warts. The characteristics of ramenta in this species are slender, densely arranged, unbranched structures, capitate and white in colour at top, differentiating it from *R. azlanii* and *R. cantleyi*. The species is distributed in a protected area, Lata Jarum Forest Reserve, Pahang [Sofiyanti et al., 2016].

R. tuanku-halimii Adam, Aizat-Juhari, Azilah & Wan: It was discovered in 2014 by the researchers led by Jumaat Haji Adam from Universiti Kebangsaan Malaysia and in 2016 the species was confirmed as the new record and named in honour of HRH the 14th Seri Paduka Baginda Yang Di-Pertuan Agong of Malaysia Almu'tasimu Billahi Muhibbuddin Tuanku Alhaj Sir Abdul Halim Mu'adzam Shah Ibni Almarhum Sultan Badlishah. The species was found to occur in Pahang (Raub District; Sungai Kenau, Sungai Yol and Matau) and Perak (Gerik District). It has the similar characteristics of *R. azlanii* and *R. sharifah-hapsahiae* but is different from *R. cantleyi, R. kerri* and *R. su-meiae*. The pattern of the window is almost covered with thick, closely spaced and almost united white rings, differentiating *R. tuanku-halimii* from *R. azlanii* and *R. sharifah-hapsahiae* [Adam et al., 2016].

R. tiomanensis Siti-Munirah, Salamah & Razelan: It was discovered by Razelan and his wife Salamah while exploring the forest area on Pulau Tioman in Malaysia in the area of Kg. Juara and reported to the first author (SM). The flower was found to have a unique combination of characteristics not matching any known species. Open flower diameter ca. 40-42 cm, perigone lobes sub-irregular, ca. 9-16 cm long, 13-21 cm wide, reddish, margins entirely to irregularly, wavy; upper surface covered with powdery white warts remarkably sparse, variously shaped; outer surface contains numerous white moles. The diaphragm is ca. 21-25 cm in diameter, rounded; upper surface glabrous, warts are absent; lower surface (windows) dark reddish and cover with sparse small rounded white warts; aperture ca. 10-14 cm diameter, irregular shape, variable lobe size, margin rim dark red band ca. 1 cm. The perigone tube is ca. 17 cm high; maroon-red cover with ramenta; upper ramenta dark simple, slender, thin, some with thick stalks, maroon-reddish, swollen white apex, unbranched, lower ramenta slender, thin, completely unbranched and fully maroon. The disk is 8 cm in diameter, flat with a rim's margin absent, not raised; disk fully visible through the aperture, pale yellowish darker at the margin. Its host is *Tetrastigma rafflesiae* and current distribution is Peninsular Malaysia, Pahang, Pulau Tioman (endemic) [Latiff, 2025].

Sumatran species. The first species described was the famous *Rafflesia arnoldii* from Bengkulu, Sumatera, Indonesia and boasted to be the largest, just over 1 m across the perigones [Ozturk and Secmen, 1991]. Currently, it is rare and hard to locate in its original locality; difficult to locate the flower in forests as the buds take many months to develop and the flower lasts for just a few days. As the remaining primary forests of Borneo and Sumatra disappear, it can be assumed that their numbers are dwindling, many are known to be nearing extinction. Some workers are developing ways to recreate the species' in an effort to stimulate the recovery but has proved unsuccessful so far, steps are also being taken to conserve the forests of Sumatera and Borneo. Other species in Sumatera are *Rafflesia bengkuluensis, R. gadutensis, R. hasseltii, R. micropylora, R. lawangensis, R. atjehensis, R. meijeri,* and *R. kemumu*.

Philippines species. Most species are found here, Meijer [1997] has revised it for Flora Malesiana and listed only 2 species R. *manillana* in Luzon and *R. schadenbergiana* in Mindanao. The number of species bursted as more explorations were conducted throughout the Philippines especially the isolated islands. Other species recognized currently are; *R. aurantia, R. baletei, R. leonardi, R. lobata, R. mira, R. philippensis, R. speciosa, R. verrucosa, R. mixta* and the latest is *R. consueloae* smallest whose diameter is ca. 9 cm across its perigones.

Javan species. Only 3 species are known to occur; *R. patma, R. zollingeri* and *R. rochussenii*.

Peninsular Thailand species. R. kerri is the only species discovered in the Malay Peninsula (which includes southern Thailand and Peninsular Malaysia). The first specimen of the species was collected from Khao Pho Ta Luang Kaeo near Renong Province on February 3, 1929 [Nais, 2001]. In 1935, the species was discovered at Bukit Tepuh (Kelantan-Thailand border) and later found in Gunung Stong State Park and Gunung Chamah, Kelantan, Peninsular Malaysia on February 12, 1992, it is easily distinguished from other species in Peninsular Malaysia by its numerous small white-pinkish warts scattered on the surface of the perigone lobes and large diameter of aperture [Wong et al., 2009].

Bornean species. *R. tuan-mudae* Beccari, named after the Tuan Muda of Sarawak, Mr. Carlo (Charles) Brooke. The early notes made by Odoardo Beccari in 1868, type collected from Mount Pueh, Semantan, Sarawak. The species was thought to be endemic to Sarawak and distributed in Mount Gading National Park, Mount Rara, Mount Penrissen but was later found distributed in Cagar Alam Gunung Raya Pasi, Singkawang, Pontianak and in Kalimantan [Nais, 2001]. A report on morphology of ovules, seeds and subprolate pollen grains [Sofiyanti and Yen, 2012]. The flower found to parasitize *T. rafflesiae* [Nais, 2001]. Wan Zakaria et al. [2016] have discovered a new host, *T. diepenhorstii*. Its distribution is mostly in Sarawak

(Mount Gading National Park, Mount Pueh, Sematan, Mount Rara, Mount Penrissen) and western Kalimantan, Indonesia.

R. tengku-adlinii Mat-Salleh & Latiff: Open flower diameter is 20.0-25.0 cm, perigone lobes 7.0-10 cm long and 12-16 cm wide, as for the lobe warts, no white warts occur, randomly distributed roundish orange warts. The diaphragm 12.5 cm wide, pentangular shape; processes 25, flattened, ramenta 3-5 mm long, very soft and dense, slightly pustulate, sometimes clavate, branched with somewhat swollen apices; window absent, lower diaphragm covered with ramenta, anther 20. Its known host is *Tetrastigma rafflesiae* and distribution is in Sabah (Trus Madi Range, Maliau Basin Conservation area).

R. pricei Meijer: It was discovered in Borneo and named after William Robert Price, a plant collector from Royal Botanic Garden, Kew; who found the species along the trail to Mamut Copper Mine at 1300 alt. It was later described by Willem Meijer [1984]. The early discovery of the species is believed not by Price because the specimen was reported to have been collected by Rev. Joseph and Mary Strong Clemens from the South-western part of Kinabalu on 17 March 1932. In 1966, another population with 125 buds was discovered by Bruce Weber and George Carson on the south-western slope of Mount Kinabalu, near Mamut and Poring. This species is also reported to occur in Bukit Retak, Brunei [Wong, 1997]. In order to protect the species from extinction, 2 sanctuaries have been established; *Rafflesia* Forest Reserve in Tambunan District and Poring-Mamut *Rafflesia* Sanctuary within Mamut Copper Mine, Ranau, Sabah. Many populations have been discovered within the area and also in Langanan Waterfall in Poring Hot Springs, Bukit Lugas, Bukit Tunturugung near Bundu Tuhan [Latiff, 2025], Ranau, Sabah. Besides, the species was also found in Sarawak, on Gunung Murud near Long Rapung, Kelabit Highlands [Wong, 1997]. An expedition in 2003 by Indonesian and Malaysian researchers found this species at Kayan Mentarang National Park, Kalimantan, Indonesia [Jayasilan et al., 2004]. The last update was by Lo et al. [2002] on the isolation of actinomycetes from the soil sample near the flower. One of the iconic species discovered in Sabah, Borneo, and it had been adopted as the logo of Flora Malesiana. Its known host is *Tetrastigma rafflesiae* and distributionis in Sabah, Sarawak and Brunei.

R. keithii Meijer: The species was named after Henry (Harry) George Keith, a former conservator of forest in Sabah. It is endemic to Borneo [Nais, 2001], found along the eastern slopes of Mt. Kinabalu, in Lohan Valley and Poring Hot Springs. Apart from being distributed within the protected areas, the species is also found in private lands. The studies on fruits and their consumers discovered *Callosciurus notatus* feeds on *R. keithii* fruit. The sticky flesh containing seeds possibly adhere to the consumer and thus get dispersed to other places [Emmons et al., 1991]. The findings also strengthen Meijer's [1985] suggestion, that squirrel as one of the possible seed dispersal agent. The conservation effort by Nais is a great success, as seed inoculation project of *R. keithii* seeds on *T. diepenhorstii* and *T. rafflesiae* gave positive results. The last research activity involving this species in Malaysia is on the isolation of actinomycetes from the soil sample near the flower by Lo et al. [2002]. It is the second largest known species whose diameter across the perigone is ca. 98 cm; known host is *Tetrastigma rafflesiae* and *T. dipenhorstii* and distribution is in Sabah, possibly also in Kalimantan, Indonesia.

R. hasseltii Suringar: It was discovered in 1877 by van Hasselt, Veth and Snelleman in Sumatera and later described by Suringar in 1879. It is found in West Sumatera, Jambi, Riau and Muara Labuh where the habitat is primary lower montane forest with altitude 400-500 a.s.l. Previously *R. hasseltii* was listed as one of the species found in Peninsular Malaysia along with *R. cantleyi* and *R. kerri* [Meijer, 1997]. However, it was mistakenly identified, in 2003 it was described as *R. azlanii* [Latiff and Wong, 2003]. From the floral morphological characteristics, *R. hasseltii* resembles *R. gadutensis* with slight differences in warts pattern. A survey by

Nais [2001] has re-confirmed *R. hasseltii* to occur also in Sarawak. Ahmad Puad et al. [2020] have eliminated the ambiguity of *R. hasselti* and announced the species as new record from Tanjung Datu National Park, Sarawak and western Kalimantan, Indonesia.

There are 5 unverified species from Borneo: Meijer [1997] claimed *R. arnoldii* occurs in Sarawak and Kalimantan, but Nais [2001] believed this is *R. tuan-mudae*. Smilarly *R. keithii* was clamined to occur on Hose Mountains in Sarawak but we believe it is also *R. tuan-mudae*. In the early 20th century 3 species were described from Kalimantan, namely *R. borneensis, R. ciliata,* and *R. witkampii* and until now they could not be confirmed due to lack of good specimens to identify. There is a species that has been photographed from banabas island, in southern part of South China Sea which is part of Indonesia. It appears to be similar to *R. cantleyi*, but yet to be verified [Latiff, 2025].

Challenges to studying Rafflesia. The plants grow entirely embedded within the body of the host plant that they parasitize [Kuijt, 1969]; it is rare in occurrence and can only be found in relatively remote lowland forests of Southeast Asia. Much of its habitat has been converted to farmland or timber concessions and in some parts of its range, the buds are harvested and sold for their purported medicinal qualities. Even once *Rafflesia* individuals become visible as flowers, these only survive a few days before decomposing; all of these factors make it difficult to even find *Rafflesia* sites and even when they are known, the sites are often not protected so there is no guarantee that they will exist in subsequent years.

The morphological characteristics have been used to differentiate the *Rafflesia* species, which include; i) open flower size, ii) warts on the perigone lobes, iii) pattern and size of diaphragm, iv) pattern of window, v) the size of aperture, vi) number of processes, vii) characters of ramenta, and viii) number of anthers [Adam et al., 2013; Susatya et al., 2017]. The flower has been regarded as the largest flower in the world [Nais, 2001]. *R. kerri* is the largest species in Peninsular Malaysia with the average diameter size 80-100 cm [Nasihah et al., 2016; Kedri et al., 2018; Norhazlini et al., 2020], whereas the size of *R. tengku-adlinii* ranges between 20-25 cm [Mat-Salleh and Latiff, 1989].

Adam et al. [2013] have used the pattern of warts to group *Rafflesia* in Peninsular Malaysia into the *R. kerri* group (lobes covered by minute, discrete warts pattern), *R. cantleyi* group (the lobes covered by rows of large discrete warts pattern) and *R. sharifah-hapsahiae* group (the lobes covered by coalesced warts); some species have the warts colour similar to the perigone lobes (*R. kerri, R. su-meiae, R. tengku-adlinii*), others like *R. parvimaculata* have numerous white warts covering perigone lobes [Sofiyanti et al., 2016], *R. pricei* has numerous elongated white warts [Meijer, 1984], and *R. hasseltii* has scarce and large white wart [Sofiyanti et al., 2007].

The structure, colour and arrangement of ramenta have been widely used by taxonomists to describe the species [Sofiyanti et al., 2016]. Susatya et al. [2017] has documented a consistent terminology to describe the structure of ramenta, which are; i) tuberculate, ii) filiform, iii) with swollen apex, iv) toadstool-like and v) fence-like and several variations within each type. The location of ramenta is also described as upper type, middle type and lower type. This classification has been proposed as a guideline/tool to re-evaluate previously described species and also in determining new species of *Rafflesia*. *R. parvimaculata* was differentiated from *R. azlanii* and *R. cantleyi* by having unbranched and white head colour of ramenta [Sofiyanti et al., 2016].

Molecular biology studies. As far as we know there is no study on its cytology, hence we don't know its diploid number, not its polyploidy possibility. Though there are many morphological studies there are no detailed ecological studies ever conducted to ascertain its role in the forest environment.

Despite having been discovered more than 2 centuries ago during an expedition by Sir Stamford Raffles in 1818 [Brown, 1821], *Rafflesia* remains an enigma to science. The mechanistic molecular level understanding of its biology that would be able to explain flower gigantism and the evolution of its parasitism still eludes us. There has been an increase in the number of studies on *Rafflesia* particularly at the molecular level in recent years. These include those that involved DNA sequencing of *Rafflesia* genes. However, today's complex research questions require a depth of information beyond the capacity of traditional DNA sequencing technologies. Next Generation Sequencing (NGS) has filled that gap and become an indispensable research tool to address the unanswered questions on the biology of *Rafflesia*. These functional genomic and transcriptomic studies on *Rafflesia* will provide new concepts into understanding the evolutionary novelty and heterotrophic ability of Rafflesia as a parasitic plant. In this paper, we review the literature published on various aspects of *Rafflesia* biology, including its taxonomy and phylogeny, development and host-parasite interaction of the important research gaps that need to be explored using high-throughput sequencing data.

Molecular approaches based on mitochondrial genome sequences can provide an effective species classification method. Several mitochondrial genes namely, cob, rp110, mttB and ccmB have been shown to display different orientation between *Rafflesia* species, while the nad1 gene sequence showed differences between the *Rafflesia* species studied [Latiff, 2025]. This indicates that mitochondrial gene sequences could be useful in the development of molecular markers for *Rafflesia* species classification. The molecular data could be expanded to scrutinize origins of different species of *Rafflesia* from different distribution locations, which can lead to a deeper understanding of the relationship between mutations in the sequence and the geographical diversity of the species.

Previous molecular studies have revealed further insights into the development of *Rafflesia*. Ramamoorthy et al. have successfully isolated and characterized the MADS-box gene, RcMADS1 from R. cantleyi [Latiff, 2025]. It was proposed that the RcMADS1 gene has an orthologous function associated with AGL24 that plays a role in flower meristem formation and flower blooming. Other molecular level fundamental studies include the transcriptome analysis of *Rafflesia* from the bud and flowering developmental stages that led to a better understanding of the genes involve during the *Rafflesia* flowering process [Lee et al., 2016]. A more recent study based on the comparative transcriptome analysis of three floral bud stages revealed that members of several transcription factor families were differentially expressed during flower development in *R. cantleyi* [Latiff, 2025]. The expression of genes involved in different phytohormone signal transduction events such as auxin transport, gibberellin biosynthesis and cytokinin were also found to be regulated during flower development. Moreover, the characterization of ARF and AUX/IAA gene families in *R. cantleyi* implies their importance in growth and development of the species, while analysis of the 14-3-3 gene family suggests its importance in vegetative growth [Latiff, 2025].

Interaction of Rafflesia with its host Plant. *Rafflesia* has been reported to parasitize a few species of *Tetrastigma, namely, T. curtisii* (Ridl.) Suesseng., *T. diepenhorstii* (Miq.) Latiff, *T. hookeri* (Lawson) Planch., *T. glabratum* Planch., *T. papillosum* (Blume) Planch. and *T. rafflesiae* (Miq.) Planch. [Meijer, 1997; Latiff, 2021; Nais, 2001, Nasihah et al., 2016]. The host specificity and disparity of distribution could be due to the evolution of *Rafflesia* [Nais, 2001]. Several studies on the genetic diversity of resistance or tolerance of host plants towards parasitic plants in agricultural systems have been previously conducted [Latiff, 2025]. The *Tetrastigma sequence* data offer essential information to derive genetic markers for species classification. Sequences, such as chloroplast and mitochondrial genes, can be developed as markers to differentiate *T. rafflesiae* from other *Tetrastigma* species. In addition, the DNA barcoding technique could be useful to study the ecological evolution and population of the vine host.

Rafflesia species are known to parasitize specific host plant of woody lianas of the species of *Tetrastigma* (*Vitaceae*, wild grapes plant) [Latiff, 1983; Nais, 2001; Chen et al., 2011]. According to Chen et al. [2011] *Tetrastigma* is distributed in Asia, ranging from India to China, across Southeast Asia, eastward towards Fiji and till subtropics Australia. The distribution of *Tetrastigma* species is wide and does not coincide with the distribution of *Rafflesia*, where *Rafflesia* could only be found in tropical rainforest of southeast Asian countries. Nais [2001] has reported seven *Tetrastigma* species parasitized by *Rafflesia* namely; *T. rafflesiae, T. diepenhorstii, T. curtisii, T. quadrangulum, T. scortechinii, T. glabratum* and *T. papillosum*. An update by Nasihah et al. [2016] mentions *T. hookeri* as new host of *R. kerri* from Lojing Highlands, Kelantan. We believe the possible hosts may be restricted to only 4 or 5 species, *T. rafflesiae* being the commonest for almost all species, *T. diepenhorstii* for *R. keithii* and *R. tuan-mudae, T. quadrangulum* for *R. kerri* in Peninsular Thailand, *T. hookeri* for *R. kerri* and possibly *T. harmandii* for the species in the Philippines. One of the authors (AL) would dismiss, *T. curtisii, T. scortechinii, T. glabratum* and *T. papillosum* as host as there is no concrete and reliable evidence to support these claims. Wan Zakaria et al. [2016] found that *R. tuan-mudae* not only parasitized *T. rafflesiae* but also *T. diepenhorstii*. The current and updated list of host plants parasitized by *Rafflesia* species in Malaysia are as follows: *T. diepenhorstii (R. tuan-mudae); T. rafflesiae (R. azlanii, R. cantleyi, R. keithii, R. kerri, R. parvimaculata, R. pricei, R. sharifah-hapsahiae, R. su-meiae, R. tengku-adlinii, R. tuan-mudae, R. tuanku-halimii); T. hookeri, T. quadrangulum (R. kerri); T. papillosum (R. pricei).*

Several studies have indicated that horizontal gene transfer (HGT) occurs from the host, *Tetrastigma* to the *Rafflesia* genomes [Barkman et al., 2004; Xi et al., 2012]. HGT is a process of intermolecular content exchange between two organisms to boost adaptation to the new environment [Latiff, 2025]. *Rafflesia* HGT involves an extensive collection of cellular functions including metabolism, respiration and protein turnover and expression levels comparable with vertical gene transfer (VGT) [Xi et al., 2012]. VGT in *Rafflesia* indicates host-like codon usage properties compared with their nearest relatives. However, the process of exchange of molecular content differs by species.

Rafflesia possesses the root-like haustorium organ, which serves as a structure to connect the parasitic plant body to the root or stem tissue of the host plant and makes a vascular connection and facilitates the transfer of nutrients and other molecules [Twyford, 2017]. One hypothesis suggests that the formation of a haustorium begins with the transfer of a set of genes from organisms that do not belong to any plant such as bacteria and fungi into the parasite genome [Latiff, 2025]. Another hypothesis suggests that the substrate required for the formation of the haustorium is derived directly from the photosynthetic plant where the original substrate is not involved in parasitism [Latiff, 2025].

Biochemical analysis of 2,6-dimethoxy-p-benzoquinonone (DMBQ), a haustorium-inducing component identified from the actual host roots, and its analogs, suggest that semiquinone intermediates formed during redox cycling between quinone and hydroquinone states could trigger haustorium development [Latiff, 2025]. Interestingly, DMBQ has been shown to induce haustorium formation in *Triphysaria* species, *Striga* species, *Agalinis* purpurea and *Phtheirospermum japonicum* [Latiff, 2025]. RNA-seq analysis has been useful in revealing the molecular mechanisms of processes unique to parasitic plants such as haustorium evolution and modification of interactions between plants [Latiff, 2025]. Further transcriptomics studies will reveal the gene regulatory network in host recognition between the species.

The "dual RNA-sequencing" approach has also been used to simultaneously monitor changes in gene expression of both host and parasite [Latiff, 2025]. The first successful application of this approach was to study the gene expression dynamics of the fungal pathogen, *Candida albicans* and the house mouse, Mus musculus [Latiff, 2025]. Subsequently, Latiff, [2025] utilized this approach in his studies on the filarial worm parasite, *Brugia malayi* and its mosquito host, *Aedes aegypti*; the protozoan parasite, *Toxoplasma gondii* and its mouse host, *Mus musculus*; and the Gram-positive bacterium, *Streptococcus gordonii* co-cultured with the fungus, *C. albicans*, respectively. In plants, it allows for the study of plant-pathogen interactions in herbaceous crops as well as trees [Latiff, 2025]. The genetic information from the dual-RNA data of the *Rafflesia* haustorium and its host tissue will be valuable in providing insights into the symbiotic relationship and interaction between *Rafflesia* and *Tetrastigma* at the molecular level.

Several other parasitic plants have been studied for their connection with the host plants. It was reported that plants of the genus *Cuscuta* gained organic and inorganic nutrients including water from the host plant through a haustorium [Latiff, 2025]. There are several factors that influence the parasitism such as the ratio of parasite biomass to the host, the number of parasites growing on a single host plant, the time taken for a complete parasite life cycle and the potential mutual evolution between the two species [Latiff, 2025]. However, a study involving *Pilostyle ingae* and its host, *Mimosa naguirei* showed that the parasite's dependence on its host did not affect the yield and quality of fruit and seed germination despite the smaller fruit size [Latiff, 2025]. Several studies were also focused on the production of effective protocols to prevent invasion of parasitic plants such as *Striga* and *Orobanche* that have led to a reduction in the agricultural production of corn, wheat and other staple crops in Africa.

The progress of NGS technologies has delivered a novel means to study host-parasite systems. We can now study the broad impact of interaction on the molecular environment apart from the behavior of a single gene under different conditions. Even though such approaches might not provide proof of function, they are able to focus subsequent functional studies onto promising targets that were previously unknown. Genomic studies conducted are to examine the interdependent genetic architectures of parasite virulence and the host resistance. Several signals can be looked for, for instance, expansions or reductions of certain gene families such as putative effectors of pathogens and associated targets in the host. Transcriptomic studies can also be aimed to illustrate the expressed fragment of the genome and how it is adopted within an organism. In addition, these studies will provide direct sequence information, quantitative expression levels and discover novel genes and splice variants [Latiff, 2025].

Potential immune roles of certain genes can also be explored using the data obtained [Latiff, 2025] stated that host immune response differs substantively with infection route of the pathogen. Further transcriptomic study also brings to light on the trans-generational priming and immune priming and specificity [Latiff, 2025]. It is possible to pool several datasets to investigate the ambiguous interactions within the same sample due to the decreasing cost of sequencing. A study by Foth et al., which focused on the vertebrate parasite from the whipworm genus *Trichuris*, revealed the important roles of the Chymotypsin A-like serine protease gene family in parasitism [Latiff, 2025]. Driven by hypotheses that functions such as those could be orthologous, such existing datasets can be used to mine *Rafflesia* datasets. Plants have complex defense mechanisms that can be condensed when pathogens or parasitic plants interfere with one of the various processes required for host defense. The wealth of data offered by these technologies is a challenge for researchers, but one with boundless potential for enlightening the field of host-parasite interaction in *Rafflesia* species.

Conservation and threats. *Rafflesia* was listed as rare plant species and vulnerable to the extinction in certain areas. The natural factors that contribute to its rarity are 1) imbalance sex ratio (2 male flowers to 1 female flower), 2) low percentage of bud reaching maturity, 3) short anthesis period, 4) random occurence of male and female flower blooming in the same area, 5) low percentage of pollination success, 6) long period taken after post-blooming to new flower formation and 6) insect infestation. The human factors have caused *Rafflesia* to the brink of extinction these are; habitat loss (due to deforestation, agriculture expansion area, development), collection by local communities for medicinal purposes and 3) uncontrolled tourist activities.

Malaysia is rich in tropical rainforests with a high biodiversity. The major threat to the flora and fauna loss and possible extinction is the habitat loss. The laws and acts are implemented in order to conserve, protect and manage the forest from human intrusion and exploitation. In 1994, Malaysia showed the commitment in conserving the biodiversity by becoming one of the countries which ratified the Convention on Biological Diversity (CBD) and produced the National Policy on Biological Diversity (NPBD) in 1998 and revised in 2005. In order to achieve the socio-economic development goals, Malaysia is still able to manage, protect and conserve its biodiversity through sustainable development. In the National Physical Plan (NPP) an Environmentally Sensitive Area (ESA) was proposed to protect the highland biodiversity from uncontrolled development and habitat loss. Through the National Forestry Policy 1978 and National Forestry Act 1984, the Forestry Department Peninsular Malaysia (FDPM) and the state Forestry Departments were entrusted to manage the sustainable utilization of forest and its products [Latiff, 2025].

In Sabah, the state has implemented the Forest Enactment 1968, classifying the forest into several classes under various categories of protection. In Sarawak, the Forest Department Sarawak is responsible in conserving the flora and fauna; establishing and maintaining the Totally Protected Areas (TPAs) - National Parks, Nature Reserves, Wildlife Sanctuaries and Permanent Forest Estates (PFEs); conduct management and research activities on nature conservation and wildlife; and issue permits and licenses for the activities in the forest. The state governments of Sabah and Sarawak are responsible in managing the cases in the forest due to their nearness to the source of forest problems and in better position to control the issues. Whereas the interstates forest issues require the federal and state government actions. In 2010, Malaysia has recorded to have 14.5 million hectares of PRF/PRE and committed to maintain the figures from decreasing. The establishment of Permanent Reserved Forest (PRF)/Permanent Reserved Estates (PRE) is able to protect the biodiversity through *in-situ*. The High Conservation Value Forests (HCVFs) purportedly to protect the forest biodiversity, ecosystem and species from encroachment activities. An effort taken by the research institutes, non-government organization (NGOs) and state level biodiversity centres, by documented the findings is very important in proposing the area as protected areas [Latiff, 2025].

Besides, ecotourism areas need a proper planning in maintaining from degradation. Several policies, laws and acts are needed to be implemented in order to; i) ensure ecotourism sites are able to provide services with good management, ii) ensure the ecotourism resources are totally protected, iii) protect the site's integrity as a national ecotourism site in the long run, iv) provide ample buffers zone to the adjacent nonforested area, v) provide alternatives within the surrounding areas such as nature experience zones and adventure park, vi) to accomodate wildlife corridors and potential flora and fauna connectivities and vii) provide connectivity to other symbiotically important ecosytems. A sustainable site plan is required for ecotourism destinations to reduce the environmental impact, where collaboration from landscape architects, engineers, environmental experts, botanists, biologists, researchers, and local community stakeholders such as Orang Asli (Indigenous people) and land owners, able to create a good input in sustainable site plan. An effort taken by the Tropical Rainforest Conservation Research Centre, an NGOs body to restore the ecosystem in *Rafflesia* conservation Area by replanting the host plant species so that *Rafflesia* could thrive and survive. An education on conservation programme should be widen enough to reach all level of citizens. As an example; R. parvimaculata was found distributed in the Forest Reserve area. Therefore, the Forestry Department has to take an approach to conserve the species by managing with the cooperation of communities in order to create an awareness and educate the communities the importance to protect this Mother Nature.

Future directions. Despite the rapid progress made within the past decade on understanding the biology of *Rafflesia*, many questions remain unanswered, and many aspects are still unexplored. DNA sequencing was introduced to study genetic variation between *Rafflesia* species in the early 2000s. NGS technologies and bioinformatics analyses further revealed the molecular aspects of taxonomy and phylogeny, developmental biology, horizontal gene transfer, flower development and senescence in Rafflesia.

The main challenge on studying *Rafflesia* is the difficulty in sampling the species in their habitat in the wild. The different developmental stages of *Rafflesia* flowers are extremely difficult to find especially due to the short blooming period. In addition, field samplings conducted suggest that *Rafflesia* buds have a high mortality rate due to lack of resources as well as attacks from herbivores, pathogens and humans' activities. These observations suggest that the formation of *Rafflesia* flowers should occur at the right time as well as in a conducive environment for ensuring the success of the species life cycle. *Rafflesia* is considered one of the most endangered plant species due to their limited distribution, specific host plant, large sex imbalance and increased threat by rapid habitat lost due to tropical rain forest degradation.

More extensive experiments can be conducted in the coming years to focus on the analysis of genomes and transcriptomes of different *Rafflesia* species over several generations. This means that unique mutations and the modifications in gene expression can be studied in greater detail, while the molecular coevolutionary processes will be observable as they occur. Knowledge gained from this wealth of data could highlight the complex interaction between Rafflesia and its host, that in turn will be crucial to preserve the diversity and population of this enigmatic plant. Information about the habitat preferences, host specificity and reproductive biology of the species will be helpful in biodiversity and conservation by revealing the environmental conditions that the populations require to survive.

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Rafflesiya - dünyanın ən böyük çiçəyi: Yüzillik yubiley

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Rafflesia cinsi çiçək morfologiyası və filogenetikası baxımından həm simvolik, həm də müəmmalıdır. Cinsə Sumatra və Filippində yayılmış 39-dan çox növ daxildir. Növün morfologiyası və sahib-parazit əlaqələri kifayət qədər yaxşı məlum olsa da, təkamül və molekulyar biologiyası müəmmalı olaraq qalır və qorunma səyləri qeyri-müəyyəndir. Bu, nəhəng ölçüsü, bənzərsiz xüsusiyyətləri, lakin botanika aləmini heyran edən xoşagəlməz qoxusu olan sirli bir çiçəkdir. Cins yalnız Cənub-Şərqi Asiyanın və Malayziyanın tropik meşələrində rast gəlinir. Malayziyadan cəmi 13 növ qeydə alınıb: 8-i Malayziya yarımadasından, 5-i Sabah və Saravakdan. Digər parazit bitkilərdən fərqli olaraq, parazit çiçək kimi tanınsa da, *Rafflesia* qanunlar və aktlarla qorunub saxlanılır və mühafizə olunur, hətta tropik meşələri məhv olmaqdan xilas etmək üçün flaqman növ kimi və bitki dünyasında simvol kimi istifadə olunur.

Açar sözlər: *Rafflesiya*, parazit çiçək, Cənub-Şərqi Asiya, tropik meşələr

Раффлезия — самый большой цветок в мире: Столетний юбилей

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Род *Rafflesia* является одновременно культовым и загадочным с точки зрения его флористической морфологии и филогенетики. Существует более 39 видов, в основном сосредоточенных на Суматре и Филиппинах. Хотя морфология, отношения хозяин-паразит у данного вида довольно хорошо известны, эволюция и молекулярная биология остаются загадочными, а усилия по сохранению неопределенны. Это загадочный цветок с гигантским размером, уникальными особенностями, но неприятным запахом, который очаровал ботанический мир. Род распространен только в тропических лесах Юго-Восточной Азии и Малайзии. Всего было зарегистрировано 13 видов из Малайзии: 8 с полуостровной Малайзии и 5 из Сабаха и Саравака. В отличие от других паразитических растений, хотя и признан паразитическим цветком, *Rafflesia* была сохранена и защищена законами и актами, даже использовалась в качестве флагманского вида для сохранения тропических лесов от уничтожения и как символ в растительном мире.

Ключевые слова: Раффлезия, паразитический цветок, Юго-Восточная Азия, тропические леса