



## TARO LEAF BLIGHT: THREAT TO TARO (*Colocasia esculenta* L. Schott) PRODUCTION

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### Abstract

Taro (*Colocasia esculenta*) is the third most important root and tuber after cassava and yam cultivated in sub-Saharan Africa, but its global yield is severely threatened by the disease- Taro Leaf Blight (TLB). The disease is associated with the oomycete *P.colocasiae* which attacks every part of the plant, especially when it is a susceptible variety. More than 80% of taro losses are due to the impact of TLB and it accounts for why many growers neglect the crop, resulting in major changes in dietary patterns and cropping systems in affected areas. Lack of funding geared toward taro research is also a major contributing factor to the crops neglect. A better understanding of *P.colocasiae* isolate in affected region, better informs disease management strategies, which over the years have included the use of resistant cultivars, chemical and biological controls, and cultural practices. The literature reviewed to describe TLB as a grave threat to taro production was retrieved from computerized databases. This paper provides an overview of the disease origin, epidemiology, and impact on cultivation, and highlights opportunities new offer of biotechnologies to reduce losses of this neglected tropical food crop. For many, this ancient crop is of cultural significance and addressing the TLB scourge is of the utmost importance.

**Keywords:** *P.colocasiae*, disease management, genomics and biotechnology

### Introduction

*Colocasia esculenta* (L.) Schott, popularly referred to as Taro, is an ancient edible aroid that serves as a source of food and income for millions of limited resourced farmers. It is a monocotyledon that belongs to the Araceae family, largely cultivated in humid regions of the tropics and subtropics, and is of great cultural importance in many taro growing regions (Power et al., 2019). Almost all parts of the crop, including its corms, cormels, leaves and petioles, can be utilized. The corms and cormels are important sources of carbohydrates and soluble starch, while its leaves and petioles contain nutritive and non-nutritive compounds that can be exploited for medicinal purposes, making taro a candidate crop for functional food development (Gupta et al., 2019). In terms of importance, taro is ranked third among root and tuber crops cultivated in sub-Saharan Africa, after yam and cassava (Onyeka, 2014). According to the FAOSTAT database, global taro yields have been declining for many years (Figure 1) and a plethora of diseases are some of the major reasons for its decline and neglect. Several viruses such as *Dasheen mosaic virus*, *Taro bacilliform virus*, *Colocasia bobone disease virus*, and *Taro vein chlorosis virus* have been implicated as diseases that cause significant damage in taro cultivation (Yusop et al., 2019). Except for the

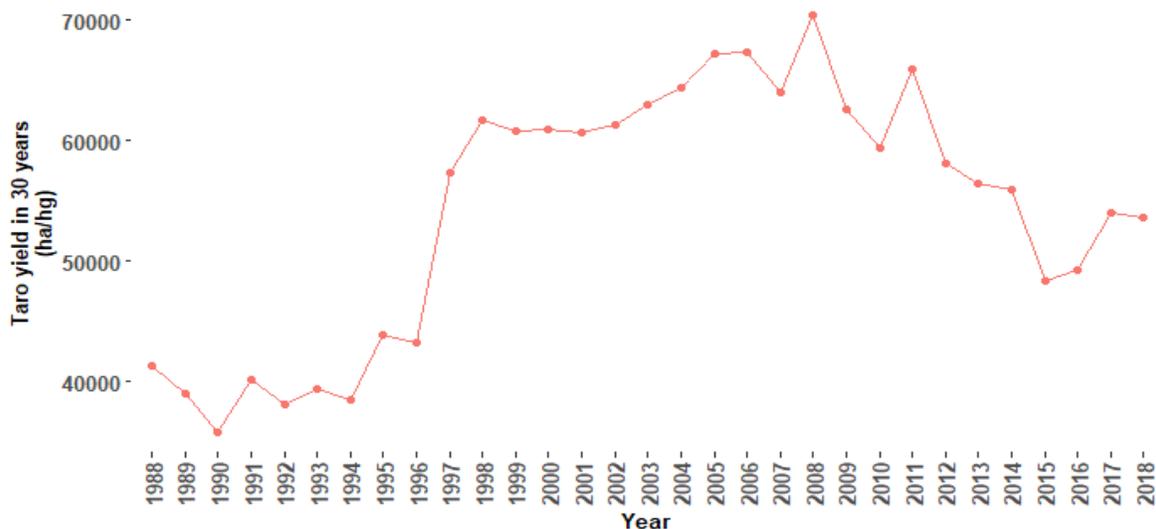
Dasheen mosaic virus disease, most viral diseases of taro do not have a global distribution and do not affect other aroids (Table 1). Taro Leaf Blight (TLB), caused by the oomycete, *Phytophthora colocasiae*, has been described to have had the most devastating effect on global taro yields (Lebot, 2009). The pathogen attacks the leaves, petioles and corms, and in the absence of a host, its survival can range from less than 21 days to more than three months in several forms such as mycelia, zoospore cysts, sporangia, chlamydospores or oospores (Otieno, 2020; Quitugua and Trujillo, 1998). The disease spreads rapidly when conditions are favourable and when left unmitigated, farmers are faced with considerable field and postharvest losses. In this review, we discuss TLB aetiology, epidemiology, impact and efforts to mitigate its spread. With advancements in molecular technologies, we highlight possibilities for improvement, where conventional methods have failed.

### Methodology

A systematic search was conducted with the terms: “taro leaf blight”, “*Phytophthora colocasiae* diversity”, “taro genomics”, “molecular detection of taro leaf blight” and “genetic improvement in root and tuber crops” on the following computerized databases: Google scholar and

NCBI-PubMed. The search was restricted from between 2010 to 2020 to ensure a contemporary exploration of the impact of TLB on taro production, molecular tools

for TLB detection and genomic research geared towards improving resistance in taro. A few older papers were included to discuss the origins and epidemiology of the



**Figure 1: Global taro yield trend from 1988-2018 (FAO, 2018)**

#### TLB symptoms and mode of transmission

TLB mostly attacks taro but there have been reported cases of attacks with lesser symptom severity and yield losses, on *Alocasia macrorrhizos*, a common aroid in the pacific region. Symptoms of the disease begin with the appearance of water-soaked lesions on leaves that rapidly expand to form large brown spots, sometimes with yellow margins (Figure 2). The disease causes leaves defoliation, resulting in limited photosynthesis and ultimately leads to the death of the crop. In post-harvest attacks, the corms quality greatly deteriorates forming firm brown rot and decay (Paiki, 1996). In susceptible varieties, the petioles are also attacked

forming brown spots that soften and fall off under the weight of its leaves. Studies have shown that the transmission of TLB occurs rapidly at night or during the day when weather conditions are very wet and humid, thus conducive for the pathogen to thrive (Misra et al., 2008). It has been observed that 3 - 4 days after the first signs of infection, whole-leaf areas are lost and in weeks whole taro fields appear blighted under favourable disease conditions. Taro is a vegetatively propagated crop and TLB is often spread through the use of planting materials infected with *P.colocasiae* sporangia and zoospores.

**Table 1: Distribution of fungal and viral diseases affecting aroids**

Pathogen	Aroid	Africa	America	Asia-Pacific
<b>Fungi/fungi-like</b>				
<i>Phytophthora colocasiae</i>	Taro	X	X	X
<i>Pythium myriotylum</i>	Taro and cocoyam*	X	X	X
<b>Virus</b>				
<i>Dasheen mosaic virus</i>	All	X	X	X
<i>Colocasia bobone disease virus</i>	Taro			Papua New Guinea and Solomon Island
<i>Taro bacilliform virus</i>	Taro			Pacific only
<i>Taro vein chlorosis virus</i>	Taro			Pacific only

\**Xanthosoma* spp

#### TLB distribution and impact

*P. colocasiae* and the leaf blight symptoms were first described in 1900 on Java, an island in Indonesian (Raciborski, 1900), and believed to have originated from South-East Asia and some evidence of that was shown by the co-existence of two mating types of *P.colocasiae*, isolated from Hian Island in China (Zhang et al., 1994).

According to Trujillo (1967), TLB was brought into the South Pacific via the Philippines and Taiwan. The disease has been implicated in the decimation of taro cultivation in Guam, Hawaii, Samoa, Papua New Guinea, Solomon Islands, Taiwan, India, Ethiopia, Equatorial Guinea, Cameroon, Nigeria and Ghana (Mbong et al., 2013; Onyeka, 2014; Omame et al., 2012;

Bandyopadhyay et al., 2011). In these countries, corm yield losses ranged from 50% to 100% and in many cases growers lost up to 97% of their preferred varieties —(Singh et al., 2012). According to Alexandra *et al.* (2020), the devastation caused by Cyclone Val of 1991,

led to the planting of thousands of taro propagules within weeks on the Samoa Island. This was an effort to save the \$12 million taro production and export industry at the time.



**Figure 2: TLB symptoms on the affected host. Clockwise from bottom: wet soaked lesion spreads to form brown spots at the margin and inside the leaf blade. The spots enlarge, forming blights. Attacked corms show a brown firm rots at its top. (culled from Pacific Pests and Pathogen - facts sheet)**

By 1993, *P.colocasiae* was detected on the southern windward side of the island. With the winds and intense rainfall, the pathogen spread rapidly and so did the decimation. Only 3% of the country's national taro varieties survived and by 1994 an estimated 92% drop in production was recorded (Hunter et al., 1998). Economic losses of about \$22 million were estimated from 1994 to 2010. In West and Central Africa, a conservative estimate of over \$1.4 million was reported to be lost annually due to the effect of TLB (Onyeka, 2014). Taro growing areas, where these devastations have occurred, has mostly led to the crops abandonment, with significant changes in dietary patterns and cropping systems. Studies have also shown that the crops narrow genetic diversity and the use of infected planting materials exacerbates the spread of the disease in these regions.

#### ***P.colocasiae* genetic variability and diagnosis**

Nath *et al.* (2015) stated that to better develop mitigating strategies against the spread of TLB, an understanding of the phenotypic and genotypic variations in pathogen populations is required. Compared to other species of *Phytophthora*, information on the genetic diversity of *P.colocasiae* is limited. Over the years, several phenotypic and molecular characterizations have been used to determine variability among *P.colocasiae* isolates from different taro growing regions. The population structure among *P.colocasiae* isolates from five countries in South-east Asia and Oceania were determined using isozymes and Random amplified polymorphic DNA (RAPD) —(Lebot et al., 2003). The study revealed significant variations among the isolates between and within countries. The same markers were

used by Mishra *et al.* (2010) to determine variations among 14 isolates sampled from different regions within India, with significant variations observed among isolates sampled in the same region. In tandem with pathogenicity, mating types and morphological characteristics, other molecular markers have been used to study the genetic diversity among *P.colocasiae* isolates from within India (Nath et al., 2012; Nath et al., 2013; Nath et al., 2015; Nath et al., 2016) and Ghana (Adomakoa et al., 2019). A major take away from all of these studies was that there was no correlation between the geographical origins and genetics and morphological characteristics of the oomycetes. Therefore, this was suggested to be due to the frequent movement of the pathogen within the study areas. This lack of correlation was also confirmed recently, using Single Nucleotide Polymorphism markers (Shrestha et al., 2014) among isolates from Vietnam, Hawaii and China. *P.colocasiae* is heterothallic and requires opposing mating types to sexually reproduce oospores with wider genetic diversity. But the occurrence of opposing mating types on the same host is a rarity. Asexually reproduced sporangia are more common and the hyper-variability revealed at a molecular level, within populations, has been attributed to mutations. Molecular diagnostic tools have also been developed for the early detection of TLB, i.e. before the appearance of symptoms (Nath et al., 2014) and this in addition to the genetic diversity informs strategies to better manage the disease.

#### **TLB disease management**

Disease management strategies used to mitigate the spread of TLB includes: cultural practices, the use of

biological (Tchameni et al., 2017) and the less cost-effective chemical controls. Protectants like Mancozeb and copper, and fungicides like Metalaxy and phosphoric acid, are some commonly recommended chemical controls (Cox and Kasimani, 1988; Omane et al., 2020). Unfortunately, results from the use of chemical controls vary and the effectiveness is dependent on weather conditions and the severity of the disease —(Singh et al., 2012). Currently, the use of resistant taro cultivars offers the most sustainable mitigating strategy against the spread of the disease. Studies have shown that the infected area increases slower in resistant cultivars than in susceptible ones (Misra et al., 2008). The target of many taro breeding programs is developing TLB resistant cultivars, and introgression has been carried out with conventional breeding methods with some success. Taro breeding is fraught with several physiological constraints including irregular flowering and a narrow genetic base with little to no TLB resistant cultivars (Obidiegwu et al., 2016). These constraints have contributed to making taro breeding a daunting task. Many international and regional taro programs have developed germplasm exchanges, to widen the genetic diversity of their taro cultivars. These programs have also developed and promoted the use of modern technologies for the conservation and distribution of resistant, pathogen-free planting materials (Alexandra et al., 2020).

#### Taro genomics and future perspectives

Singh *et al.* (2012) noted that, compared to other taro growing regions in the world, documentation of the impact of TLB prevalence has mostly been restricted to the Pacific region. Some other researchers have also noted that the consequences of TLB prevalence in Africa are under-researched. These highlight a major problem, which is a lack of funding for taro research in developing countries where taro cultivation is important for daily sustenance and income. Due to the effect of unmitigated TLB spread, yield losses of up to 80% have been reported in susceptible varieties, especially when conditions are conducive. Genetic improvement through conventional breeding in taro is time-consuming and efforts to implement genomic research into breeding for TLB resistant cultivars (Sharma et al., 2008) are limited. Genomic resources of *P. colocasiae* and *C. esculenta* are required to develop better mitigation strategies against the spread of TLB. Recently, Bellinger *et al.* (2020) developed a *de novo* taro genome assembly and coupled with a genetic linkage map, generated from genotyping by sequencing data, identified markers associated with TLB resistance. With recent advancements and reducing cost of sequencing technologies, taro genomic research will enable opportunities for developing TLB resistant cultivars through molecular breeding (genomic selection or marker assisted selection) to enhance natural resistance, identification of resistance genes, exploiting functional genomics that allows the understanding of host-pathogen interactions and genetically engineering resistance. Engineering resistance through genetic transformation using

*Agrobacterium*-mediated protocols produced transgenic lines with rice chitinase and wheat oxalate oxidase. These genes induced resistance to the oomycetes *Sclerotium rolfsii* and *P.colocasiae* (He *et al.*, 2015) in taro. Genome editing technologies, such as clustered regularly interspaced short palindromic repeats –Cas9 (CRISPR - associated protein 9) system, have shown promise for genetic improvement of crops. Implementing CRISPR can eliminate the inefficiencies observed in classical transformation systems. In addition to developing resistance, conservation of these materials is also important. While conducting germplasm exchanges, it is imperative to safeguard resistant cultivars by implementing the use of biotechnology tools such as, tissue culture and molecular diagnostics, in these exchanges. This conserves pathogen-free planting materials for breeding programs and distribution to farmers, thus combating the spread of the disease early, and ensuring taro food security potentials and as a candidate for functional food development.

#### Conclusion

The threat to taro as a food security crop remains, due to the global prevalence of TLB. Compounding this is lack of funding geared towards taro research, especially in sub-Saharan Africa. There needs to be concerted effort by farmers, researchers and policy-makers in addressing declining taro production and the role climate change can play in exacerbating the spread of TLB. Though, limited, molecular and genomic technologies have been exploited to better understand the pathogen origins, diversity and host-pathogen interactions. Implementing new biotechnologies into taro breeding programs and germplasm exchanges are encouraged because they can improve the development and conservation of resistant cultivars.

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