ISOLATION, IDENTIFICATION AND CHARACTERIZATION OF *CLEOME GYNANDRA* L. BACTERIAL SEED ENDOPHYTES FROM NORTHERN NAMIBIA

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ABSTRACT

Endophytic microorganisms are symbionts found inside host tissue without eliciting disease, symptoms or causing any damage. They play an integral role in spermatophyte life cycles and are endowed with multi-functional traits that promote the host's health, growth and yield. Cleome gynandra L. (C. gynandra), is an unexplored "orphan" plant that has a diverse array of such endophytic microbial populations. C. gynandra (Ombidi in Oshiwambo; Ombowa in Herero; Gomabeb in Damara/Nama) is a neglected droughttolerant wild annual crop spread in semi-arid regions of Northern Namibia. This plant has shown great potential in agronomy, climate adaptation, economy and traditional medicine, making it stand out as a prominent contender among climate-adapted future crops. Little, however, is known about C. gynandra plant growth promoting (PGP) seed endophytes. The study aimed to isolate and identify endophytic bacteria associated with C. gynandra spermatophyte and characterize their functional plant growth promoting potential which could be used to improve plant growth and yield. Twenty morphologically distinct isolates were assessed. They exhibited various abilities to produce growth regulators that contribute to ammonia production (85%), atmospheric nitrogen fixation (40%), fluorescence production (10%), hydrogen cyanide production (30%), indole acetic acid (IAA) production (100%), phosphate solubilization (15%) and siderophore production (80%). Phylogenetic analysis showed that all the isolates (excluding *Phytobacter ursingii*) belonged to the *Proteobacteria* phylum. The application of endophytic plant growth promoting bacteria (PGPB) is considered to have the potential for improving plant growth in extreme environments. Three best PGP producing isolates, namely Enterobacter cloacae, Klebsiella pneumoniae and Kluyvera cryocrescens were selected for greenhouse trials using Brassica napus L. (Rape English Giant) seeds. In comparison to the control groups, there was a statistically significant difference for root length (p=0.024), plant height (p=0.037) wet (p=0.000) and dry (p=0.000) mass in the microbial experimental group. This indicated that the microbe treatments had an effect on growth parameters. From this study, it is concluded that C. gynandra seeds harbour a reservoir of endophytic bacteria with the ability to improve plant growth and with the potential for use as inoculants (biofertilizers) to establish sustainable crop production systems.

Keywords: agriculture, *C. gynandra*, endophytes, plant growth-promoting, seed bacteria, seed inoculants.

List of Publications

The work, or parts thereof, presented in this thesis have been published as part of the citations below:

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Shipoh, **P.M.**, Chimwamurombe, P.M. and J.D Uzabakiriho (2020). *Cleome gynandra* L. Seed Endophytes Induce Rape (*Brassica napus* L.) Seedling Germination Rate and Promote Rape Plant Growth and Leaf Yield. Paper in preparation of journal submission.

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Dedication

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Declaration

I, Panduleni Mwahepekange Shipoh, hereby declare that this study is a true reflection

of my research, and that this work, or part thereof has not been submitted for a degree at

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CHAPTER 1: INTRODUCTION

1.1 Background of the study

Agriculture plays a vital role in most low income and middle-income countries where most households depend on smallholder agriculture for their livelihoods (Ng'etich, Aguyoh and Ogweno, 2012; Singh, 2013). As of 2018, 19.71% of the Namibian population were employed in the agriculture sector which contributed 974.80 USD Million to the GDP in the fourth quarter of 2018 (National Planning Commission, 2018). Modern agricultural systems have been focusing on a very limited number of high-input and high-yielding crop species for food production throughout the world (Chivenge *et al.*, 2015). With the advent of climate change, coupled with the rapid increase in population and urbanization, it has been predicted that the survival of these systems in the 21st century will face daunting challenges (Masuka, Goss and Mazarura, 2012; Mabhaudhi *et al.*, 2017).

The agriculture sector should undergo imperative metamorphosis to reduce the environmental impacts while increasing productivity and lead to better livelihoods and poverty reduction (Padulosi, Thompson and Rudebjer, 2013; Wangolo *et al.*, 2015). The development of resilient crops that can yield under uncertain and extreme climatic and poor soil growing conditions would significantly play a prominent role in mitigating these problems. Diversifying production and consumption habits to include underutilized crops can influence and contribute to improved nutrition and household food security, and elevate relegated indigenous crops to the status of neglected and underutilized crop species (Chivenge *et al.*, 2015; Mabhaudhi *et al.*, 2017). African indigenous crops can play a pivotal role in this endeavour (Ng'etich, Aguyoh and Ogweno, 2012). These species of plant are known to better withstand adverse weather conditions via increased hardiness

and reduced external inputs compared to the cultivated crops (Masuka, Goss and Mazarura, 2012). The production of African indigenous vegetables has been constrained by limited information on fertilization requirements coupled with inadequate scientific knowledge (Cruz-Garcia and Price, 2012; Ng'etich, Aguyoh and Ogweno, 2012; Gido, Bett and Bokelmann, 2016).

Some African indigenous leaf vegetables, which are also categorized as "orphan crops" are adapted to local environments in which they are grown and play an integral role in African agricultural and food systems (Adebooye and Opabode, 2004; Chivenge *et al.*, 2015). They are also known to have adequate amounts of essential dietary micronutrients and being a valuable source of nutrition in rural communities (Gido, Bett and Bokelmann, 2016). Available information on African leafy vegetables is limited, making commercialization, crop development and sustainable conservation difficult (Agbo *et al.*, 2009; Masuka, Goss and Mazarura, 2012).

During the past decade, microorganisms have garnered importance in sustainable agriculture due to the benefits they have on soil and crop productivity (Ramakrishna, Yadav and Li, 2019). Endophytes are microorganisms that dwell inside plants without causing any harm (Schulz and Boyle, 2006; Truyens *et al.*, 2014). For many decades, endophytes have been known for their growth benefits and health promotion (Ryan *et al.*, 2008; Reinhold-Hurek and Hurek, 2011). They are ubiquitous to the majority of plant tissue. Seed endophytes are of particular interest as they are vertically transmitted between plant generations through seedlings (Barea, 2015; Abbamondi *et al.*, 2016; Shahzad *et al.*, 2018). However, seed-borne endophytic microbes have not been fully explored yet (Shahzad *et al.*, 2018). They are potential producers of various phytohormones that can improve biomass, yield and stress mitigation, and are easily

selected by plants for mutually beneficial interactions because they are naturally occurring (Rosenblueth and Martínez-romero, 2006; Ryan et al., 2008; Maheswari, Anbukkarasi and Hemalatha, 2014; Shahzad et al., 2018). While previous studies (Shilla et al., 2019) have centred around Cleome gynandra L. (Cat's Whisker) origin, morphology and taxonomy, none have focused on their seed endophytes nature. There are currently no structured agricultural practices that can effectively lead to their sustainable harvesting (Masuka, Goss and Mazarura, 2012; Onyango, Onwonga and Kimenju, 2016). The use of plant growth promoting endophytes as seed inoculants have shown promising prospects to increase crop yield, through the plants' mechanisms and in the most environmentally friendly manner as possible (Golding, 2012; O'Callaghan, 2016). The diversity of C. gynandra seed endophytes and their potential for agricultural practices in Namibia has not been explored. This study aimed to isolate endophytic bacteria from Cleome gynandra seeds and explore their potential and use in the Namibian agriculture landscape. To our knowledge, this study is the first report on the diversity of culturable endophytic seed bacteria associated with Cleome gynandra growing in Namibia. The outcome of this study will form the basis of knowledge on these endophytic seed bacteria and how they can be selected for utilization of plant growth promotion.

1.2 Statement of the problem

C. gynandra forms a substantial part of the diets of the Aawambo community in various parts of the country (Kolberg, 2001; Omondi et al., 2017). It has great nutritional (high levels of calcium, iron, magnesium and zinc), economic and agricultural potential (Omondi et al., 2017). Despite these exciting traits, very little attention has been given to it because it is a neglected and underutilized crop (Padulosi, Thompson and Rudebjer,

2013). There are currently no sustainable agronomic systems in place that can be used to successfully harvest and domesticate *C. gynandra* (Masuka, Goss and Mazarura, 2012) in Namibia. Research has shown that seed plant growth promoting endophytes have been linked to plant growth and yield (Chaturvedi, Singh and Gupta, 2016). This study aimed to determine whether or not *C. gynandra* seeds harbour endophytic bacteria that could contribute to its's growth and yield, which can potentially be used as a bio-inoculant on domesticated crops and increase their horticultural potential.

1.3 Objectives of the study

The specific objectives of this study were to:

- (i) isolate, identify and characterize putative PGP *C. gynandra* seed endophytes from 4 geographical locations;
- (ii) determine the phylogenetic classification of *C. gynandra* seed endophytes;
- (iii) determine the effect of PGP isolates from *C. gynandra* on germination rates, plant growth and yield of *Brassica napus* (Rape English Giant) crops.

1.4 Significance of the study

C. gynandra endophytes stand out as a prominent contender for climate-adaptive agriculture. The outcome of this study will provide a greater understanding of its seed endophyte bacterial population. This knowledge might improve its sustainable agricultural production in Namibia, with potential benefits of providing an alternative source of income for local communities and in turn, providing affordable agricultural practices to local farmers that will contribute to the countries growing population.

1.5 Limitations of the study

Since a culture-dependent method was used, it is possible that available endophytes were not all isolated as not all strains could be cultured. This could have reduced the chance of genetic diversity among the isolates identified.

1.6 Delimitation of the study

The study was conducted within the boundaries of the Omusati, Oshana, Ohangwena and Oshikoto regions. Regions have artificial lines as boundaries between them, inevitably meaning that they share features such as soil composition and have identical physical conditions (Mendelsohn, 2007). This indicates that more diverse variations of the seed endophytes might not be found.

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CHAPTER 2: LITERATURE REVIEW

2.1 Introduction

Indigenous vegetables and endophytic bacteria have become a new focus in modern agriculture (Adebooye and Opabode, 2004; Bhattacharyya and Jha, 2012). Previous and current literature have reviewed the potential production of indigenous crops and the use of endophytic bacteria as biofertilizers (Hynes *et al.*, 2008; Agbo *et al.*, 2009; Gido, Bett and Bokelmann, 2016; Timmusk *et al.*, 2017; Kalayu, 2019). This review chapter will focus on the following themes: background of *Cleome gynandra*, seed endophytic bacteria interactions and importance, plant growth promoting endophytes modes of action and potential of endophytic bacteria as biofertilizers. Furthermore, this chapter will focus on the application of seed endophytic bacteria and its application to Namibian agriculture.

2.2 Cleome gynandra L. (C. gynandra)

Ombidi (in Oshikwanyama and Oshimbadja); ombivi (in Oshimbalanhu); omboga (in all other Oshiwambo language dialects); ombowayozondu, ombowa, ombowayozongombe (in Herero language), gomabeb (in Damara/Nama language); Cat's whisker, spider plant (English) (Kolberg, 2001; P.T Shipoh 2018, pers. comm., 12 December).

Cleome gynandra L. (**Figure 2.1**), synonym Gynandropsis gynandra (L.) Briq., is a wild annual leafy vegetable spread around Namibia (Kolberg, 2001). It is dominant in the northern Namibian regions (**Figure 2.2**) of Omusati, Oshana, Ohangwena and Oshikoto, which hosts 40% of the Namibian population (Starkey *et al.*, 2017), though, it is not restricted to these areas only (Kolberg, 2001). It belongs to the *Capparaceae* family (formerly *Capparidaceae*), *Cleomoideae* subfamily and is a phylogenetic near relative to

the *Brassicaceae* family (Chweya and Mnzava, 1997; Wu *et al.*, 2017), with 15 species native to Namibia (Craven, 1999) and *C. gynandra* being the most widely used species as a leafy vegetable (Kolberg, 2001). *C. gynandra* grows as a weed in Southern Africa and is characterized by its long taproots, with fewer secondary roots (Chweya and Mnzava, 1997).

C. gynandra has shown great agronomic, medicinal, economic and adaptive potential (Wangolo et al., 2015). It has a C₄ photosynthetic pathway, an adaptation that allows it to survive arid environments (Chweya and Mnzava, 1997; Marshall et al., 2007). Its seeds have high levels of polyunsaturated oil, allowing the oil to be edible (Mnzava, 1990), to make soap and used to kill lice (Burkill, 1985). The use of its oil is not practised in Namibia (P.T. Shipoh 2018, pers. comm., 12 December). The plant has a variety of medicinal properties such as the ability to induce childbirth labour (Kamatenesi-Mugisha and Oryem-Origa, 2007; Kujeke, Edziwa and Icishahayo, 2017), treat scorpion stings, snake bites and fevers (Manandhar, 2002) and displayed antifungal properties (Imanirampa and Alele, 2016). The African spider has been known to have pest repellent properties (Guarino, 1997; Opiro et al., 2013) and through its sale, provide a source of income in some African countries (Chweya and Mnzava, 1997; Muhanji et al., 2011).



Figure 2.1: Cleome gynandra L. plant. (Masuka, Goss and Mazarura, 2012).

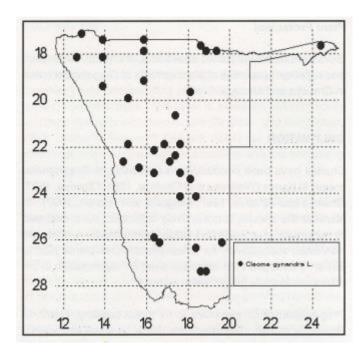


Figure 2.2: Geographical distribution of *Cleome gynandra* L. in Namibia (Kolberg, 2001).

C. gynandra is a wildflower with an origin that is not very clear (Lokesha, 2018). It is believed to have originated in sub-Saharan Africa and southern Asia, but to date, it is spread out worldwide in tropical, subtropical and pacific regions (Bremer and Wannorp, 1975; Lokesha, 2018; Shilla et al., 2019). It is a herbaceous plant with edible leaves that can grow between 0.5 to 1.5m tall, depending on environmental conditions (Guarino, 1997; van Rensburg et al., 2007). Leaf shape is compound and palmate (covered with glandular hair), with the plant bearing three to seven leaflets (Guarino, 1997; Masuka, Goss and Mazarura, 2012). It is an annual plant that grows best during summer (between December and March) when it is supplied with adequate amounts of water during the rainy season and when it has complete sunlight exposure at temperatures of 18°C to 25°C (Kakujaha-Matundu, 1996; Kolberg, 2001; van Rensburg et al., 2007). C. gynandra has variable pigmentation in its stems and flowers. Stems vary from green, pink to purple while flowers come in shades of white, light pink or purple (Mishra, Moharana and Dash, 2011; Masuka, Goss and Mazarura, 2012). It has been reported that the purple stems are more nutritious while other reports have claimed that the green stems are more resistant to insects, but more susceptible to diseases (Silué, 2009). Although C. gynandra pollination mechanisms are not fully understood, it is believed that the plant has evolved strategies that are specific to self-pollinating plant species (Lokesha, 2018). The plants properties, coupled with its ability to grow in arid conditions make it versatile and suitable for various agricultural prospects (Onyango, Onwonga and Kimenju, 2016).

Human contribution does not dictate its growth as it grows wild (Rodin, 1985; Edmonds and Chweya, 1997). The plant is available in areas with an abundance of animal manure, noting that it is mostly found near cattle posts and cultivated fields (Rodin, 1985; Shackleton *et al.*, 1998). Its seeds are considered stubborn as they have a hard shell,

allowing for them to only be propagated by cattle, and can remain dormant for up to six months or longer depending on the region (Chweya and Mnzava, 1997). Dormancy can however be artificially disrupted by incubation of the seeds at 40 °C for one to five days (Lokesha, 2018). Cattle eat the flowers, seeds/seed pods which are then expelled into its dung, which is used as a fertilizer and spread out onto the field, allowing the plant to grow when conditions are deemed conducive. According to subsistence farmers in the area, the plant is only harvested for consumption during the months of November, December and January (P.T. Shipoh 2018, pers comm., 12 December; Kolberg, 2001; van Rensburg *et al.*, 2007). If it is harvested any time after that, it is known to have a bitter taste and considered a weed (Guarino, 1997; Kolberg, 2001; van Rensburg *et al.*, 2007; Silué, 2009) which is why it gets destroyed from then on as the farmers begin to prepare for the harvesting season.

There are very few genetic diversity studies that have been done on *Cleome gynandra* L., that are specific to Africa, where the species is widely distributed. Not much literature has reported on its breeding or harvesting. The plant is known to be widely distributed in tropic and sub-tropic areas, which can attribute to its diversity. Genetic variation can be attributed to edaphic factors, mutation load and morphological traits such as differences in aroma (Lokesha, 2018). Morphological variation is not much but can be narrowed down to aromatic and non-aromatic individual plants (Kolberg, 2001). Previous studies have attempted to assess genetic diversity by identifying species according to taxonomic descriptions and through the use of molecular markers such as allozymes and inter-simple sequence repeats (Omondi *et al.*, 2016).

2.3 Cleome gynandra nutritional content and its importance

There are several underutilized naturally occurring, green leafy vegetables with promising nutritional value (Kavitha and Ramadas, 2013; Gido, Bett and Bokelmann, 2016). *C. gynandra* is a nutritive vegetable that can retain most of its nutrients after cooking in comparison to other leafy vegetables in its category (Silué, 2009). Understanding this retainability will allow subsistence farmers to further improve the nutritional value of this plant (Silué, 2009; Muhanji *et al.*, 2011).

Table 2.1: Nutrient comparison of raw *C. gynandra* leaves to exotic vegetables (Adapted from Kolberg, 2001).

Vegetable	Vit. A	Vit. C	Iron	Calcium	Protein
	mg/100g	mg/100g	mg/100g	mg/100g	g/100g
Lettuce (<i>Lactuca sativa</i> L.)	0.2 - 7.8	3 - 33	0.5 - 4.0	17-107	0.8 - 1.6
Spinach (Spinacia	2.8 - 7.4	1 - 59	0.8 - 4.5	60 - 595	2.3 - 3.1
oleraecea) Cleome gynandra L.	6.7 - 18.9	127 - 484	1 - 18.8	213 - 434	3.1 - 7.7

Table 2.2: Activities of vitamins and minerals (Adapted from Hedges and Lister, 2005).

Name	Major Function
Vitamin A	Essential for eyesight and eye health
Vitamin C	Needed for healthy connective tissue
Iron	Component for haemoglobin in blood
Calcium	Structural component for teeth and bones
Protein	Essential for growth and maintenance

In comparison to lettuce and spinach, *C. gynandra* has a significantly higher overall nutrient content (**Table 2.1**). *C. gynandra* is an important vegetable in rural areas across several African countries as it is the main source of vitamins and minerals (Omondi *et al.*, 2017) (**Table 2.2**). Exotic vegetables have taken a permanent place in most households which have allowed modern agronomy to cater for and conserve their genetic resources

and boost their productivity (Ng'etich, Aguyoh and Ogweno, 2012). With leafy vegetables such as *C. gynandra* being nutritionally superior to exotic vegetables, knowledge of its overall agronomy, broadening food bases and domestication should be at the forefront of modern agricultural practices (Chivenge *et al.*, 2015; Wangolo *et al.*, 2015; Chataika *et al.*, 2020).

2.4 Seed Endophytes

Seed-borne endophytes are vertically transmitted and live in close relationships with their host throughout successive generations (Truyens et al., 2014; Verma, Kharwar and White, 2019; Tyc et al., 2020). Seeds play an integral role in spermatophyte life cycles: they can remain dormant until favourable conditions allow them to germinate and develop into a new plant (Nelson, 2004; Shahzad et al., 2018). Seeds can benefit from seed-associated microbe interactions as they assist in seed preservation (Bednarek and Osborn, 2009; Geisen et al., 2017). When seeds germinate, their intake of water leads to an exudate secretion that attracts endophytes, which in turn colonises the rhizosphere and spermosphere (Nelson, 2004). They allow seedlings to, directly and indirectly, promote their host's growth (Figure 2.3), as they are tolerant to abiotic stress and resistant to pests and pathogens (Nelson, 2004; Parsa et al., 2016). Endophytes also produce secondary metabolites for plant environmental adaptation and crop yield improvement (Liu, Kloepper and Tuzun, 1995; Ramamoorthy et al., 2001). Direct mechanisms include nitrogen (N₂) fixation, phosphate solubilization, indole-3-acetic acid (IAA) production, while indirect mechanisms include siderophore production and ammonia (NH₃) production (Goswami, Thakker and Dhandhukia, 2016; Premachandra, Hudek and Brau, 2016). Secondary metabolite production comes in the form of fluorescence production and hydrogen cyanide (HCN) production (Allu, Kumar and Audipudi, 2014; Kamei, Dolai and Kamei, 2014). Seed endophytes have been of particular interest in recent studies as they are transmitted from generation to generation (Truyens *et al.*, 2014; Shahzad *et al.*, 2018). Seed-borne endophytes ensure that the next developing plant will be favoured by mutualism and grow to an optimum capacity (Rudgers *et al.*, 2009; Truyens *et al.*, 2014). To the best of my knowledge, no previous studies have been done on seed endophytes of *C. gynandra*.

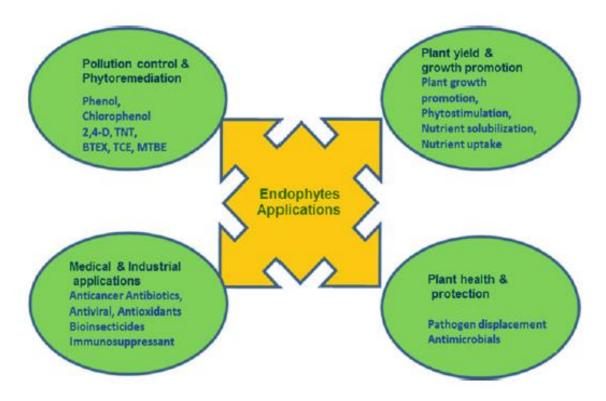


Figure 2.3: Application of endophytes in various fields (Arora and Ramawat, 2017).

2.5 Plant-Microbe Interactions: How Seeds Get Their Microbiome

Plant microbiomes are communities where endophytes dwell in plants (Hardoim *et al.*, 2012; Mitter *et al.*, 2017). Seeds were reported to be the initial source of endophytes or

pathogens in a plant (Baker and Smith, 1966). The internal seed microbiome is inherited via the seed from previous generations to survive conditions of seed storage and desiccation (Truyens *et al.*, 2014; Mitter *et al.*, 2017). Although studies report that seeds of most plant species harbour endophytes (Schardl, Leuchtmann and Spiering, 2004), seed-vectored endophytes have been poorly investigated (Marianela *et al.*, 2018; Verma, Kharwar and White, 2019). The concept of seeds being an important source of bacterial endophytes has only become accepted as of late (Mano and Morisaki, 2008). It has been revealed that a wide array of endophytes can be obtained from plant tissue (Hardoim *et al.*, 2012).

Studies have centred around the concept of root colonisation by beneficial endophytes in the rhizosphere. The rhizosphere is an area of soil that borders the root system of a plant (Barea et al., 2005; Ahemad and Kibret, 2014). This area facilitates metabolic processes and serves as a vector for nutrient uptake (Bowen and Rovira, 1999; Bednarek and Osborn, 2009). For endophytes to grow optimally in the rhizosphere, the soil should have a neutral pH, a good supply of organic and inorganic nutrients, and lastly, good water holding capacity. In meeting the needs of the endophytes, the plant will release secondary metabolites (Stone and Williams, 1992; Demain, 1999; Kai, Effmert and Piechulla, 2016). These secondary metabolites will interact symbiotically with the endophytes to improve the plants' overall growth indirectly by inhibiting plant pathogens and directly by solubilizing nutrients (Whipps, 2001; Premachandra, Hudek and Brau, 2016). Root exudates attract beneficial bacteria and other soil microorganisms for interaction in the rhizosphere (Walker et al., 2003). However, for the endophytes to be successful in colonising the root, they would have to compete against the other microbes in the surrounding area (Weller et al., 2002; Compant, Clement and Sessitsch, 2010). Secondary metabolites have been known to confer a competitive edge over other microorganisms, which in turn further contributes to root colonisation (Premachandra, Hudek and Brau, 2016). These metabolites are secreted by specific bacterial strains allowing for better competition among the natural flora in the root zone of the plant (Haas and Défago, 2005; Carvalhais et al., 2013). This promotes their competitive capabilities. Some endophytes have shown the ability to colonise internal tissues in conjunction with rhizosphere colonisation, which has allowed them to display plant growth promoting traits (Bais et al., 2006; Araujo et al., 2008). Colonisation occurs when bacteria penetrate cracks occurring on the root surface or directly by the root tip (Figure 2.4; Figure 2.5). Some bacteria have developed further adaptations such as nodules or specific mechanisms for root penetration. In some interactions, colonisation can take place through fissures at the lateral root base and the cortical intercellular crack entry (Compant, Clement and Sessitsch, 2010). In other interactions, colonisation occurs in the interior of hairy root tissues and specialized organs called nodules (Garg and Geetanjali, 2007). Previous studies have indicated that endophytes make use of the various individual or combined mechanisms to allow complete root colonisation. Plant-microbe interactions can be classified according to the direction they occur in the rhizosphere: interaction with protozoa and metazoa (Ronn, Vestergard and Ekelund, 2012); interspecific and intraspecific communication in the bacterial community (Tyc et al., 2014) and bacterial interaction with the plant (Bednarek and Osborn, 2009).

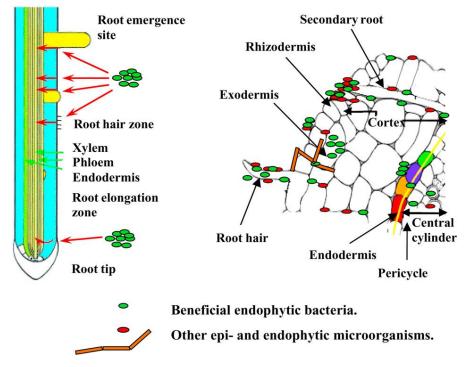


Figure 2.4: Sites of endophytic bacteria colonisation in plants (Compant, Clément and Sessitsch, 2010).

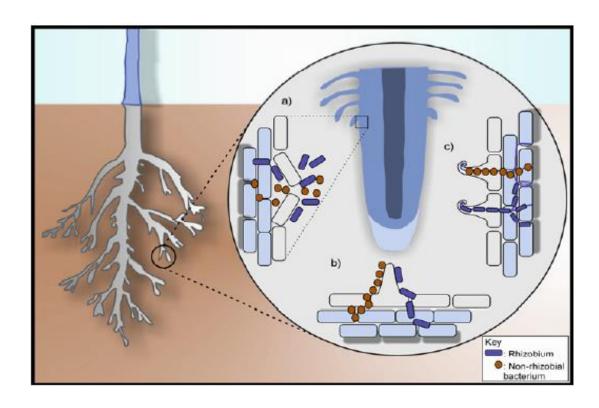


Figure 2.5: Mode of entry to plant roots as follows: a) Through epidermal cell layers; b) Through root hair colonisation; c) Through colonisation of infection threads (Ibanez *et al.*, 2017).

2.6 Plant growth promoting seed endophytes and their importance.

Endophytes are transferred to the seed from vegetative parts of the plant (lateral acquisition) and inherited from parent to offspring via gametes (vertical acquisition) (Shade, Jacques and Barret, 2017). Endophytes enter the seed through parent to offspring transmission where they are dispersed as the seed germinates. They get transferred to other seeds which they enter laterally and thus the cycle continues (Barea, 2015; Cope-Selby et al., 2017; Shearin et al., 2017). This ensures that the endophytes will be present in new plants to come (Truyens et al., 2014). Endophytic bacteria are known to enhance plant growth in crops to improve their nutrition through nitrogen fixation and phosphate solubilization (Rodríguez and Fraga, 1999; Yadegari et al., 2010; Ahemad and Kibret, 2014). Besides biofertilization, endophytic bacteria are also reported to promote plant growth and yield through the production of phytohormones like IAA, an auxin produced to stimulate root growth (Ahemad and Kibret, 2014; Chaturvedi, Singh and Gupta, 2016). As biopesticides, endophytes can indirectly control plant pests and diseases or induce resistance response like siderophores would (Goswami, Thakker and Dhandhukia, 2016). In return, the plant protects endophytes and provides them with nutrients in the form of photosynthates. Phytochemicals such as alkaloids, flavonoids and amino acids have also shown potential plant growth promoting functionality through auxin transport, seed dormancy and ion regulation, as well as defense against plant pathogens (Field, Jordán and Osbourn, 2006; Pérez-Montaño et al., 2014; Vejan et al., 2016). Endophytes are increasingly gaining scientific and commercial interest because of this potential to improve plant quality and growth, and their close association with internal tissues of host plants (Ahemad and Kibret, 2014; Santoyo *et al.*, 2016). In general, the most commonly reported seed endophytes belong to the genera *Bacillus* and *Pseudomonas*, with *Acinetobacter, Paenibacillus, Staphylococcus, Micrococcus* and *Pantoea* (Sivasakthi, Usharani and Saranraj, 2014; Truyens *et al.*, 2014) (**Figure 2.6**).

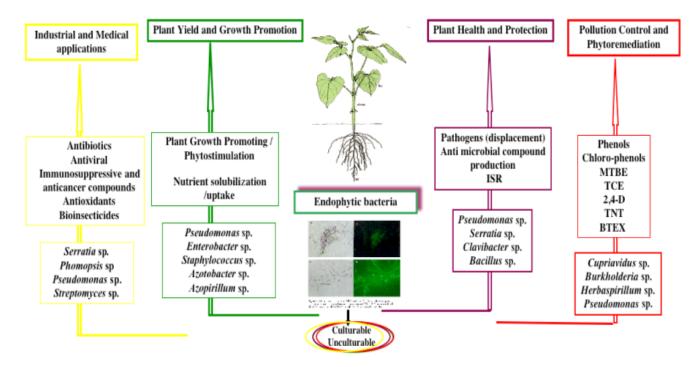


Figure 2.6: Shows a schematic diagram of various plant-bacterial endophyte interactions and their applications that have been previously studied (Ryan *et al.*, 2008).

2.7 Mode of action of Plant Growth Promoting Bacteria (PGPB) as

biofertilizers

2.7.1 Direct mechanisms of action:

2.7.1.1 Nitrogen fixation

Nitrogen is an element that living organisms require in order to synthesize proteins and nucleic acids, making it essential for plant growth (Shridhar, 2012; de Souza, Ambrosini

and Passaglia, 2015). Biological nitrogen fixation (BNF) is the process where atmospheric nitrogen is converted into ammonia by nitrogen fixing bacteria using the nitrogenase enzyme to make it bioavailable (Egamberdieva and Kucharova, 2008; Franche, Lindström and Elmerich, 2009). Nitrogen fixing bacteria can be classified as symbiotic (forming a symbiotic relationship with a host) or non-symbiotic (free-living bacteria) (Shridhar, 2012). Nitrogenase (protein complex) is required to make the nitrogen fixation process possible in plants (Mahmud et al., 2020). Nitrogenase is made up of enzymes and metal co-factors with the first one being dinitrogenase and the second being dinitrogenase reductase (Bulen and LeComte, 1966). Molybdenum nitrogenase is one of the three naturally occurring nitrogenases (Mahmud et al., 2020). It is the most abundant nitrogenase as it has the most significance in nitrogen fixing bacteria and is produced by all natural diazotrophs (Dos Santos et al., 2012; McGlynn et al., 2013). The nitrogen fixing genes (nif genes) are found in symbionts and non-symbionts (Ahemad and Khan, 2011). These genes are required for the synthesis of nitrogenase by encoding enzyme complexes, nitrogen fixation functions and nodulation (Mahmud et al., 2020). Nitrogen can serve as a limiting factor in crop production. The presence of these genes will regulate the function of nitrogenase, enable the plant to synthesize proteins and thus contribute to its growth (Dixon and Kahn, 2004). It has been reported over the years that there is a limited number of nitrogen fixing bacteria, but in more recent years, studies revealed that most microorganisms have nitrogen fixation as one of their traits (Franche, Lindström and Elmerich, 2009). Endophytic species belonging to the genera that have nitrogen fixing capabilities include Rhizobium, Azotobacter, Bacillus, Enterobacter, Klebsiella, Pseudomonas, Arthrobacter and Azospirillum (Dixon and Kahn, 2004; Tilak et al., 2005; Sivasakthi, Usharani and Saranraj, 2014). Rhizobium are well-known symbiotic nitrogen fixing bacteria that interact with leguminous plants by infecting their roots, forming nodules that serve as the site where endophytes fix nitrogen and make it readily available for the plant (Gonzalez-lopez and Pozo, 2005). Non-legume plants can fix nitrogen through plant organs other than the roots, intracellularly and extracellularly (Santi, Bogusz and Franche, 2013). *Azospirillum* (endophytic diazotroph) and *Azotobacter* are free-living nitrogen fixing bacteria that are linked to programs associated with non-legume plants worldwide (Shridhar, 2012). They develop and colonize the interior of the roots and surface of the host plant, with this interaction being considered the focal point of BNF (Gonzalez-lopez and Pozo, 2005).

2.7.1.2 Phosphate solubilization

Phosphorus is a key nutrient that is considered to limit plant growth (Ezawa, Smith and Smith, 2002; Vejan *et al.*, 2016). Microorganisms play an essential role in the natural phosphate cycle. This cycle takes place through the cyclic oxidation and reduction of phosphorous compounds, where phosphine is oxidized to phosphate (Rodríguez and Fraga, 1999). Soluble phosphorus is readily absorbed as HPO₄²⁻ and H₂PO₄⁻ which will be used by the plant (Rodríguez and Fraga, 1999). It has an essential role in biochemical pathways which are particularly important for photosynthesis and BNF (Khan, Zaidi and Wani, 2007). Phosphate solubilizing endophytes are found in soil but are not abundantly spread (Mohammadi, 2012). This leads to competition for phosphate adsorption sites with other microbes that are more abundantly distributed throughout the rhizosphere (Mohammadi, 2012). This results in inadequate phosphate supply to the plant (Mohammadi, 2012). To overcome this, plants should be inoculated with a microbe that specifically solubilizes phosphate to allow the plant to receive it in a higher concentration

(Rodríguez and Fraga, 1999; Pradhan and Sukla, 2005). Studies show that the contribution phosphorus-solubilizing endophytes have towards plant nutrition has led to overall improvements in plant growth (Krasilinikov, 1957; Islam *et al.*, 2007). Phosphate solubilizing endophytes being used as inoculants allows for increased uptake of phosphorus, thus leading to crop yield increases (Rodríguez and Fraga, 1999; Walpola and Yoon, 2012). Previous studies indicated that bacteria able to express phosphate solubilization are among the *Klebsiella*, *Enterobacter*, *Pseudomonas*, *Bacillus*, *Agrobacterium*, *Rhizobium*, *Aereobacter*, *Achromobacter*, *Burkholderia*, *Micrococcus*, *Flavobacterium*, *Proteus*, *Serratia*, *Citrobacter* and *Erwinia* genera (Rodríguez and Fraga, 1999; Khan, Zaidi and Wani, 2007; Yousefi *et al.*, 2011; Walpola and Yoon, 2012; Singh *et al.*, 2014).

2.7.1.2.1 Mechanisms of Phosphate Solubilizing Microbes:

2.7.1.2.1.1 Inorganic phosphate solubilization

Inorganic phosphate solubilization is absorbed by lowering the soil or medium pH (**Figure 2.7**) and through chelation (Khan *et al.*, 2009). In alkaline soils, phosphates can precipitate and form insoluble calcium phosphate (Khan *et al.*, 2009). The solubility of calcium phosphate increases when the soil pH decreases and once the pH is lowered, phosphorus is made available (Fankem *et al.*, 2006; Khan *et al.*, 2009). Phosphate solubilizing microbes lower the soil pH through the secretion of organic acids (Ingle and Padole, 2017). Through metabolic processes such as oxidative respiration or fermentation, the microbes can produce organic acids, with the strength of the acid produced determining how efficient solubilization will be (Kalayu, 2019). Chelation enables phosphate solubilizing microbes to dissolve inorganic phosphate by competing with phosphate for absorption sites on the soil and through the chelation of cations bound

to phosphorous (Ingle and Padole, 2017). The chelation reaction involves the carboxyl and hydroxyl groups of acids chelating the cations bound to phosphorus which converts it to a more soluble form. These acids also compete for fixation sites on insoluble oxides such as Al and Fe. They react with them causing them to stabilize and thus allow them to be called 'chelates' (Walpola and Yoon, 2012).

2.7.1.2.1.2 Organic Phosphate Mineralization

Microorganisms need to mineralize (hydrolyse) substrates using the phosphatase enzyme (**Figure 2.7**) for them or the plant to utilize phosphorus in its organic form, with the process taking place at the expense of plant and animal remains (Khan *et al.*, 2009; Kalayu, 2019). This process plays an essential role in phosphorus cycling and makes use of a variety of enzymes that can either be alkaline or acidic (Alori, Glick and Babalola, 2017). Soil bacteria mineralize organic phosphorus by producing extracellular enzymes such as phytases, phospholipases and phosphoesterases (Walpola and Yoon, 2012).

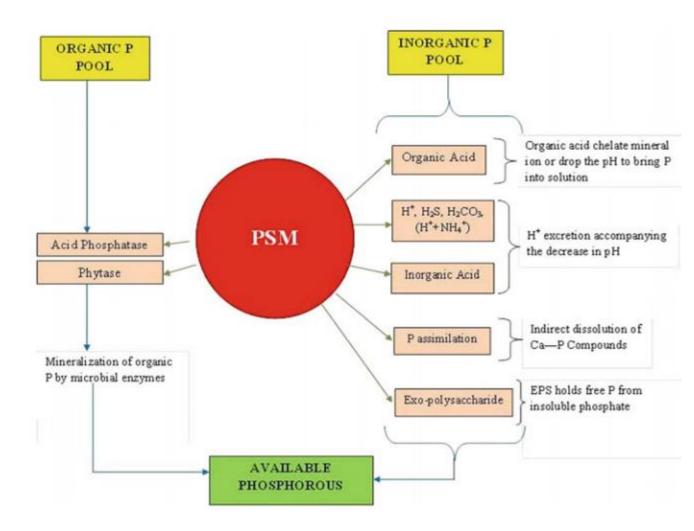


Figure 2.7: Mechanisms of phosphate solubilization/mineralization from organic/inorganic substances produced by phosphate solubilizing microorganisms (Walia *et al.*, 2017).

2.7.1.3 Indole-3-acetic acid (IAA) production

Indole-3-acetic acid (IAA) is an abundant naturally occurring auxin that belongs to a group of phytohormones, which are found in plants and stimulates root growth (**Figure 2.8**), with up to 80% of microorganisms being able to synthesize it (Vessey, 2003; Miransari and Smith, 2014; Gupta *et al.*, 2015). It influences an array of cellular functions which regulate plant growth and development. It is synthesized and secreted by PGPB, from which it gets absorbed directly on the seed or root surface of the plant by tryptophan

(an amino found in root exudates) available on root exudate or seed (Saleem et al., 2007). Microorganisms inhabiting the rhizosphere synthesize and release IAA as a secondary metabolite because of the rich supply of substrates released from the roots (Shahab, Ahmed and Khan, 2009). IAA plays a vital role in plant-microbe interactions, varying from phytostimulation to pathogenesis. IAA also serves as a reciprocal signalling molecule that affects gene expression and regulates plant development through cellular responses in several microorganisms (Ahemad and Kibret, 2014). These responses include cell expansion, division and differentiation (Sivasakthi, Usharani and Saranraj, 2014). Studied *Pseudomonas* strains such as *P. fluorescens* and *P. putida* were able to synthesize indole-3-acetic acid (Khakipour et al., 2008).

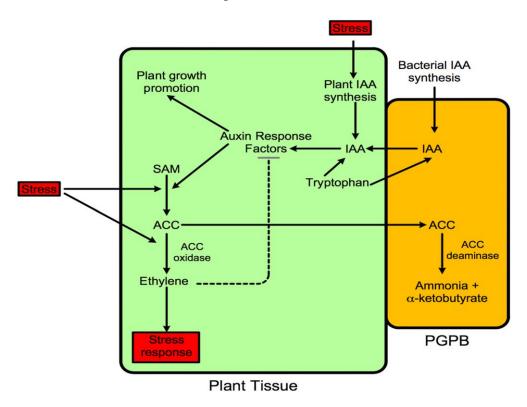


Figure 2.8: Schematic representation of plant growth stimulation by plant growth promoting phytohormones (Olanrewaju, Glick and Babalola, 2017).

As more bacterial species are analyzed, more precise routes for IAA bacterial biosynthesis pathways (Figure 2.9) are identified and classified according to intermittent compounds (Ljung et al., 2002; Spaepen, Vanderleyden and Remans, 2007; Maheshwari, Dheeman and Agarwal, 2015). The tryptamine (TAM) pathway involves TAM being directly converted to indole-3-acetaldehyde (IAAld) by amine oxidase. Decarboxylation which is brought on with indole-3-pyruvate decarboxylase leads to the formation of IAA (Hartmann, Singh and Klingmuller, 1983). With the tryptophan side-chain oxidase (TSO) pathway, tryptophan is directly converted to IAAld by indole-3-pyruvate and is then oxidized to IAA simultaneously (Oberhansli, Defago and Haas, 1991). The main step of the indole-3-acetonitrile (IAN) pathway consists of the conversion of indole-3-acetamide via nitrilase where IAN is produced by tryptophan via indole-3-acetaldoxime (Patten and B. R. Glick, 1996; Zhao et al., 2001). The indole-3-acetamide (IAM) pathway is considered the best pathway characterized by bacteria (Spaepen, Vanderleyden and Remans, 2007). It entails the conversion of tryptophan into IAA through two steps. The first step sees tryptophan being converted to IAM which is produced by the enzymatic action of tryptophan-2-monooxygenase. The second step sees IAA being obtained by the enzymatic hydrolysis of IAM by IAM hydrolase (Bar and Okon, 1993; Prinsen et al., 1993; Spaepen, Vanderleyden and Remans, 2007; Maheshwari, Dheeman and Agarwal, 2015). The IAAld pathway centres around tryptophan being converted into indole-3pyruvate by the aminotransferase enzyme and decarboxylated into IAAld by indolepyruvate decarboxylase. The terminal step involves IAAld being oxidized into IAA (Ljung et al., 2002; Maheshwari, Dheeman and Agarwal, 2015).

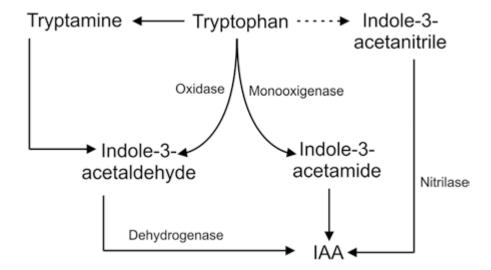


Figure 2.9: Indole-3-acetic acid biosynthesis pathways (Maheshwari, Dheeman and Agarwal, 2015).

2.7.1.4 Ammonia production

Ammonia is an important nutrient for plant growth and also serves as an anti-fungal metabolite (Whipps, 2001). Accumulation of ammonia in the soil creates alkaline conditions which suppress the growth of certain fungi (Bhattacharyya and Jha, 2012). Ammonia production is exhibited by microorganisms via metalloenzyme systems such as nitrogenase (Dixon and Kahn, 2004). Nitrogenases are enzymes that catalyze the biological reduction of atmospheric nitrogen to ammonia (Dixon and Kahn, 2004). The organism breaks down the complex nitrogenous material and releases ammonia in the soil which is taken up by the plant as a nutrient source (Bhattacharyya and Jha, 2012).

2.7.2 Indirect mechanisms of action:

2.7.2.1 Siderophore production

Iron (Fe) is one of the bulk minerals present in plenteous amounts on earth, yet it is unavailable in the soil for the plants (Rajkumar *et al.*, 2010). Iron is an important nutrient for microorganisms and plants as it plays a vital role in metabolic processes such as

photosynthesis, respiration and BNF (Kobayashi and Nishizawa, 2012). In instances where iron solubility in the soil is low, bacterial endophytes have been able to overcome this limitation by using a chelating agent known as a siderophore (Neilands and Leong, 1986; Krewulak and Vogel, 2008). The design of siderophores is intended to facilitate the formation of tight and stable complexes with ferric iron (Miethke and Marahiel, 2007). The mechanisms for Fe (II) uptake in endophytes have been elucidated. Fe (II) is widely available for living cells, however, it is oxidized to Fe (III) in the majority of microbial habitats (Hynes et al., 2008). This is due to enzymatic oxidation as it is being assimilated by spontaneous reaction with molecular oxygen and circulation in a host organism, resulting in low concentrations or its lack of availability (Miethke and Marahiel, 2007; Premachandra, Hudek and Brau, 2016). As iron's bioavailability is relatively low, the role of siderophores has become essential in locating the iron environments and making it available to the plant (Chaitanya et al., 2014). Siderophores have a high affinity to solubilize and bind iron together, allowing it to be transported. Bacterial endophytes belonging to the Bacillus, Azotobacter, Pseudomonas and Enterobacter genera have shown siderophore production capabilities, with the potential to promote plant growth and improve crop yield (Husen, 2003; Tian et al., 2009). In the presence of siderophores, plant nutrition can improve and thus plant growth can increase.

2.7.2.2 Secondary Metabolite Production:

2.7.2.2.1 Fluorescence Production

Fluorescence producing bacteria have been considered the most promising PGPB as they can promote plant growth by the production of secondary metabolites such as phytohormones, hydrogen cyanide and antibiotics (Sivasakthi, Usharani and Saranraj, 2014). The proposed phytohormones produced are mainly, auxins, cytokinins,

gibberellins and ethylene which regulate plant growth and development in their respects (Kumar, Behl and Narula, 2001). Auxins regulate root growth, cytokinins and gibberellins inhibit plant pathogens and lastly, ethylene stimulates seed germination (Walsh, Morrissey and O'Gara, 2001). The most prominent fluorescence producing genus is *Pseudomonas* (Gupta *et al.*, 2015).

2.7.2.2 HCN production

HCN is a secondary metabolite that is produced naturally by a vast number of organisms including soil bacteria, plants, insects, algae and fungi and is known to serve as a biological control against pathogens as it has toxic properties, which however do not negatively affect the host plant (Haas and Défago, 2005; Kamei, Dolai and Kamei, 2014). Recent studies suggested that HCN could bind iron in the rhizosphere, indirectly making phosphate more readily available, directly increase other nutrient availability and by doing so, result in increased plant growth (Rijavec and Lapanje, 2016; Sagar *et al.*, 2018). *Pseudomonas* and *Bacillus* are genera of plant growth promoting bacterial strains that are noted for having HCN production as a common trait (Ahmad, Ahmad and Khan, 2008).

2.8 Endophytic bacteria as seed inoculants

Microbial inoculants have been used to serve as seed treatments as they deliver the microbe directly to the rhizosphere where plant-microbial activities take place. Seed inoculant treatments have been praised for their success to improve plant nutrient uptake and availability (O'Callaghan, 2016; Murphy, Doohan and Hodkinson, 2018). There are however factors that affect inoculant quality and effectiveness such as cost-effectiveness, time-consuming production and viable storage conditions (O'Callaghan, 2016). Studies

have focused on how to overcome these barriers. Endophytic PGPB have been of particular interest as an inoculant because their root colonisation ability has provided a favourable environment for plant function and development (de Souza, Ambrosini and Passaglia, 2015).

2.9 Endophytic bacteria and their potential role in Namibian agriculture

To date, there are no farming methods that can be used to successfully cultivate/domesticate *Cleome gynandra* L. in Namibia. To fully understand the farming methods of a specific crop, factors such as soil structure and fertility, sunlight concentration, temperature, climate and water management should be taken into account. Subsistence farmers do not have the means to look into these factors which is why any scientific contribution to farming methods would be in their interest. Namibia is a country that has farming as one of its most prominent economic activities (Mendelsohn, 2006). With this in mind, providing a reliable agricultural system that can easily be replicated is a necessity. The understanding of endophytes and their mechanisms can bring us one step closer to determining how they can be applied as effective treatments for the cultivation of indigenous vegetables. This will in turn improve the horticultural capability of indigenous plant species in Namibia.

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CHAPTER 3

CHARACTERIZATION OF PLANT GROWTH PROMOTING BACTERIAL SEED ENDOPHYTES OF *CLEOME GYNANDRA* L. FROM NORTHERN REGIONS OF NAMIBIA

Abstract

Endophytic bacteria have the ability to enhance plant health, growth and yield. In addition, they have the potential to act as bioinoculants. Cleome gynandra L. (C. gynandra) is a wild drought-tolerant and underutilized leafy vegetable found in the rural semi-arid northern regions of Namibia. It has shown exceptional potential in traditional medicine, agronomy, economy and climate adaptation. The objectives of this study were to morphologically characterize isolated bacterial strains and assess their plant growth promoting (PGP) capabilities. Twenty morphologically distinct isolates were obtained and assessed for plant growth promoting traits. Isolated endophytes exhibited capabilities to produce growth regulators as follows: nitrogen fixation (40%), indole acetic acid production (IAA) (100%), siderophore production (80%), ammonia production (85%), fluorescence production (10%), hydrogen cyanide production (30%) and phosphate solubilization (15%). Phylogenetic analysis of these isolates revealed that all the isolates belonged to the Proteobacteria phylum (excluding Phytobacter ursingii). It was concluded that C. gynandra seeds harbour endophytic bacteria that could improve plant growth in hostile environments, enhance crop productivity and be used for biotechnological applications in agriculture.

Keywords: agriculture, bacterial seed endophytes, *C. gynandra*, plant growth promotion, seed inoculants.

Introduction

Rapid population growth in the 20th century, coupled with environmental damage and climate change, has brought about challenges to the agricultural yield output of the traditionally grown field crops to feed the world population (Glick, 2012; Majeed, Muhammad and Ahmad, 2018). To address the expected food needs, conventional agricultural production was intensified to ensure food security (Timmusk *et al.*, 2017; Majeed, Muhammad and Ahmad, 2018). This was achieved through the Green Revolution that enabled the sharp increase of input of synthetic chemical fertilizers and pesticides, irrigation and the development of high yielding crop hybrids (Chauhan *et al.*, 2012; Abraham *et al.*, 2014; Gange and Gadhave, 2018). These fertilizers have become essential components of modern agriculture because they provide essential plant nutrients such as nitrogen, phosphorus and potassium (Chauhan *et al.*, 2012).

The excessive use of industrial chemicals fertilizers, herbicides and pesticides has led to environmental hazards such as leaching and nutrient-rich run-off that cause eutrophication of surface water bodies; greenhouse gas emissions; groundwater contamination, food poisoning and soil quality degradation (Pingali, 2012; Abraham *et al.*, 2014). Therefore, an alternative and more sustainable approach which can reduce the use of chemical application and improve agriculture to ensure food security must be put in place (Jha *et al.*, 2013; Chandini *et al.*, 2019).

A plant growing under field conditions harbours a well-structured and regulated complex microbial community that inhabit the rhizosphere, as well as the epiphytic and endophytic phyllosphere (Backer *et al.*, 2018; Numan *et al.*, 2018). Many of the bacteria found in and around plants have the ability to stimulate and facilitate plant growth and

consequently are called plant growth promoting bacteria (PGPB) (Akila et al., 2011; Glick, 2012; Jha et al., 2013; Gupta et al., 2014). These bacteria stimulate the plant by invading internal plant tissue with their main point of entry being the rhizosphere (root zone) (Gaiero et al., 2013; Ibanez et al., 2017). Endophytes are microorganisms that dwell inside plants without causing any harm (Schulz and Boyle, 2006; Mercado-Blanco and Lugtenberg, 2014). A study conducted on maize seeds indicated that its endophytic bacterial community can be conserved during evolution and natural selection (Johnstonmonje and Raizada, 2011). Seed endophytes are of particular interest for they are vertically transmitted from generation to generation (Rosenblueth and Martínez-romero, 2006; Truyens et al., 2014). They are endemic to nature and are thought to influence the plant's physiology through regulating the plants nutrient and hormone levels (Hardoim et al., 2012). In the rhizosphere, roots are invaded through root hair colonisation, infection threads between root hairs and disrupted epidermal cell layers (Compant, Clement and Sessitsch, 2010; Reinhold-Hurek and Hurek, 2011). Another form of colonisation that plant growth promoting bacteria use is the infection of seeds to ensure their existence in new plants (Ibanez et al., 2017).

All plants studies to date have shown to symbiotically harbour endophytic microorganisms that help them in several ways such as acting as biofertilizers and biopesticides (Rosenblueth and Martínez-romero, 2006; Araujo *et al.*, 2008; Cocq *et al.*, 2017). These studies have centred on crops of economic importance leaving out indigenous plants such as *C. gynandra* (Chweya and Mnzava, 1997; Maheswari, Anbukkarasi and Hemalatha, 2014; Omondi *et al.*, 2017; López *et al.*, 2018). Plant growth promoting bacteria have been used as soil inoculants to improve the yields of agricultural crops (Khalid, Arshad and Zahir, 2004; Golding, 2012; de Souza, Ambrosini and

Passaglia, 2015; Chaturvedi, Singh and Gupta, 2016). Their efficiency transpires through a variety of mechanisms that develop during the early stages of seedling development as seed endophytes become a part of the host plant rhizosphere (Yang, Kloepper and Ryu, 2009; White *et al.*, 2017; Verma, Kharwar and White, 2019). This contributes to plant growth promoting traits such as nitrogen fixation, siderophore production, indole-3-acetic acid (IAA) production, phosphate solubilization, ammonia production, hydrogen cyanide production and fluorescence production (Adesemoye and Egamberdieva, 2013; Abbamondi *et al.*, 2016). These mechanisms either directly facilitate resource acquisition or indirectly inhibit pathogen activity on plant growth (Ahemad and Kibret, 2014; Gupta *et al.*, 2015; Verma and White, 2017). Bacterial species belonging to the genera *Pseudomonas Azospirillum*, *Azotobacter*, *Klebsiella*, *Enterobacter*, *Alcaligenes*, *Arthrobacter*, *Burkholderia*, *Bacillus*, and *Serratia* have been reported to have plant growth promoting capabilities (Matiru and Dakora, 2004; Truyens *et al.*, 2014; Agbodjato *et al.*, 2015).

Cleome gynandra L., is a leafy vegetable that is indigenous to rural areas in Namibia on agricultural land and near human settlements (Guarino, 1997). (Guarino, 1997; van Rensburg et al., 2007). It is probably a native of Africa and is now widely distributed in tropical and subtropical regions throughout the world (Chweya and Mnzava, 1997). Mostly collected from the wild, C. gynandra is known to be very nutritious and consumed in most African countries (Guarino, 1997; Silué, 2009; Kujeke, Edziwa and Icishahayo, 2017). It is an annual herb that is identified by its white flowers, long seed pods and compound leaves that are divided into folioles. C. gynandra is a plant with a C4 photosynthetic pathway that enables it to withstand high temperatures, intense sunlight and drought (Silué, 2009; Shahzad et al., 2018). With its natural habitat consisting of

wastelands and many other soil types, make this plant indubitably suitable for various agricultural prospects (Chweya and Mnzava, 1997). This study aimed to isolate and assess *C. gynandra* seed endophytes diversity, characterize their plant growth promoting traits and test their agricultural potential as plant growth promoting (PGP) factors.

3.1 Materials and Methods

3.1.1 Study area and sample collection

A 100 whole healthy *C. gynandra* seed pods were collected. These seeds were used as the source material for endophytic bacteria isolation. All seeds used in this study were collected in May 2018 from the Omusati, Oshana, Ohangwena and Oshikoto regions in the Northern part of Namibia (**Figure 3.1**; **Figure 3.2**). Individual samples were placed in sterile plastic bags that contained silica gel to remove excess moisture, and stored at 4°C until further processing in the laboratory of the Department of Biological Sciences of the University of Namibia. There was a total of five sampling points from each region (**Table 3.1**). The soil in these regions is mostly composed of cambisols, calcisols and arenosols (Mendelsohn, 2007). The soil texture is sandy, fine and soft with good water-retention capacity, however, it has moderate fertility as it is not rich in essential nutrients (Mendelsohn *et al.*, 2002). The rainy season is from October to April with these regions receiving an average rainfall from 250-300mm, 350-400mm and occasionally 500-550mm per annum (Mendelsohn *et al.*, 2002).

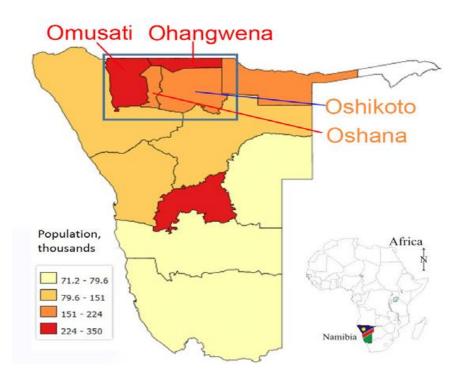


Figure 3.1: Map depicting the central northern regions of Namibia (Starkey *et al.*, 2017).

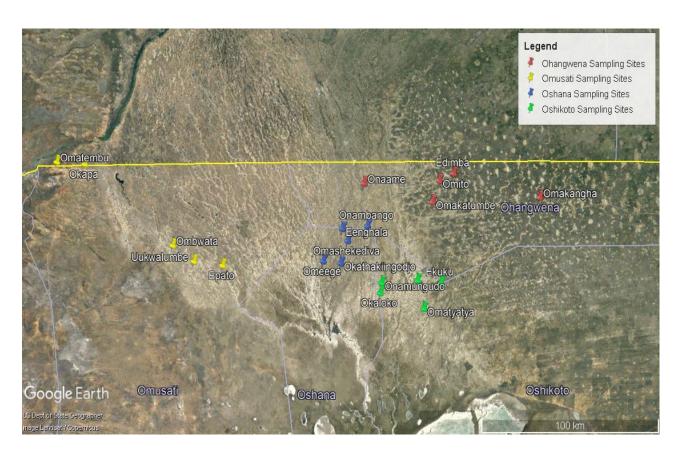


Figure 3.2: Map depicting the sampling sites. Google Earth Pro (Version 7.3.2.5776) [software]. Mountain View, CA: Google Inc. (2018).

Table 3.1: Sampling sites GPS coordinates

Site name	Latitude coordinate	Longitude coordinate
Omusati Region:		
Uukwalumbe	S17°51.437'	E015°02.209'
Ombwata	S17°47.100'	E014°55.525'
Epato	S17°52.596'	E015°11.287'
Okapa	S17°24.929'	E014°27.628'
Omatembu	S17°24.182'	E014°18.585'
Oshana Region:		
Omeege	S17°51.723'	E015°43.123'
Omashekediva	S17°46.310'	E015°50.886'
Eenghala	S17°43.069'	E015°49.236'
Okathakiingodjo	S17°52.311'	E015°48.655'
Onambango	S17°42.401'	E015°57.140'
Ohangwena Region:		
Edimba	S17°28.434'	E016°24.433'
Onaame	S17°30.975'	E015°56.196'
Omakangha	S17°34.919'	E016°51.698'
Omito	S17°30.336'	E016°19.894'
Omakatumbe	S17°36.045'	E016°17.706'
Oshikoto region:		
Omatyatya	S18°04.557'	E016°14.875'
Okaloko	S18°00.275'	E016°01.097'
Ompugulu	S17°57.007'	E016°12.890'
Onamungudo	S17°57.613'	E016°01.516'
Ekuku	S17°57.670'	E016°20.237'

3.1.2 Endophytic bacteria isolation

The collected plant material (seed pods) were first disinfected with 70% ethanol for 1 minute and then treated with 10% sodium hypochlorite solution for 10 minutes. The samples were then rinsed with distilled water three times to remove any surface microorganisms that might interfere with further testing. To verify successful surface sterilization, 300 μ l of the final rinse water was plated onto trypticase soy agar (TSA) plates (15 g Agar, 15 g Casein Peptone, 5 g Sodium Chloride, 5 g Soya Peptone, 1000 ml

in distilled water) and served as a control. Plates were incubated at 28°C for 15 days with periodic examination for microbial growth (Coêlho *et al.*, 2011).

Endophytic bacteria were isolated from seed pods collected in the 4 Northern regions of Namibia. Entire seed pods were ground using a mortar and pestle. The plant extract was then mixed with 6ml of aqueous 0.9% NaCl solution and incubated at 28°C for three hours to allow endophytes to be released. The extract was then serially diluted up to the dilution factor 10⁻⁴ after which 0.1 ml aliquots were then plated on TSA. All plates, the control included, were incubated for 2 weeks at 28°C (Araujo *et al.*, 2002). Colonies were selected every 5 days based on morphological differences. Pure cultures were obtained by sub culturing single morphologically distinct colonies onto fresh TSA plates (Araujo *et al.*, 2002). Bacterial cultures for each isolate were prepared by growing them in nutrient broth at 28°C for 24 hours. After incubation, 500 μl of each culture and 500 μl of prepared 50% glycerol were mixed in a 1.5 ml Eppendorf tube, to form a 1:1 volume ratio. The isolates were labelled accordingly and stored in a -80°C freezer.

3.1.3 Genomic DNA extraction and 16S rRNA gene amplification

Based on cell and colony morphology, twenty different morphotypes were identified from C. gynandra seed endophytes. Total genomic DNA of overnight pure cultures was extracted using a ZR Fungal/Bacterial DNA MiniPrepTM Kit from Zymo Research (USA), in accordance with the manufacturer's instructions. The extracted DNA was stored at 4°C until use. The DNA was subjected to PCR amplification using the universal primers 27f (5'-AGAGTTTGATCCTGGCTCAG3-') and 1492r (5'-GGTTACCTTGTTACGACTT-3'), targeting the 1.5 kb region of the 16S rRNA genes (Hynes et al., 2008) using an ESCO SwiftTM MaxPro Thermal Cycler (Esco Group,

Singapore). The final PCR reaction mixture contained 25 µl DreamTaq Green PCR Master Mix 2× (ThermoScientific: Thermofisher, USA), 16 µl Nuclease-free water, 2 µl of each primer (1µM concentration) and 5 µl isolated Genomic DNA as a template which amounted to a total volume of 50 µl (Coêlho et al., 2011). The PCR conditions were as follows: pre-denaturation at 95°C for 4 min, 35 cycles of denaturation at 95°C for 1 min, annealing at 50°C for 30 sec, extension at 72°C for 1 min and a final extension at 7 °C for 10 min, with the holding temperature being 4°C (Kang, Lee & Cho, 2013). Amplicons were quantified by running a 1% agarose gel stained with ethidium bromide (0.5 μg/ml) and visualized using a Clear View UV Transilluminator (Cleaver Scientific Ltd, United Kingdom). PCR product sequencing and purification were conducted at Inqaba Biotec (Pretoria, South Africa). The obtained sequences were edited using Chromas (Version 2.6.4). and aligned using BioEdit Sequence Alignment Editor (Version 7.0.5.3). The consensus sequences were subjected to the BLASTn search program for nucleotide sequence homology (Altschul et al., 1997). The obtained sequences were compared with the sequences in the National Center for Biotechnology Information (NCBI) database using the Standard Nucleotide BLAST. The search was made specific to the 16S ribosomal RNA sequences (Bacteria and Archaea) database for bacterial identification.

3.1.4 Phylogenetic analysis

A phylogenetic tree was constructed from the obtained consensus sequences. Evolutionary analyses were conducted in Molecular Evolutionary Genetics Analysis X (MEGA X) (Kumar *et al.*, 2018). The identified sequences were aligned using the Clustal X program (Larkin *et al.*, 2007). The evolutionary history was inferred using the Neighbour-Joining method (Satou and Nei, 1987). The optimal tree with the sum of

branch length (0.138924950) is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein, 1985). The tree was drawn to scale with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura, 1980) and are in the units of the number of base substitutions per site. This analysis involved 57 nucleotide sequences. All positions containing gaps and missing data were eliminated (complete deletion option). There was a total of 464 positions in the final dataset.

3.1.5 Bioassays for plant growth promoting traits:

3.1.5.1 Siderophore production

The isolates were evaluated for the qualitative production of siderophores on blue agar chrome azurol s (CAS) plates (60.5 mg CAS (C₂₃H₁₃Cl₂Na₃O₉S) in 50 ml water mixed with 10 ml iron (III) solution (1 mM FeCl₃.6H₂O, 10 mM HCl), 72.9 mg HDTMA (hexadecyltrimethylammonium bromide) in 40 ml water, 42.23g Kings B medium, 900 ml distilled water) (Schwyn and Neilands, 1987). Wells were formed onto each CAS agar plate. Three hundred microlitres of 24-hour old broth cultures of the isolates were placed into each well. CAS plates were then incubated at 28°C for 3-6 days. The development of yellow to orange halo was indicative of siderophore production (Chaitanya *et al.*, 2014). Distilled water was used as a negative control and *Klebsiella pneumonia* was used as a positive control (Louden, Haarmann and Lynne, 2011). All assays were carried out in triplicate.

3.1.5.2 Phosphate solubilization

The phosphate solubilization abilities of the isolated strains were tested on Pikovskaya medium (0.5 g Yeast extract, 0.5 g Ca₃(PO₄)₂, 0.1 g MgSo₄, 10 g C₆H₁₂O₆, 0.0001 g Fe(II)SO₄, 0.2 g KCl, 0.0001 g MnSO₄ & 20 g Agar in 1000 ml of distilled water), where growth is associated with the capacity to use inorganic phosphate in the form of Ca₃(PO₄)₂ as the sole source of insoluble phosphate (Pikovskaya, 1948). Isolates were spot inoculated onto the plates and incubated at 28°C for 7 days. The appearance of a transparent zone around the bacterial colonies indicated the phosphate solubilization ability of the isolate. Distilled water was used as a negative control and *Klebsiella pneumonia* was used as a positive control (Minaxi *et al.*, 2012). Assays were carried out in triplicate.

3.1.5.3 Determination of indole production

Indole production was tested in bacterial suspension grown in nutrient broth in the dark supplemented with tryptophan (2 mg ml-1) as the precursor of IAA and compared to the ones grown without the addition of the tryptophan for day 5 and 7 respectively. Isolates were incubated for two weeks at 28°C (Lwin *et al.*, 2012). IAA presence was checked in a culture supernatant (50 μl) mixed with 100 μl of Salkowski reagent (4.5 g of FeCl₃ per litre in 10.8 M H₂SO₄) in a 96 well plate, in triplicates, forming a 1:2 ratio (Gordon and Weber, 1950). The plate was subsequently incubated at room temperature, under dark condition for 30 – 40 minutes. The development of a pink colour indicated IAA production (Lwin *et al.*, 2012). Absorbency was measured using a SpectraMax® M2 Microplate Reader and SoftMax® Pro 6.4 Software (Molecular Devices Inc, USA) at 530 nm to determine the concentration of IAA which was then compared to a standard graph (Minaxi

et al., 2012). Absorbency was subjected to One Way ANOVA. Pure IAA was used to prepare the standard concentrations for the graph (Appendix 1), which was used to compare the concentrations measured from the spectroscopy. IAA solution (5%) was used as a positive control whereas nutrient broth was used as a negative control (Minaxi et al., 2012).

3.1.5.4 Ammonia production

To screen for ammonia production, 1 ml of 24-hour old bacterial cultures were inoculated separately in peptone water (10 ml) and incubated at 36±°2C for 48-72 hours. Nessler's reagent (0.5 ml) was added to the bacterial suspension. Ammonia production was indicated by the development of a brown to yellow colour (Cappuccino and Sherman, 1992). Distilled water was used as a negative control and *Klebsiella pneumonia* was used as a positive control (Agbodjato *et al.*, 2015).

3.1.5.5 Amplification of Nitrogenase *nif*H gene

To test for putative nitrogen fixing bacteria, the approximately 400 bp nifH gene was PCR amplified (5''by nested using the primer sets FGPH19 TACGGCAARGGTGGNATHG-3') and PoIR (5'-ATSGCCATCATYTCRCCGGA-3') for the first PCR run and PoIF (5'-TGCGAYCCSAARGCBGACTC-3') and AQER (5'-GACGATGTAGATYTCCTG-3') primer sets for the second PCR run (Zhan and Sun, 2011). The reactions were carried out in an ESCO Swift™ MaxPro Thermal Cycler (Esco Group, Singapore). The reaction mixture for the first stage of nested PCR contained 12.5 μl DreamTag Green Master Mix 2× (ThermoScientific: Thermofisher, USA), 10.5 μl Nuclease-free Water, 0.5 µl of each primer at a concentration of 0.5 µM and 1 µl of Genomic DNA, totalling a volume of 25 μl (Dias *et al.*, 2012). The reaction conditions were as follows: pre-denaturation at 94°C for 4 min, 30 cycles of denaturation at 94°C for 1 min, annealing at 55°C for 1 min, extension at 72°C for 2 min and a final extension at 72°C for 5 min. The reaction mixture for the second stage of the nested PCR contained 12.5 μl DreamTaq Green Master Mix 2× (ThermoScientific: Thermofisher, USA), 10.5 μl Nuclease-free Water, 0.5 μl of each primer at a concentration of 0.5 μM and 1 μl of template from the first nested PCR stage, totaling a volume of 25 μl (Dias *et al.*, 2012). The reaction conditions were as follows: pre-denaturation at 94°C for 4 min, 30 cycles of elongation at 94°C for 1 min, annealing at 56°C for 1 min, extension at 72°C for 2 min and a final extension at 72°C for 5 min. Products were held at 4°C. The positive control strain used was *Enterobacter* sp and the negative control was nuclease free water. The products were visualized using a 1.2% agarose gel and 100 bp ladder (Dias *et al.*, 2012).

3.1.6 Screening for Secondary metabolite production:

3.1.6.1 Hydrogen cyanide (HCN) production

Endophytic bacteria isolates were screened for HCN production on TSA plates supplemented with glycine (4.4g/L). Using 24-hour old broth culture of the isolates, a loop-full of each isolate was streaked onto the plates. Whatman number 1 filter paper was soaked in 0.5% picric acid solution and then place on the underside of each Petri dish lid. Parafilm was used to seal the plates, which were then incubated for 5-7 days at 30°C (Freeman *et al.*, 1975). The cyanogenic potential was indicated by the change of colour in the filter paper from yellow to brown or reddish-brown (Allu, Kumar and Audipudi, 2014). Assays were carried out in triplicate.

3.1.6.2 Fluorescence production

Fluorescence production was determined using King's B agar (20 g Peptone, 1.5 g K₂HPO₄, 1.5 g MgSO₄, 20 g Agar, 1000 ml distilled water), (King, Ward and Raney, 1954). Endophytic bacteria were streaked on the plates. The plates were incubated for 48 hours at 28±2°C. After the incubation period, the plates were observed for fluorescence production under UV light (Allu, Kumar and Audipudi, 2014). Assays were carried out in triplicate.

3.2 Results and Discussion

Bacterial isolates were selected based on morphological features such as colour (red, yellow and white), colony size (small), and texture (smooth). A total of 20 endophytic bacterial isolates, that have plant growth promoting capabilities, were isolated from seeds of *Cleome gynandra* L. located in the four central northern regions of Namibia. It should however be noted the number of isolates is not a true reflection of the diverse microbial community as some microbes could be unculturable while others required specific enrichment media to grow (Kandjimi, Uzabakiriho and Chimwamurombe, 2015). Isolates were categorized by their traits. They elicited traits as follows (**Table 3.2**); 16 siderophore producers, 3 phosphate solubilizers, 20 IAA producers (**Appendix 2**), 17 ammonia producers, 6 hydrogen producers, 2 fluorescence producers and 8 nitrogen fixers.

3.2.1 *C. gynandra* bacterial seed endophyte isolation and identification

Seed endophytes have been isolated from various sources previously (Verma and White, 2017; Tyc *et al.*, 2020), however, no reports are available on the seed endophytes isolated

from Cleome gynandra. Through 16S rRNA sequence identification and the BLASTn search tool, this study's C. gynandra seed endophytic bacteria were identified and classified into five genera, namely Klebsiella, Enterobacter, Phytobacter, Kluyvera, Kosakonia (Table 3.3) Additional classification indicated that all isolates belonged to the phylum Proteobacteria, class Gammaproteobacteria, order Enterobacterales and family Enterobacteriaceae. A total of 80 isolates were initially isolated from C. gynandra seeds and only 20 isolates (five from each region) were selected based on their distinctive morphological traits and were further screened in vitro for a wide range of PGP traits. Tested PGP traits included nitrogen fixation, mineral phosphate solubilization, IAA production, siderophore production, ammonia production, hydrogen cyanide production and fluorescence production. The isolate that occurred most frequently in all the regions was Enterobacter cloacae. The isolates that were unique to each region were Klebsiella aerogenes (OSC-2) for Oshana region, Enterobacter mori (OHC-3) and Phytobacter ursingii (OHC-4) for Ohangwena region, Kluyvera cryocrescens (OKC-9) for Oshikoto region and Kosakonia sacchari (OMC-6) for Omusati region.

3.2.2 Phylogenetic analysis of 16S rRNA isolates

The most similar reference sequences with the highest homology, query coverage and the lowest E values were selected and aligned by the Clustal X program. An outgroup was not used because outgroups that do not have polymorphic sites matching up to the sequences increase the likelihood of conflict in the tree, which leads to incorrect root assignment (Wheeler, 1990; Huelsenbeck, Bollback and Levine, 2002) Phylogenetic analyses revealed that the majority (90%) of the endophytic isolates shared high sequence similarities (greater than 98%) with their identified relative species (**Table 3.3**). The

constructed tree (**Figure 3.4**) contains the closest related strains for each isolate. Isolates are shown to belong to the *Klebsiella*, *Enterobacter*, *Phytobacter*, *Kluyvera* and *Kosakonia* genera, which all fall under the Enterobacteriaceae family. A study conducted on soil bacterial communities in Mexico produced similar results as endophytic bacteria belonging to the *Proteobacteria* phyla were found to be one of the dominant phyla at 38% (Lüneberg *et al.*, 2018). However, studies conducted in arid environments have shown the presence of *Bacillus* (Marasco *et al.*, 2013; Soussi *et al.*, 2016). Its absence in this study could be due to soil properties not being conducive for its growth resulting in it being less abundant. Although the isolates displayed high identity similarities, a significant number of them had low bootstrap values. It can be concluded that the low values could be caused by the rate of evolution and mutation of their genes, unrelated sequences being aligned together or sequences being too similar.

3.2.3 Plant Growth Promoting Traits and Screening for Secondary Metabolites

The endophytic isolates were subjected to six tests to determine their plant growth promoting capabilities as presented in **Table 3.2**. Siderophore producing bacteria have evolved to develop specialized mechanisms to solubilize iron from organic substances, promote plant growth directly and indirectly by supplying plants with this solubilized iron and protect the host plant against pathogens (Arora, Tewari and Singh, 2013; Gupta *et al.*, 2015; Ferreira *et al.*, 2019). Findings from this study have shown that the production of iron-chelating was the most common plant growth promoting trait observed among 80% of the isolates, namely *K. aerogenes, K. grimontii, K. pneumoniae, E. cloacae, E. mori* and *K. sacchari*. Similar results were reported for bacterial genera *Pseudomonas, Enterobacter, Rhizobium* and *Bacillus* in the tobacco rhizosphere, where 85% of the

Ammani, 2013). Siderophores reduce the population of deleterious microorganisms which creates less competition for iron in the rhizosphere (Sharma *et al.*, 2003), making them more prevalent and giving them higher potential in the rhizosphere (Leong, 1986; Neilands and Leong, 1986). Plants from the Omusati region had the highest proportion (5/20) of siderophore producers whereas those from the Oshana region had the lowest at three. Plant samples from the Ohangwena and Oshikoto regions had four siderophore producers respectively.

Phosphate solubilizing plant growth promoting bacteria have garnered the attention of agricultural microbiologists as soil inoculants used to improve plant growth and yield because they enhance the availability of phosphorus to the plants (Bhattacharyya and Jha, 2012). From the four regions only three isolates (15% of all isolates), namely Enterobacter cloacae (OSC-1) from Oshana region, Klebsiella pneumonia (OKC-7) from Oshikoto region and Enterobacter cloacae (OMC-1) from Omusati region, formed solubilization halos on Pikovskaya medium. Isolates from Ohangwena region were unable to solubilize phosphate. Such a low percentage of isolates that show phosphate solubilization ability is not unique to our study as other studies also show limited numbers of 37% of microbes being able to solubilize phosphate (Sagar et al., 2018). The ability of plant growth promoting rhizobacteria strains to solubilize insoluble phosphorus (P) and convert it to plant-available form is an important characteristic under conditions where P is a limiting factor for crop production (Pradhan and Sukla, 2005; Khan, Zaidi and Wani, 2007; Ramesh et al., 2014). Studies have demonstrated that phosphate solubilizing endophytes have the potential to plant growth under drought conditions (Mapelli et al., 2013; Soussi et al., 2016). This may be considered a positive indicator of utilizing the microbes as biofertilizers for crop production and beneficial for sustainable agriculture (Walpola and Yoon, 2012).

IAA is the most studied auxin and there is strong evidence that IAA producing endophytes can increase and improve plant yield (Glick, 2012). Most microorganisms (80%) can detect IAA produced by plants (Patten and Glick, 1996) which can account for it being discovered in high percentages. In an attempt to better select endophytic isolates with high plant growth promotion potential traits, IAA production was tested. The results revealed that all 20 isolates had IAA producing capabilities. The 20 isolates produced IAA at varying concentrations, ranging from 0.1523 – 0.2921 µg IAA/ml⁻¹ (**Appendix 2**). Among endophytic strains, Enterobacter cloacae (OSC-5) and Phytobacter ursingii (OHC-4) outstood for producing significantly higher amounts of IAA compared to the other strains, with the highest amount (0.2921 µg IAA/ml⁻¹) coming from the Oshana region. The lowest amount was produced from Enterobacter cloacae (OKC-8) at 0.1523 μg IAA/ml⁻¹, isolated from the Oshikoto region (**Figure 3.3**). A study conducted on peppers grown under drought stress showed that 100% of endophytes were able to produce IAA (Marasco et al., 2012). Other studies showed that 89% of strains produced IAA, with the highest producing strains Agrobacterium and Rhizobium producing IAA above 7.8 µg IAA/ml⁻¹ (Khalid, Arshad and Zahir, 2004; El-deeb et al., 2012; Abbamondi et al., 2016), which is significantly higher than the amounts obtained in this study. Statistical analysis (Appendix 3) revealed a p-value of 0.000. Because the p-value is below the significant level of 0.05, it has been determined that there is a significant difference between the means. This could be a result of the rate at which each microbe can produce IAA. Ammonia producing endophytes provide a nutrient source for the host plant. Ammonia production is a trait that yielded the second number of positive producers with 17 out of 20 (85%) isolates testing positive. These isolates include *E. cloacae*, *K. pneumoniae*, *P. ursingii*, *K. cryoscrescens*, *K. grimontii* and *K. sacchari*. *Bacillus* strains isolated from maize produced similar rates of ammonia with 80% of them being producers (Agbodjato *et al.*, 2015). The highest number came from Oshikoto and Omusati region with five ammonia producers each while the lowest came from the Oshana region with only three producers.

The amplified nitrogenase *nifH* gene fragments were successfully amplified from the genomic DNA of 8 out of the 20 isolates with the expected length of ± 320 pairs. Four bacterial species were identified to contain the *nifH* gene using nested PCR and they were *Klebsiella aerogenes* (OSC-2), *Enterobacter cloacae* (OSC-5, OSC-3, OSC-1, OSC-7, OHC-2), *Klebsiella pneumoniae* (OHC-1) and *Kluyvera cryocrescens* (OKC-9). These bacteria are metabolically versatile and are found in a diverse range of environments (Pérez-Montaño *et al.*, 2014). They have been suggested as sugarcane endophytic plant promoters and nitrogen-fixing bacteria (Zhu *et al.*, 2013; Chen *et al.*, 2014). In previous studies and in the absence of chemical nitrogen fertilizers, *Klebsiella* showed nitrogen-fixing capabilities when it was inoculated into wheat in greenhouse and field experiments (Iniguez, Dong and Triplett, 2004). The use of nitrogen-fixing bacteria as an inoculant increased the average yield of sweet cherries by 21.7% (Esitken *et al.*, 2006) and increased dry weight and nitrogen content of roots, shoots and seedlings in sugarcane at a statistically significant 95% confidence level (Lin *et al.*, 2012).

Hydrogen cyanide (HCN) is a volatile secondary metabolite produced by deleterious rhizobacteria where it is used as a biocontrol against weeds and other plant pathogens (Kamei, Dolai and Kamei, 2014). HCN producing rhizobacteria have recently shown contributions to geochemical processes such as chelation of iron, which in turn increase

nutrient availability and thus indirectly improved plant growth (Rijavec and Lapanje, 2016; Sagar *et al.*, 2018). The Ohangwena, Oshikoto and Omusati regions yielded two hydrogen cyanide producers respectively, with Oshana region producing none. This is a low yield considering that a vast number of organisms can naturally produce hydrogen cyanide (Kamei, Dolai and Kamei, 2014). HCN producing endophytes in this study made up 30% of the isolates, and they belong to the *Enterobacter* and *Klebsiella* genera. A similar percentage (40%) was recorded for bacteria (*Bacillus, Pseudomonas, Enterobacter, Acinetobacter* and *Micrococcus*) isolated from beans (Kumar *et al.*, 2012). Fluorescence production brought in the lowest yield of results with only two isolates from the Ohangwena region, namely *Klebsiella pneumonia* (OHC-1) and *Phytobacter ursingii* (OHC-4), yielding positive results.

Fluorescence producing endophytes and their potential as inoculants have been realized as they were able to yield increased growth in chickpea, potato, sugar beet and radishes (Sivasakthi, Usharani and Saranraj, 2014). A similar report on a red chilli plant indicated that all tested bacteria (belonging to *Pseudomonas* genera) were able to produce fluorescence (Allu, Kumar and Audipudi, 2014).

The present study observed all isolates being able to elicit more than one plant growth promoting trait. *Enterobacter cloacae* (OMC-1) was able to display five plant growth promoting characteristics that correspond with reports that have shown *Enterobacter* spp. possess multiple plant growth promoting activities (Tsuda *et al.*, 2001; Hynes *et al.*, 2008; Khalifa *et al.*, 2016). Several strains of *Enterobacter cloacae* have been considered to be plant growth promoting rhizobacteria (Liu *et al.*, 2013). *E. cloacae* has been widely distributed in nature primarily being isolated from the rhizosphere and has shown nitrogen fixation abilities, with one specific strain displaying biocontrol potential against pathogens

found in corn and cucumbers (Hinton and Bacon, 1995). A study in India showed that *E. cloacae* has been recovered from a soybean rhizosphere and enhanced the soybean growth through the mobilization of phosphate (Ramesh *et al.*, 2014). The *Enterobacter cloacae* strain in this study displayed siderophore production, phosphate solubilization, ammonia production, hydrogen cyanide production and indole-3-acetic acid production. Arid ecosystems have diverse microbial communities that dwell within them (Soussi *et al.*, 2016). Endophytic bacteria found in this ecosystems are suggested to support and improve plant health and growth as well as make them resistant to abiotic stresses such as drought (Marasco *et al.*, 2012; Soussi *et al.*, 2016). Further clarification on factors that lead plant growth promoting bacteria to regulate drought resistance will allow for these bacteria to have better potential in biotechnology and agriculture (Marasco *et al.*, 2013; Soussi *et al.*, 2016).

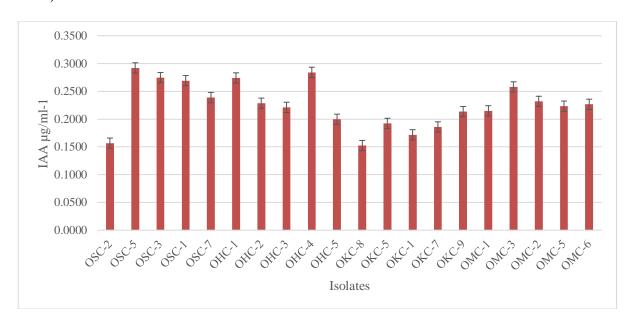


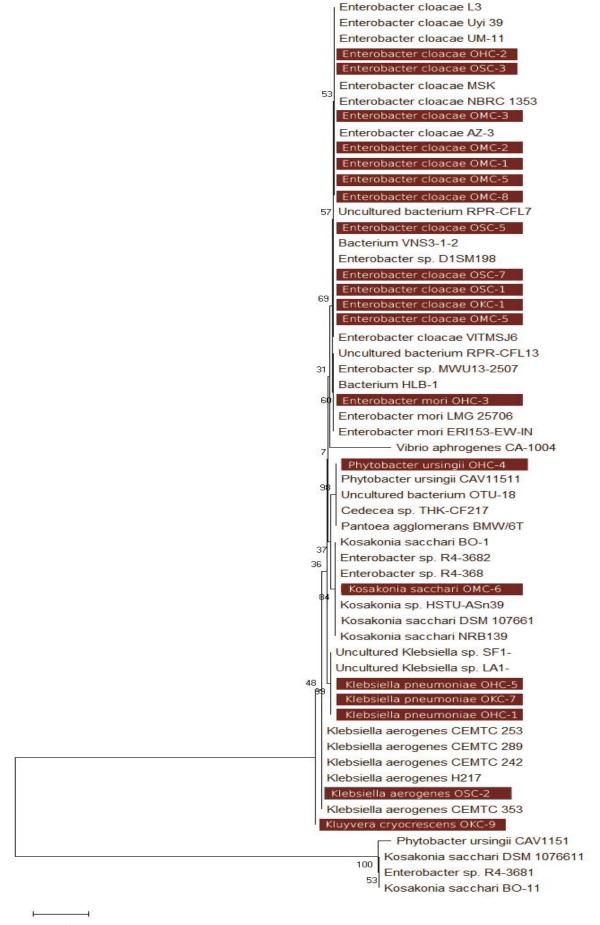
Figure 3.3: Average IAA production ($\mu g/ml^{-1}$) by isolated endophytes. Vertical bars indicate mean \pm SE.

 Table 3.2: Screening for PGP and secondary metabolite traits

Isolate	nifH	Siderophore Production	Phosphate Solubilization	NH3 Production	HCN Production	Fluorescence Production	IAA Production
Klebsiella aerogenes (OSC-2)	+	+	-		-	-	+
Enterobacter cloacae (OSC-5)	+	-	-	+	-	-	+
Enterobacter cloacae (OSC-3)	+	+	-	+	-	-	+
Enterobacter cloacae (OSC-1)	+	-	+	-	-	-	+
Enterobacter cloacae (OSC-7)	+	+	-	+	-	-	+
Klebsiella pneumoniae (OHC-1)	+	+	-	+	-	+	+
Enterobacter cloacae (OHC-2)	+	+	-	-	+	-	+
Enterobacter mori (OHC-3)	-	+	-	+	+	-	+
Phytobacter ursingii (OHC-4)	-	-	-	+	-	+	+
Klebsiella pneumoniae (OHC-5)	-	+	-	+	-	-	+
Enterobacter cloacae (OKC-8)	_	+	-	+	-	-	+
Enterobacter cloacae (OKC-5)	-	+	-	+	-	-	+
Enterobacter cloacae (OKC-1)	-	-	-	+	+	-	+
Klebsiella pneumoniae (OKC-7)	-	+	+	+	+	-	+
Kluyvera cryocrescens (OKC-9)	+	+	-	+	-	-	+
Enterobacter cloacae (OMC-1)	-	+	+	+	+	-	+
Enterobacter cloacae (OMC-3)	-	+	-	+	-	-	+
Klebsiella grimontii (OMC-2)	-	+	-	+	+	-	+
Enterobacter cloacae (OMC-5)	-	+	-	+	-	-	+
Kosakonia sacchari (OMC-6)	-	+	-	+	-	-	+

Table 3.3: Source of bacterial isolates and BLAST results of 16S rRNA

Isolate	Most Related Species	Percentage	Accession	Site Name	Region
Designation		Identity	Number		
OSC-2	Klebsiella aerogenes KCTC 2190	98%	NR102493.2	Omashekediva	Oshana
OSC-5	Enterobacter cloacae subsp. dissolvens	100%	NR044978.1	Eenghala	Oshana
	strain LMG 2683				
OSC-3	Enterobacter cloacae strain DSM 30054	99%	NR117679.1	Eenghala	Oshana
OSC-1	Enterobacter cloacae subsp. dissolvens strain ATCC 23373	99%	NR118011.1	Okathakiingodjo	Oshana
OSC-7	Enterobacter cloacae subsp. dissolvens strain LMG 2683	100%	NR044978.1	Onambango	Oshana
OHC-1	Klebsiella pneumoniae strain DSM 30104	98%	NR117686.1	Edimba	Ohangwena
OHC-2	Enterobacter cloacae strain DSM 30054	99%	NR117679.1	Edimba	Ohangwena
OHC-3	Enterobacter mori LMG 25706 strain	100%	NR116430.1	Omakangha	Ohangwena
	R18-2				
OHC-4	Phytobacter ursingii strain ATCC 27989	100%	NR159305.1	Omito	Ohangwena
OHC-5	Klebsiella pneumoniae strain DSM 30104	97%	NR117686.1	Omakatumbe	Ohangwena
OKC-8	Enterobacter cloacae strain DSM 30054	99%	NR117679.1	Omatyatya	Oshikoto
OKC-5	Enterobacter cloacae strain DSM 30054	99%	NR117679.1	Ompugulu	Oshikoto
OKC-1	Enterobacter cloacae subsp. dissolvens strain ATCC 23373	99%	NR118011.1	Onamungudo	Oshikoto
OKC-7	Klebsiella pneumoniae strain DSM 30104	97%	NR117686.1	Ekuku	Oshikoto
OKC-9	Kluyvera cryocrescens strain NBRC 102467	99%	NR114108.1	Ekuku	Oshikoto
OMC-1	Enterobacter cloacae strain DSM 30054	99%	NR117679.1	Uukwalumbe	Omusati
OMC-3	Enterobacter cloacae strain DSM 30054	99%	NR117679.1	Epato	Omusati
OMC-2	Enterobacter cloacae strain ATCC 13047	99%	NR102794.2	Okapa	Omusati
OMC-5	Enterobacter cloacae subsp. dissolvens strain ATCC 23373	99%	NR118011.1	Omatembu	Omusati
OMC-6	Kosakonia sacchari strain SP1	98%	NR118333.1	Omatembu	Omusati



0.10

Figure 3.4: A neighbor-joining phylogenetic tree based on 16S rRNA gene sequences of endophytic seed bacteria (isolates are labelled according to their designation from Table 3.4 and are highlighted in red). Bootstrap confidence values were obtained with 1000 replicates and bootstrap values of more than 50% are shown at branch points. The scale bar represents the observed number of substitutions per nucleotide site (0.10).

Namibia is an arid country that is characterized by extreme ecological environments to which plants have to adapt (Mendelsohn et al., 2002). Organisms such as plants and bacteria that thrive in such extreme conditions adopt mechanisms and survival strategies to alleviate abiotic stresses (Soussi et al., 2016). These conditions will therefore select endophytes that would help them curb or mitigate these types of stresses from generation to generation (Marasco et al., 2012, 2013). Plant growth promoting bacteria are important components of sustainable agriculture as they are cost-effective, safe and can enhance plant growth and yield (Glick, 2012; Blaszczyk et al., 2014). Direct and indirect benefits of plant growth promotion have been reported to be successful due to the presence of endophytic seed bacteria (Magnani et al., 2010; Mercado-Blanco and Lugtenberg, 2014). Research findings in this study are in agreement with other research conducted on isolated strains and their plant growth promoting potential. Strains that can display multiple traits are more desirable for agricultural use as bioinoculants, biocontrol agents and biofertilizers. The correct selection of isolates being used as inoculants is crucial. Strains should be tested for effectiveness through plant growth promotion activity. To ensure the selected endophytes are safe to use and will not invade the environment or other plants, tests can be done in early product development to exclude pathogenic microorganisms (Berg, 2009). Enterobacter cloacae (OMC-1), Klebsiella pneumonia (OHC-1) and Kluyvera cryocrescens (OKC-9) were the three isolates that displayed the most diverse and highest amount of plant growth promoting traits. Evidence of plant growth promoting

activity indicates that these isolated strains can successfully improve overall plant health and improve crop yield (Ryan *et al.*, 2008). Cost-effective production systems using inexpensive materials (Visnovsky *et al.*, 2008) and food industry by-products (Costa *et al.*, 2001), make microbial inoculants an economically feasible option to chemical fertilizers (O'Callaghan, 2016). Endophytic seed bacteria isolated in this study need to be further studied for prospective agricultural applications.

3.3 Conclusion

This study revealed that *Cleome gynandra* L. seeds harbour endophytes. Twenty bacterial isolates were isolated from *C. gynandra* seeds obtained from the Oshana, Omusati, Ohangwena and Oshikoto regions respectively. The isolated endophytes (100%) displayed plant growth promoting traits including siderophore production, phosphate solubilization, indole-3-acetic acid production, ammonia production, hydrogen cyanide production, fluorescence production and nitrogen fixation. All isolates belong to the *Proteobacteria* phylum. The lack of genetic diversity could be attributed to abiotic stresses that prevented other microbes from thriving and being more abundant. It can be concluded that findings from this study have highlighted that endophytic seed bacteria have potential application in sustainable agriculture methods. The understanding of the plant growth potential of the endophytes in this study will provide the information required for future commercialization. Further research and development on all plant growth promoting seed endophytes and their interactions are required.

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CHAPTER 4

CLEOME GYNANDRA L. SEED ENDOPHYTES PROMOTE RAPE (BRASSICA NAPUS L.) SEEDLING GERMINATION RATE, PLANT GROWTH AND LEAF YIELD

Abstract

Endophytic seed bacteria have been considered for agricultural applications as they are known to elicit plant growth promoting traits such as nitrogen fixation, siderophore production, phosphate solubilization, fluorescence production, hydrogen cyanide and indole-3-acetic acid (IAA) production. They improve plant health, growth and potentially increase the plant yield. Endophytic bacteria have recently garnered attention as potential bioinoculants. Few studies have tested them in this application and developed them for commercial use. The objective of this study was to evaluate the effects of microorganismbased bio-fertilizers in single, double and triple strain combinations isolated from *Cleome* gynandra L. on the domesticated crop Brassica napus L. (Rape English Giant). Endophyte strains used in this study were, Enterobacter cloacae, Klebsiella pneumoniae and Kluyvera cryocrescens. Plant growth parameters observed were wet mass, dry mass, chlorophyll readings, root length, plant height and leaf yield. There was a statistically significant difference for plant height (p=0.037), root length (p=0.024), and wet (p=0.000) and dry (p=0.000) mass between the treatments. The post hoc LSD test determined that the single strain (K. pneumoniae) and triple strain combination (E. cloacae, K. pneumoniae and K. cryocrescens) performed the best against the other treatments, controls and in all growth parameters. This study concluded that C. gynandra seeds contain endophytic bacteria with the potential to improve plant growth for the production of rape seed and could be used as inoculants to establish a sustainable crop production system.

Keywords: commercialization, endophytic seed bacteria, plant growth promotion, seed inoculant, yield enhancing

Introduction

Endophytes are organisms that occur and interact within intracellular or intercellular plant tissue (Schulz and Boyle, 2006; Reinhold-Hurek and Hurek, 2011; Cocq *et al.*, 2017). Those plant tissues include roots, stems, leaves, fruits and seeds (Rosenblueth and Martínez-romero, 2006; Hardoim *et al.*, 2012; White *et al.*, 2017). Endophytes have been investigated for their potential plant growth promoting properties and their fitness to biotic and abiotic stress (Araujo *et al.*, 2008; Mercado-Blanco and Lugtenberg, 2014). There is an increasing body of evidence that suggests that seed endophytes are of interest as they have shown plant growth, enhanced plant tolerance to biotic and abiotic stresses and enhanced plant defence mechanisms (Reinhold-Hurek and Hurek, 2011; Truyens *et al.*, 2014; Shahzad *et al.*, 2018).

Plant growth promoting endophytes have been utilized to stimulate plant growth through the production of auxins, secondary metabolites and through direct and indirect mechanisms of action (Bhattacharyya and Jha, 2012; Vejan *et al.*, 2016). Mechanisms of action in this study include (i) nitrogen fixation and ammonia production to increase nitrogen availability for plant uptake (Gabriela *et al.*, 2015); (ii) production of volatile secondary metabolites in particular hydrogen cyanide, to improve overall plant growth (Ryu *et al.*, 2003); (iii) production of auxin indole-3-acetic acid to regulate plant growth (de Souza, Ambrosini and Passaglia, 2015); (iv) production of siderophores to make iron available in the soil for plant uptake (Flores-Felix, Silva and Rivera, 2015); (v) production of fluorescence to inhibit plant pathogens (Arora, Khare and Oh, 2008); (vi) phosphate solubilization to increase the availability of phosphate for plant uptake (Wani, Khan and Zaida, 2007). Plant growth promoting bacteria have shown potentiality to confer resistance to water stress in tomatoes (Mayak, Tirosh and Glick, 2004). A study

conducted on peppers showed that endophytes have plant growth promoting traits that perform in synergy, which allowed the plant to be drought-resistant under water stress (Marasco *et al.*, 2013).

Farming practices require the use of costly and harmful chemical fertilizers to sustain the high yield needed to keep up with the demand for agricultural produce (Sansanwal *et al.*, 2017; Trivedi *et al.*, 2018). Researchers have shown an interest in organic agricultural approaches in farming (Orhan *et al.*, 2006; Glick, 2012; de Souza, Ambrosini and Passaglia, 2015). Endophytes have been used successfully as biofertilizers, to improve plant growth and sustain plant and soil health (Orhan *et al.*, 2006; Kalayu, 2019). The best method for endophytes being applied to agricultural systems has not been established, however, reports have shown that using endophytes as soil or seed inoculants has been successful (Cocq *et al.*, 2017; Murphy, Doohan and Hodkinson, 2018). Endophytic inoculants have been noted to increase nitrogen uptake, nodulation, growth and yield of crops (Bhattacharyya and Jha, 2012). In comparison to well-studied rhizosphere, seed endophytes are poorly understood (Cankar *et al.*, 2005).

Cleome gynandra L., also commonly known as the Cat's Whisker, is an indigenous, wild and underexploited leafy green vegetable (Guarino, 1997; Wasonga et al., 2015; Kujeke, Edziwa and Icishahayo, 2017). It grows on a wide range of soils but thrives on well-manured, fertile soil (van Rensburg et al., 2007; Shilla et al., 2019). Its status of being a weed causes the plant to be neglected and prevents the crop from being improved for breeding (higher leaf yield, longer vegetation growth period) (Chweya and Mnzava, 1997; Chataika et al., 2020). C. gynandra has been reported to be highly nutritious and possessing insecticidal properties (Chweya and Mnzava, 1997; Abukutsa-Onyango, 2007). Despite its limitations such as producing a low yield (Chweya and Mnzava, 1997),

Cleome's seeds have shown the potential to harbour plant growth promoting endophytes. This makes *C. gynandra* seed endophytes suitable candidates to serve as seed inoculants. Rape English Giant (*Brassica napus* L.) is an annual leafy vegetable crop that is considered a profitable agricultural enterprise worldwide (Loehr, Seif and Nyambo, 1998; Kuntashula *et al.*, 2004). Its leaves are rich in ascorbic acid, thiamine and vitamin A (Ganya, Svotwa and Katsaruware, 2018). It grows in a wide variety of soils, has a short growing season and has a high water demand due to its large leaf surface area (Walton *et al.*, 1999; Ganya, Svotwa and Katsaruware, 2018).

The *Brassica* genus belongs to the *Brassicaceae* family (Rieger, Preston and Powles, 1999). This family is a near relative to the *Capparaceae* family to which *C. gynandra* belongs (Chweya and Mnzava, 1997). Because they are such close relatives, Rape English Giant was deemed a suitable candidate for the greenhouse trials in the present study. This study aimed to test the effectiveness of using plant growth promoting bacteria (PGPB) isolated from *Cleome gynandra* L. seeds as a seed inoculant with the potential to enhance in vivo growth of the domesticated crop *Brassica napus* L.

4.1 Materials and Methods

4.1.1 Research Site Location

The experiment was carried out from May 2019 to July 2019 at the University of Namibia's Greenhouse Facility (22.6122°S, 17.0584°E). The altitude of the location is 1655 m above sea level with average greenhouse temperatures ranging from 15 to 32 °C. No rainfall was recorded during the experiment.

4.1.2 Bacterial Isolation and Screening for Plant Growth Promoting Traits

Protocol for isolation and screening of plant growth promoting traits has been outlined in chapter 3.

4.1.3 Bacterial Inoculum and Treatment Preparation:

4.1.3.1 Bacterial Strains and Inoculant Preparation

Three bacterial strains isolated from *Cleome gynandra* L. seeds exhibiting several plant growth-promoting traits (**Table 4.1**) were used in this study. The bacterial cultures were subjected to the McFarland's method for turbidity. Prepared McFarland solution (BaCl₂ (0.048M, 0.5 ml) was added to 99.5 ml of 0.18M H₂SO₄) was read in a spectrophotometer at the wavelength of 625nm. Three selected bacterial strains were inoculated in sterile nutrient broth and incubated at 28°C for 24 hours. The turbidity of the bacterial cultures were read in a spectrophotometer at 625 nm and adjusted to the 0.5 McFarland scale (Lwin *et al.*, 2012; Eduardo *et al.*, 2018).

Table 4.1: Bacterial isolates and the plant growth promoting traits they display.

Isolate	PGP Trait
Enterobacter cloacae	Siderophore production, Phosphate solubilization, NH ₃ production, HCN
	production, IAA production
Klebsiella pneumoniae	nifH, Siderophore production, NH ₃ production, Fluorescence production,
	IAA production
Kluyvera cryocrescens	nifH, Siderophore production, NH ₃ production, IAA production

 NH_3 = Ammonia HCN = Hydrogen cyanide IAA = Indole-3-acetic acid nifH

= Nitrogen fixation

4.1.3.2 Treatments

Isolates were selected based on several plant growth promoting traits (**Table 4.1**). Three bacterial strains, namely, *Enterobacter cloacae* (OMC-1), *Klebsiella pneumoniae* (OHC-1) and *Kluyvera cryocrescens* (OKC-9), were chosen as treatments for the pot experiment based on their performance amongst multiple (more than three) plant growth promoting

properties. Strains were used in a singular and consortia form (**Table 4.2**). Treatments were arranged in a randomized complete block design with nine blocks and three replicates.

Table 4.2: Treatments used for experiment.

Treatment Label	Treatment
T_1	A (Enterobacter cloacae)
T_2	B (Klebsiella pneumoniae)
T_3	C (Kluyvera cryocrescens)
T_4	AB
T_5	AC
T_6	BC
T_7	ABC
T_8	Water
T ₉	Fertilizer (Nuleaf Organic Fertilizer)

4.1.3.3 Effect of Endophytic Bacterial Inoculation on Rape Seed

Germination and Mean Germination Time

Sterile Whatman no. 1 filter paper was placed in sterile petri dishes and labelled according to each treatment. Endophytes were grown in 10 ml of nutrient broth for 24 hours at 28°C. Each bacterial treatment (0.5 ml) was added to 1.5 ml of distilled water to moisten the filter paper. Starke Ayres® Nutrifeed (0.5 ml) in combination with 1.5 ml distilled water was used as a positive control (T9) and 2 ml of distilled water was used as a negative control (T8). Using sterile forceps, seeds (five), were gently placed and spread into petri dishes. The time for this step was recorded (08H00). The petri dishes containing the seeds were placed in a dark cupboard at room temperature. Aseptic measures such as sterilization of all equipment were used to avoid contamination. The filter paper was moistened with 1 ml of distilled water every 12 hours. Germination percentage

(Germination Percentage = seeds germinated/total seeds \times 100) was recorded every 24 hours for 6 days as described by Manmathan and Lapitan (2013).

4.1.3.4 Effect of Endophytic Bacterial Inoculation on Growth

Starke Ayres ® Rape English Giant seeds were inoculated with 50 ml of each bacterial treatment. The seeds were left to soak in the treatment for 24 hours after which the seeds were drained. Five seeds were sown into equally measured, soil filled plant pots at 1 cm depth (Lwin *et al.*, 2012).

4.1.3.5 Pot Trial Experiment of *C. gynandra* Seed Endophyte as Seed

Inoculants

In this experiment, plants pots (12 cm x 9 cm) were sterilized using a bleach solution and filled with approximately 222 g of dry soil. The pots were arranged in a randomized complete block design with three replicates for each treatment, totalling 310 pots in the greenhouse. Each treatment was applied directly to the seeds. Plants were watered daily with equal amounts of water (approximately 250 ml). The temperature was measured daily for the duration of the experiment. Chlorophyll concentration readings were measured every three days, on the fourth youngest leaf on the main stem after the leaves emerged (± 20 days after germination) using the Konica Minolta Chlorophyll Meter SPAD-502Plus (Konica Minolta Inc, Japan). After 45 days, fresh mass, root length, and leaf yield were determined and compared. The plants were then dried at 70°C for six hours and weighed to determine the dry mass (Lwin *et al.*, 2012).

4.1.4 Data Analysis

Growth parameter measurements were recorded on the same day to avoid any differences based on the developmental stages of the plants' growth. The collected data were subjected to multivariate analysis of variance (MANOVA) using IBM® SPSS® Statistics software (Corp, 2019). The means were separated using post hoc LSD at a 0.05 significance level.

4.2 Results and Discussion

4.2.1 Germination Assay

A positive germination percent is considered to be 99% and above (Lwin *et al.*, 2012). In this study, T₁ (*E. cloacae*), T₄ (*E. cloacae*; *K. pneumoniae*), T₇ (*E. cloacae*; *K. pneumoniae*; *K. cryocrescens*) and T₈ (Negative control) displayed the highest positive effect on germination with all of them having a germination percent of 100%. Treatment 5 (*E. cloacae*; *K. cryocrescens*), 6 (*K. pneumoniae*; *K. cryocrescens*), and 9 (Positive control) yielded the lowest results with a germination percent of 87% indicating that these treatments neither promoted nor inhibited the germination rate.

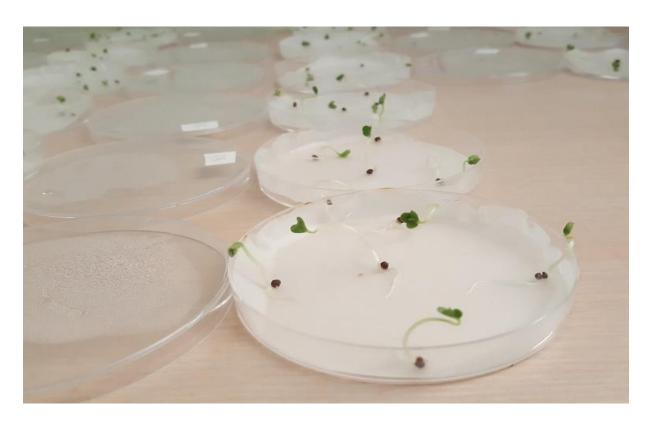


Figure 4.1: Germination assay.

 Table 4.3: Germination Percent of Each Treatment.

Treatments	Germination Percent
$T_1(E.\ cloacae)$	100%
$T_2(K. pneumoniae)$	93%
T_3 (K. cryocrescens)	93%
T ₄ (E. cloacae; K. pneumoniae)	100%
T ₅ (E. cloacae; K. cryocrescens)	87%
$T_6(K. pneumoniae; K. cryocrescens)$	87%
T ₇ (E. cloacae; K. pneumoniae; K.	100%
cryocrescens)	
T ₈ (Water) Control	100%
T ₉ (Fertilizer) Control	87%

4.2.2 Pot Trial Experiment and Plant Growth Parameters

Final harvest of plants was done after 45 days where root length, plant height, leaf yield and fresh mass were recorded. The expected time frame for germination was four days. Treatments T_1 (*E. cloacae*) to T_7 (*E. cloacae*; *K. pneumoniae*; *K. cryocrescens*) were able

to germinate within two days. This is an indication that the selected microbes were able to increase the germination rate by 50%. This could be due to the rate of colonisation that different endophytes possess. Treatments in this study have shown the ability to have a positive effect on the germination rate on a domesticated crop. All the isolated strains resulted in significantly higher germination rates with a 50% improvement under the following single and combination treatments: T₁ (*E. cloacae*), T₄ (*E. cloacae*; *K. pneumoniae*), T₇ (*E. cloacae*; *K. pneumoniae*; *K. cryocrescens*) and T₈ (Negative control). The leaves grew in a pattern of three folioles per stalk with T₇(*E. cloacae*; *K. pneumoniae*; *K. cryocrescens*) producing the largest leaf size. All inoculated treatments recorded higher leaf number in comparison to uninoculated controls except for T₇ (*E. cloacae*; *K. pneumoniae*; *K. cryocrescens*). There was an increase in the root length from the treatments in comparison to the controls. T₂ (*K. pneumoniae*) had the highest value for root length at 21.21 cm, recording an increase of 3% more than the controls, while the lowest value went to T₈ at 13.36 cm (**Table 4.4**).

There was an increase in the root length from the treatments in comparison to the controls. However, the bacterial treatments were not able to increase the plant height when compared to the positive and negative controls (**Table 4.4**). The lowest value for plant height was recorded as 19.47 cm for T_8 , whereas the highest value for plant height was 25.59 cm for $T_7(E.\ cloacae; K.\ pneumoniae; K.\ cryocrescens)$. The results for plant height are in agreement with a study conducted Zahir *et al.*, (2010). The bacterial treatments were not able to increase the chlorophyll levels when compared to the positive and negative controls (**Figure 4.3**), however, $T_7(E.\ cloacae; K.\ pneumoniae; K.\ cryocrescens)$ produced the highest values at 6% on day one, four and ten and 7% on day seven, while T_1 (*E. cloacae*) yielded the lowest values overall. This is supported by findings from

previous research done by Yildirim et al., (2011) on broccoli. The negative control had higher levels of chlorophyll in comparison to the positive control and microbial treatments. This could be attributed to the negative control synthesizing more chlorophyll in order to absorb more light. Results show that the positive control produced the highest amounts for wet and dry mass, in comparison to the microbial treatments. Although most microbial treatments scored significantly lower than the control, treatment T₄ (E. cloacae; K. pneumoniae) was able to produce amounts 30% lower for wet mass and 10% lower for dry mass respectively. The negative control had a higher wet mass in comparison to some microbial treatments. This could be due to its nitrogen levels, which have been linked to increased wet mass. Research on Cleome gynandra L., has seen an increase in wet and dry mass with an application of a nitrogen rich fertilizer (Ng'etich, Aguyoh and Ogweno, 2012). The results presented from the previous study are similar to the present study as wet and dry mass amounts were highest in T₉ (Positive control) which was a nitrogen containing fertilizer. Single strain Klebsiella pneumoniae (T₂), as well as consortia of and combination strains Enterobacter cloacae and Kluyvera cryocrescens (T₅) were able to increase the relative yield of multiple growth parameters in comparison to the positive and negative control (**Table 4.4**). The maximum effect on all growth parameters was observed on the combination treatment T₇ (E. cloacae; K. pneumoniae; K. cryocrescens). This could be due to their synergistic effects amongst each other, which could in turn indirectly improve the plant growth. In a report conducted by Iniguez, Dong and Triplett (2004), Klebsiella, a known nitrogen-fixing bacteria (Wei et al., 2014), was reported to increase chlorophyll levels, plant height and root and shoot weight in wheat plants under greenhouse conditions, which thus supports the results in this study. Enterobacter cloacae, Klebsiella pneumoniae and Kluyvera cryocrescens are endophytic bacteria that have been reported to possess multiple plant growth promoting activities (Chelius and Triplett, 2000; Khan, Zaidi and Wani, 2007; Tian *et al.*, 2009; Singh, 2013; Khalifa *et al.*, 2016). Some inoculants that had negative effects or no effect on growth parameters could be attributed to the production of phytotoxins that inhibited plant growth (Brown and Rovira, 1999).

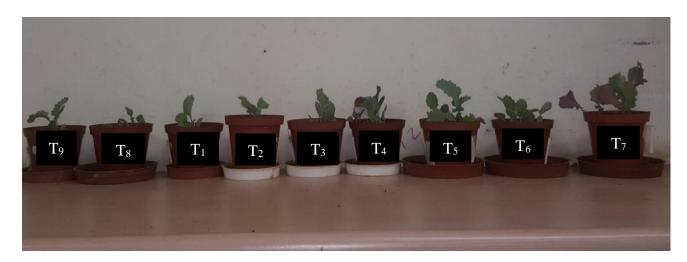
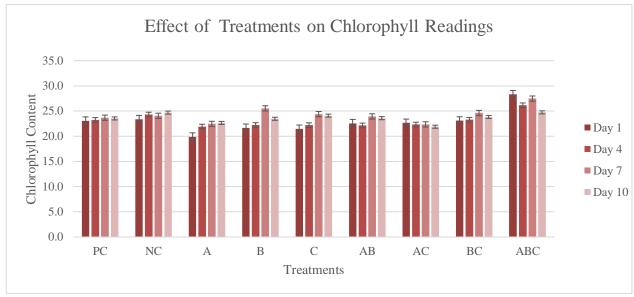


Figure 4.2: Displaying the effects of each treatment on plant growth.



PC = Positive Control (Fertilizer)

NC = Negative Control (Water)

 $\mathbf{A} = Enterobacter\ cloacae$ $\mathbf{B} = Klebsiella\ pneumoniae$

 $\mathbf{C} = Kluyvera\ cryocrescens$

Figure 4.3: The effects of each treatment on chlorophyll content. Vertical bars indicate the mean \pm SE.

Table 4.4: Comparison of treatment effects on leaf number, root length, plant height, wet mass and dry mass.

Treatment	Leaf Number	Root Length (cm)	Plant Height (cm)	Wet Mass (g)	Dry Mass (g)
T_1	15.10±3.62	15.73±3.36	21.83±3.64	1.59±0.99	0.71±0.59
T_2	12.77 ± 3.80	21.21±32.97	21.21±3.76	1.09 ± 0.53	0.48 ± 0.27
T_3	15.03±4.16	15.89 ± 4.24	22.69±5.31	1.28 ± 0.66	0.45 ± 0.28
T_4	16.30±3.33	16.60 ± 4.02	22.76±4.27	3.18±1.42	1.10 ± 0.63
T_5	15.23±2.99	13.76±3.83	22.15±4.12	2.98 ± 1.34	0.86 ± 0.47
T_6	14.60±4.21	16.46 ± 2.86	23.85 ± 2.74	2.68±1.10	0.94 ± 0.46
T_7	6.40 ± 2.46	17.44 ± 2.93	25.59 ± 3.26	2.67 ± 1.90	0.89 ± 0.67
T_8	8.85 ± 4.04	13.36±4.01	19.47±4.96	2.15±1.50	0.34 ± 0.28
T ₉	8.21±3.41	17.09±4.18	23.80±4.66	5.18±2.89	1.22±0.70

Data are presented as mean±standard deviation

 $T_1 = A$ (Enterobacter cloacae)

 $T_6 = BC$

 $T_2 = B$ (Klebsiella pneumoniae)

 $T_7 = ABC$

 $T_3 = C$ (Kluyvera cryocrescens)

 Γ_8 = Water (Negative

Control)

 $T_4 = AB$ $T_9 = Fertilizer (Positive Control)$ $T_5 = AC$

A test of normality determined that plant height was the only collection of data that were normally distributed based on the examination of its normal Q-Q plots (**Appendix 3**). All the data collected were subjected to a multivariate analysis of variance (MANOVA) (Appendix 3). Multivariate analysis has been used to identify and analyze multiple important traits of different bacterial species in previous studies (Al Khanjari et al., 2008; Yada et al., 2010), which has also been done in the present study. It was determined that there was a significant difference for root length (p = 0.024), plant height (p = 0.037), wet mass (p = 0.000) and dry mass (p = 0.000). In the case of the leaf number, T_7 (E. cloacae; K. pneumoniae; K. cryocrescens) was the only one to indicate that it had no significant (p = 0.092) effect on the number of leaves yielded in comparison to the positive control. T₅ (E. cloacae; K. cryocrescens) was the only inoculant that significantly promoted root length in comparison to the other inoculants and controls. Inoculant T₆ showed significance with regards to plant height. Treatment T_2 (K. pneumoniae) and T_3 (K. cryocrescens) had the highest means for wet mass compared to the other treatments and controls. Treatment T_3 (*K. cryocrescens*) showed that there was no significant difference (p = 0.059) compared to the negative control for dry mass while T₄ (E. cloacae; K. pneumoniae), T_6 (K. pneumoniae; K. cryocrescens) and T_7 (E. cloacae; K. pneumoniae; K. cryocrescens) displayed no difference against the positive control. All treatments showed that there was no significant difference in chlorophyll readings with regards to the positive and negative control. Treatments with the best overall performance were T_2 (K. pneumoniae) and T₇ (E. cloacae; K. pneumoniae; K. cryocrescens) which was determined by the post hoc LSD test (Hilton and Armstrong, 2006) (**Appendix 3**).

The primary goal of agriculture is to produce high quality, safe and affordable food for the increasing world population (Avis et al., 2008; Backer et al., 2018). An emerging trend in agriculture has seen chemical fertilizers being replaced with microbial counterparts to reduce health concerns (Conn and Franco, 2004; Timmusk et al., 2014; Kalayu, 2019). The best strategy for endophyte application in agriculture systems is not known (Cocq et al., 2017). The use of microbes as seed inoculant under field trials and greenhouse conditions has been documented in many studies, reporting these bacteria to produce plant growth regulators (Ozturk, Caglar and Sahin, 2003; Zahir, Arshad and Frankenberger, 2004) and have promising agronomic potential as seed inoculants (Zaida et al., 2009; Minaxi et al., 2012; de Souza, Ambrosini and Passaglia, 2015). The use of microbial inoculation has been successful in sugar cane (Silva et al., 2012), however, field efficacy has not been thoroughly studied. Interactions between plant growth promoting bacteria and plants are not well understood, with regards to field applications and different environments (Niranjan, Shetty and Reddy, 2005). In some cases, it has been unsuccessful due to problems with the establishment of biological agent and other uncontrollable variables (O'Callaghan, 2016; Cocq et al., 2017). Availability of more information will enable the development and acceptance of new agricultural technologies which can improve plant development (Akanbi et al., 2007). Determining the behaviour of endophytes under different conditions is critical to understanding their life cycle in order to assess their risk of becoming pathogenic, through shifts in abiotic conditions or adaptation to the new host. (Redman, Dunigan and Rodriguez, 2001; Robinson et al., 2016). Based on previous research (Murphy, Doohan and Hodkinson, 2018; Shahzad et al., 2018), the improved growth parameters evaluated in this study could be attributed to the plant growth promoting capabilities of the microorganisms selected. The information provided in this study looks to contribute to the understanding of endophytes and how they can be applied to efficient agricultural systems.

4.3 Conclusion

This study provided evidence that *Cleome gynandra* L. seeds from Oshana, Omusati, Ohangwena and Oshikoto regions respectively, harbour bacterial endophytes with several plant growth promoting traits and can serve as seed inoculants on domesticated crops. Findings from this study have confirmed that *C. gynandra* endophytic seed bacteria have promising potential as seed inoculants. They have displayed capabilities to improve the leaf number, plant height, root length and increase the germination rate of *Brassica napus* L. seeds. It is recommended that more greenhouse experiments and field trials are required to understand the endophytes capabilities and contribute to the commercialization of the bacterial strains.

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CONCLUSION

Many endophytes associated with plants are known to confer plant growth promoting traits. This thesis revealed that *Cleome gynandra* L. seeds collected from the Oshana, Omusati, Ohangwena and Oshikoto regions respectively, harbour endophytes. Twenty bacterial isolates possessing plant growth promoting and secondary metabolite producing capabilities were isolated from *C. gynandra* seeds. The endophytes (excluding *Phytobacter ursingii*) belong to the *Proteobacteria* phyla and their importance as plant growth promoters can be deduced from all the research published to date. Although

research suggests beneficial microorganisms are essential to agriculture, only a few microorganisms have been used as seed treatments/inoculants. As bio-inoculants, seed endophytes can improve the overall health and growth of plants. Bacterial strains in this study have shown the ability to serve as seed inoculants on the domesticated crop Brassica napus L. (Rape English Giant), which is a phylogenetic relative of C. gynandra. They were able to increase the germination rate by 50% as well as have an effect on plant height, root length and leaf number. Further investigations and greenhouse/field trials are required to ensure that endophytic bacteria from this study can be commercialized and applied as bioinoculants. The use of endophytes that are native to plant and soil types in indigenous crops in Namibia should be encouraged in order to move towards protecting current natural resources and provide environmental sustainability. They could contribute to sustainable, cost effective and more environment-friendly methods of agriculture. Although endophytes can be mass produced and are suited for biotechnological application, studies only focus on culturable endophytes (Mercado-Blanco and Lugtenberg, 2014). There are still knowledge gaps on seed endophytes and their mechanisms. With a more in-depth understanding of bacterial seed endophytes, current and future scientists will be able to unlock the biotechnological potential of plant-microbe interactions and open them to a host of new applications. The process of commercialization requires the isolation of strains, screening, mass production, industry linkage, quality control and field efficacy testing (Nandakumar et al., 2001). Successful commercialization would depend on the linkage between scientific academic bodies, industries (Nakkeeran, Fernando and Siddiqui, 2005) and government bodies. This thesis serves as a reference for future research and development on all plant-growth promoting seed endophytes and their interactions pertaining to *Cleome gynandra* L.

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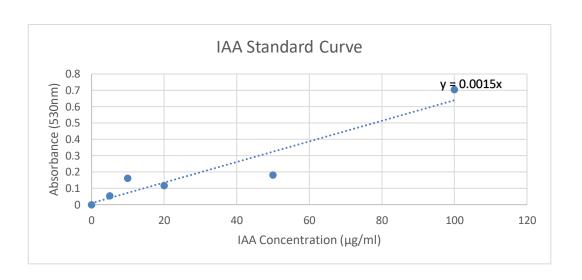
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Appendices

Appendix 1

IAA standard curve graph.



Appendix 2

 Table 1:
 Screening for IAA production

Isolate	Replicat	es (Absorb	oance=530)	Average	Standard	IAA Producer
	1	2	3		Deviation	
OSC-2	0.2153	0.1168	0.1376	0.1572	± 0.0512	+
OSC-5	0.2659	0.3086	0.3018	0.2921	± 0.0229	+
OSC-3	0.2747	0.2819	0.2674	0.2747	± 0.0073	+
OSC-1	0.2125	0.3349	0.2599	0.2691	± 0.0617	+
OSC-7	0.2329	0.248	0.2353	0.2387	± 0.0081	+
OHC-1	0.1963	0.2985	0.3274	0.2741	± 0.0689	+
OHC-2	0.2092	0.2335	0.2428	0.2285	± 0.0173	+
OHC-3	0.2077	0.2157	0.2397	0.2210	± 0.0167	+
OHC-4	0.2295	0.307	0.3156	0.2840	± 0.0474	+
OHC-5	0.234	0.18	0.1848	0.1996	± 0.0299	+
OKC-8	0.165	0.1529	0.139	0.1523	±0.0130	+
OKC-5	0.1965	0.2122	0.168	0.1922	±0.0224	+
OKC-1	0.1948	0.144	0.1762	0.1717	± 0.0257	+
OKC-7	0.2013	0.1653	0.1911	0.1859	±0.0186	+
OKC-8	0.2566	0.1916	0.1922	0.2135	±0.0374	+
OMC-1	0.2296	0.2083	0.2066	0.2148	±0.0128	+
OMC-3	0.2575	0.2473	0.2689	0.2579	±0.0108	+
OMC-2	0.2317	0.2249	0.2389	0.2318	± 0.0070	+
OMC-5	0.3069	0.1891	0.1737	0.2232	± 0.0729	+
OMC-6	0.256	0.2017	0.2222	0.2266	±0.0274	+

Appendix 3
Statistical analysis data generated from SPSS software

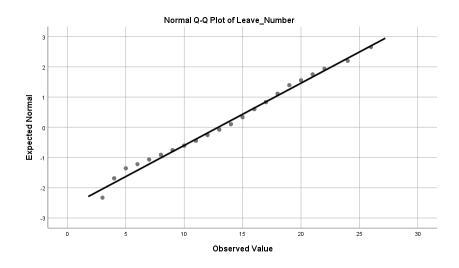
Overall Normality Test

Tests of Normality

	Kolmogorov-Smirnov ^a			Shapiro-Wilk		
	Statistic	df	Sig.	Statistic	df	Sig.
Leave_Numbe	.087	250	.000	.979	250	.001
r						
Root_Length	.255	250	.000	.244	250	.000
Plant_Height	.040	250	.200*	.995	250	.603
Wet_Mass	.168	250	.000	.844	250	.000
Dry_Mass	.156	250	.000	.872	250	.000

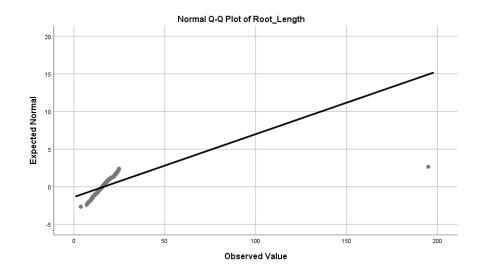
^{*.} This is a lower bound of the true significance.

Leaf Number Q-Q Plot

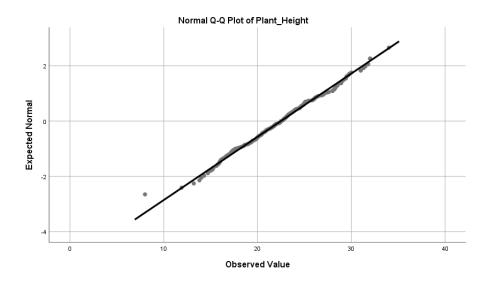


Root Length Q-Q Plot

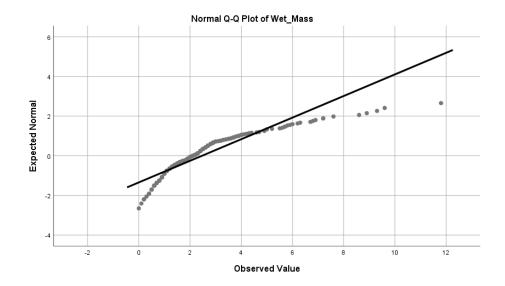
a. Lilliefors Significance Correction



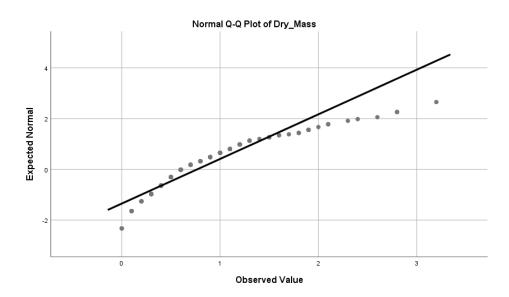
Plant Height Q-Q Plot



Wet Mass Q-Q Plot



Dry Mass Q-Q Plot



Chlorophyll Readings One Way ANOVA

ANOVA

Chlorophyll Averages

1 0	Sum of				
	Squares	df	Mean Square	F	Sig.
Between	1317.884	203	6.492	1.742	.151
Groups					

Within Groups	41.000	11	3.727	
Total	1358.884	214		

Between-Subjects Factors

20	Between Subjects Luctors				
		Value Label	N		
Growth	1	A	30		
Parameters		(Enterobacter			
		cloacae)			
	2	B (Klebsiella	30		
		pneumoniae)			
	3	C (Kluyvera	30		
		cryocrescens)			
	4	AB	30		
	5	AC	30		
	6	BC	30		
	7	ABC	20		
	8	Positive	24		
		Control			
	9	Negative	26		
		Control			

Descriptive Statistics

	Growth Parameters	Mean	Std. Deviation	N
Leaf_Numbe r	A (Enterobacter cloacae)	15.100	3.6232	30
	B (Klebsiella pneumoniae)	12.767	3.8028	30
	C (Kluyvera cryocrescens)	15.033	4.1563	30
	AB	16.300	3.3337	30
	AC	15.233	2.9906	30
	BC	14.600	4.2067	30
	ABC	6.400	2.4581	20

	Positive Control	8.208	3.4133	24
	Negative Control	8.846	4.0368	26
D	Total	12.904	4.8536	250
Root_Length	A (Enterobacter cloacae)	15.727	3.3594	30
	B (Klebsiella	21.207	32.9656	30
	pneumoniae)	1.7.000	1 22 52	
	C (Kluyvera	15.890	4.2363	30
	cryocrescens)	4 4 7 0 7	4.000	
	AB	16.597	4.0227	30
	AC	13.757	3.8324	30
	BC	16.457	2.8551	30
	ABC	17.440	2.9305	20
	Positive Control	17.092	4.1815	24
	Negative Control	13.362	4.0092	26
	Total	16.382	11.9672	250
Plant_Height	A (Enterobacter cloacae)	21.830	3.6419	30
	B (Klebsiella	21.217	3.7578	30
	pneumoniae)			
	C (Kluyvera	22.687	5.3146	30
	cryocrescens)			
	AB	22.757	4.2698	30
	AC	22.147	4.1248	30
	BC	23.847	2.7356	30
	ABC	25.590	3.2643	20
	Positive Control	23.796	4.6646	24
	Negative Control	19.473	4.9580	26
	Total	22.495	4.3738	250
Wet_Mass	A (Enterobacter	1.593	.9903	30
	cloacae)	1.000	5222	20
	B (Klebsiella	1.090	.5333	30
	pneumoniae)	1 077	((1)	20
	C (Kluyvera	1.277	.6611	30
	cryocrescens)	2.102	1 1200	20
	AB	3.183	1.4208	30
	AC	2.977	1.3392	30
	BC	2.683	1.1014	30

	ABC	2.670	1.8991	20
	Positive Control	5.183	2.8874	24
	Negative Control	2.146	1.4957	26
	Total	2.471	1.8353	250
Dry_Mass	A (Enterobacter cloacae)	.710	.5909	30
	B (Klebsiella pneumoniae)	.477	.2700	30
	C (Kluyvera cryocrescens)	.447	.2751	30
	AB	1.097	.6338	30
	AC	.857	.4681	30
	BC	.943	.4599	30
	ABC	.890	.6711	20
	Positive Control	1.221	.7009	24
	Negative Control	.338	.2801	26
	Total	.767	.5688	250

Post Hoc Tests

Growth Parameters

Multiple Comparisons

LSD

			Mean			95% Confide	nce Interval
Dependent	(I) Growth		Difference			Lower	Upper
Variable	Parameters	(J) Growth Parameters	(I-J)	Std. Error	Sig.	Bound	Bound
Leaf_Number	A (Enterobacter	B (Klebsiella	2.333*	.9388	.014	.484	4.183
	cloacae)	pneumoniae)					
		C (Kluyvera	.067	.9388	.943	-1.783	1.916
		cryocrescens)					
		AB	-1.200	.9388	.202	-3.049	.649
		AC	133	.9388	.887	-1.983	1.716
		BC	.500	.9388	.595	-1.349	2.349
		ABC	8.700*	1.0496	.000	6.632	10.768
		Positive Control	6.892*	.9957	.000	4.930	8.853
		Negative Control	6.254*	.9742	.000	4.335	8.173
	B (Klebsiella	A (Enterobacter	-2.333*	.9388	.014	-4.183	484
	pneumoniae)	cloacae)					
		C (Kluyvera	-2.267*	.9388	.017	-4.116	417
		cryocrescens)					
		AB	-3.533*	.9388	.000	-5.383	-1.684
		AC	-2.467*	.9388	.009	-4.316	617
		BC	-1.833	.9388	.052	-3.683	.016
		ABC	6.367*	1.0496	.000	4.299	8.434
		Positive Control	4.558*	.9957	.000	2.597	6.520
		Negative Control	3.921*	.9742	.000	2.001	5.840

	C (Kluyvera	A (Enterobacter	067	.9388	.943	-1.916	1.783
	cryocrescens)	cloacae)					
		B (Klebsiella	2.267*	.9388	.017	.417	4.116
		pneumoniae)					
		AB	-1.267	.9388	.179	-3.116	.583
		AC	200	.9388	.831	-2.049	1.649
		BC	.433	.9388	.645	-1.416	2.283
		ABC	8.633*	1.0496	.000	6.566	10.701
		Positive Control	6.825*	.9957	.000	4.864	8.786
		Negative Control	6.187*	.9742	.000	4.268	8.106
	AB	A (Enterobacter	1.200	.9388	.202	649	3.049
		cloacae)					
		B (Klebsiella	3.533*	.9388	.000	1.684	5.383
		pneumoniae)					
		C (Kluyvera	1.267	.9388	.179	583	3.116
		cryocrescens)					
		AC	1.067	.9388	.257	783	2.916
		BC	1.700	.9388	.071	149	3.549
		ABC	9.900*	1.0496	.000	7.832	11.968
		Positive Control	8.092*	.9957	.000	6.130	10.053
		Negative Control	7.454*	.9742	.000	5.535	9.373
	AC	A (Enterobacter	.133	.9388	.887	-1.716	1.983
		cloacae)					
		B (Klebsiella	2.467*	.9388	.009	.617	4.316
		pneumoniae)					
		C (Kluyvera	.200	.9388	.831	-1.649	2.049
		cryocrescens)					

		AB	-1.067	.9388	.257	-2.916	.783
		BC	.633	.9388	.501	-1.216	2.483
		ABC	8.833*	1.0496	.000	6.766	10.901
		Positive Control	7.025*	.9957	.000	5.064	8.986
		Negative Control	6.387*	.9742	.000	4.468	8.306
	ВС	A (Enterobacter cloacae)	500	.9388	.595	-2.349	1.349
		B (Klebsiella pneumoniae)	1.833	.9388	.052	016	3.683
		C (Kluyvera cryocrescens)	433	.9388	.645	-2.283	1.416
		AB	-1.700	.9388	.071	-3.549	.149
		AC	633	.9388	.501	-2.483	1.216
		ABC	8.200*	1.0496	.000	6.132	10.268
		Positive Control	6.392*	.9957	.000	4.430	8.353
		Negative Control	5.754*	.9742	.000	3.835	7.673
	ABC	A (Enterobacter cloacae)	-8.700*	1.0496	.000	-10.768	-6.632
		B (Klebsiella pneumoniae)	-6.367*	1.0496	.000	-8.434	-4.299
		C (Kluyvera cryocrescens)	-8.633*	1.0496	.000	-10.701	-6.566
		AB	-9.900*	1.0496	.000	-11.968	-7.832
		AC	-8.833*	1.0496	.000	-10.901	-6.766
		BC	-8.200*	1.0496	.000	-10.268	-6.132
		Positive Control	-1.808	1.1008	.102	-3.977	.360
		Negative Control	-2.446*	1.0814	.025	-4.576	316

	Positive Control	A (Enterobacter	-6.892*	.9957	.000	-8.853	-4.930
		cloacae)					
		B (Klebsiella	-4.558*	.9957	.000	-6.520	-2.597
		pneumoniae)					
		C (Kluyvera	-6.825*	.9957	.000	-8.786	-4.864
		cryocrescens)					
		AB	-8.092*	.9957	.000	-10.053	-6.130
		AC	-7.025*	.9957	.000	-8.986	-5.064
		BC	-6.392*	.9957	.000	-8.353	-4.430
		ABC	1.808	1.1008	.102	360	3.977
		Negative Control	638	1.0292	.536	-2.665	1.390
	Negative Control	A (Enterobacter	-6.254*	.9742	.000	-8.173	-4.335
		cloacae)					
		B (Klebsiella	-3.921*	.9742	.000	-5.840	-2.001
		pneumoniae)					
		C (Kluyvera	-6.187*	.9742	.000	-8.106	-4.268
		cryocrescens)					
		AB	-7.454*	.9742	.000	-9.373	-5.535
		AC	-6.387*	.9742	.000	-8.306	-4.468
		BC	-5.754*	.9742	.000	-7.673	-3.835
		ABC	2.446*	1.0814	.025	.316	4.576
		Positive Control	.638	1.0292	.536	-1.390	2.665
Root_Length	A (Enterobacter	B (Klebsiella	-5.480	3.0876	.077	-11.562	.602
	cloacae)	pneumoniae)					
		C (Kluyvera	163	3.0876	.958	-6.245	5.919
		cryocrescens)					
		AB	870	3.0876	.778	-6.952	5.212

	AC	1.970	3.0876	.524	-4.112	8.052
	BC	730	3.0876	.813	-6.812	5.352
	ABC	-1.713	3.4520	.620	-8.513	5.087
	Positive Control	-1.365	3.2748	.677	-7.816	5.086
	Negative Control	2.365	3.2041	.461	-3.946	8.677
B (Klebsiella pneumoniae)	A (Enterobacter cloacae)	5.480	3.0876	.077	602	11.562
	C (Kluyvera cryocrescens)	5.317	3.0876	.086	765	11.399
	AB	4.610	3.0876	.137	-1.472	10.692
	AC	7.450*	3.0876	.017	1.368	13.532
	BC	4.750	3.0876	.125	-1.332	10.832
	ABC	3.767	3.4520	.276	-3.033	10.567
	Positive Control	4.115	3.2748	.210	-2.336	10.566
	Negative Control	7.845*	3.2041	.015	1.534	14.157
C (Kluyvera cryocrescens)	A (Enterobacter cloacae)	.163	3.0876	.958	-5.919	6.245
	B (Klebsiella pneumoniae)	-5.317	3.0876	.086	-11.399	.765
	AB	707	3.0876	.819	-6.789	5.375
	AC	2.133	3.0876	.490	-3.949	8.215
	BC	567	3.0876	.855	-6.649	5.515
	ABC	-1.550	3.4520	.654	-8.350	5.250
	Positive Control	-1.202	3.2748	.714	-7.653	5.249
	Negative Control	2.528	3.2041	.431	-3.783	8.840
AB	A (Enterobacter cloacae)	.870	3.0876	.778	-5.212	6.952

	B (Klebsiella	-4.610	3.0876	.137	-10.692	1.472
	pneumoniae)					
	C (Kluyvera	.707	3.0876	.819	-5.375	6.789
	cryocrescens)					
	AC	2.840	3.0876	.359	-3.242	8.922
	BC	.140	3.0876	.964	-5.942	6.222
	ABC	843	3.4520	.807	-7.643	5.957
	Positive Control	495	3.2748	.880	-6.946	5.956
	Negative Control	3.235	3.2041	.314	-3.076	9.547
AC	A (Enterobacter	-1.970	3.0876	.524	-8.052	4.112
	cloacae)					
	B (Klebsiella	-7.450*	3.0876	.017	-13.532	-1.368
	pneumoniae)					
	C (Kluyvera	-2.133	3.0876	.490	-8.215	3.949
	cryocrescens)					
	AB	-2.840	3.0876	.359	-8.922	3.242
	BC	-2.700	3.0876	.383	-8.782	3.382
	ABC	-3.683	3.4520	.287	-10.483	3.117
	Positive Control	-3.335	3.2748	.310	-9.786	3.116
	Negative Control	.395	3.2041	.902	-5.916	6.707
BC	A (Enterobacter	.730	3.0876	.813	-5.352	6.812
	cloacae)					
	B (Klebsiella	-4.750	3.0876	.125	-10.832	1.332
	pneumoniae)					
	C (Kluyvera	.567	3.0876	.855	-5.515	6.649
	cryocrescens)					
	AB	140	3.0876	.964	-6.222	5.942

	AC	2.700	3.0876	.383	-3.382	8.782
	ABC	983	3.4520	.776	-7.783	5.817
	Positive Control	635	3.2748	.846	-7.086	5.816
	Negative Control	3.095	3.2041	.335	-3.216	9.407
ABC	A (Enterobacter	1.713	3.4520	.620	-5.087	8.513
	cloacae)					
	B (Klebsiella	-3.767	3.4520	.276	-10.567	3.033
	pneumoniae)					
	C (Kluyvera	1.550	3.4520	.654	-5.250	8.350
	cryocrescens)					
	AB	.843	3.4520	.807	-5.957	7.643
	AC	3.683	3.4520	.287	-3.117	10.483
	BC	.983	3.4520	.776	-5.817	7.783
	Positive Control	.348	3.6205	.923	-6.783	7.480
	Negative Control	4.078	3.5566	.253	-2.928	11.084
Positive Control	A (Enterobacter	1.365	3.2748	.677	-5.086	7.816
	cloacae)					
	B (Klebsiella	-4.115	3.2748	.210	-10.566	2.336
	pneumoniae)					
	C (Kluyvera	1.202	3.2748	.714	-5.249	7.653
	cryocrescens)					
	AB	.495	3.2748	.880	-5.956	6.946
	AC	3.335	3.2748	.310	-3.116	9.786
	BC	.635	3.2748	.846	-5.816	7.086
	ABC	348	3.6205	.923	-7.480	6.783

	Negative Control	A (Enterobacter	-2.365	3.2041	.461	-8.677	3.946
		cloacae)					
		B (Klebsiella	-7.845*	3.2041	.015	-14.157	-1.534
		pneumoniae)					
		C (Kluyvera	-2.528	3.2041	.431	-8.840	3.783
		cryocrescens)					
		AB	-3.235	3.2041	.314	-9.547	3.076
		AC	395	3.2041	.902	-6.707	5.916
		BC	-3.095	3.2041	.335	-9.407	3.216
		ABC	-4.078	3.5566	.253	-11.084	2.928
		Positive Control	-3.730	3.3850	.272	-10.398	2.938
Plant_Height	A (Enterobacter	B (Klebsiella	.613	1.0740	.568	-1.502	2.729
	cloacae)	pneumoniae)					
		C (Kluyvera	857	1.0740	.426	-2.972	1.259
		cryocrescens)					
		AB	927	1.0740	.389	-3.042	1.189
		AC	317	1.0740	.768	-2.432	1.799
		BC	-2.017	1.0740	.062	-4.132	.099
		ABC	-3.760*	1.2008	.002	-6.125	-1.395
		Positive Control	-1.966	1.1392	.086	-4.210	.278
		Negative Control	2.357*	1.1145	.035	.161	4.552
	B (Klebsiella	A (Enterobacter	613	1.0740	.568	-2.729	1.502
	pneumoniae)	cloacae)					
		C (Kluyvera	-1.470	1.0740	.172	-3.586	.646
		cryocrescens)					
		AB	-1.540	1.0740	.153	-3.656	.576
		AC	930	1.0740	.387	-3.046	1.186

	BC	-2.630*	1.0740	.015	-4.746	514
	ABC	-4.373*	1.2008	.000	-6.739	-2.008
	Positive Control	-2.579*	1.1392	.024	-4.823	335
	Negative Control	1.744	1.1145	.119	452	3.939
C (Kluyvera	A (Enterobacter	.857	1.0740	.426	-1.259	2.972
cryocrescens)	cloacae)					
	B (Klebsiella	1.470	1.0740	.172	646	3.586
	pneumoniae)					
	AB	070	1.0740	.948	-2.186	2.046
	AC	.540	1.0740	.616	-1.576	2.656
	BC	-1.160	1.0740	.281	-3.276	.956
	ABC	-2.903*	1.2008	.016	-5.269	538
	Positive Control	-1.109	1.1392	.331	-3.353	1.135
	Negative Control	3.214*	1.1145	.004	1.018	5.409
AB	A (Enterobacter	.927	1.0740	.389	-1.189	3.042
	cloacae)					
	B (Klebsiella	1.540	1.0740	.153	576	3.656
	pneumoniae)					
	C (Kluyvera	.070	1.0740	.948	-2.046	2.186
	cryocrescens)					
	AC	.610	1.0740	.571	-1.506	2.726
	BC	-1.090	1.0740	.311	-3.206	1.026
	ABC	-2.833*	1.2008	.019	-5.199	468
	Positive Control	-1.039	1.1392	.363	-3.283	1.205
	Negative Control	3.284*	1.1145	.004	1.088	5.479
AC	A (Enterobacter	.317	1.0740	.768	-1.799	2.432
	cloacae)					

	B (Klebsiella	.930	1.0740	.387	-1.186	3.046
	pneumoniae)					
	C (Kluyvera	540	1.0740	.616	-2.656	1.576
	cryocrescens)					
	AB	610	1.0740	.571	-2.726	1.506
	BC	-1.700	1.0740	.115	-3.816	.416
	ABC	-3.443*	1.2008	.005	-5.809	-1.078
	Positive Control	-1.649	1.1392	.149	-3.893	.595
	Negative Control	2.674*	1.1145	.017	.478	4.869
BC	A (Enterobacter	2.017	1.0740	.062	099	4.132
	cloacae)					
	B (Klebsiella	2.630^{*}	1.0740	.015	.514	4.746
	pneumoniae)					
	C (Kluyvera	1.160	1.0740	.281	956	3.276
	cryocrescens)					
	AB	1.090	1.0740	.311	-1.026	3.206
	AC	1.700	1.0740	.115	416	3.816
	ABC	-1.743	1.2008	.148	-4.109	.622
	Positive Control	.051	1.1392	.964	-2.193	2.295
	Negative Control	4.374*	1.1145	.000	2.178	6.569
ABC	A (Enterobacter	3.760^{*}	1.2008	.002	1.395	6.125
	cloacae)					
	B (Klebsiella	4.373*	1.2008	.000	2.008	6.739
	pneumoniae)					
	C (Kluyvera	2.903*	1.2008	.016	.538	5.269
	cryocrescens)					
	AB	2.833*	1.2008	.019	.468	5.199

	AC	3.443*	1.2008	.005	1.078	5.809
	BC	1.743	1.2008	.148	622	4.109
	Positive Control	1.794	1.2594	.156	687	4.275
	Negative Control	6.117*	1.2372	.000	3.680	8.554
Positive Control	A (Enterobacter	1.966	1.1392	.086	278	4.210
	cloacae)					
	B (Klebsiella pneumoniae)	2.579*	1.1392	.024	.335	4.823
	C (Kluyvera	1.109	1.1392	.331	-1.135	3.353
	cryocrescens)					
	AB	1.039	1.1392	.363	-1.205	3.283
	AC	1.649	1.1392	.149	595	3.893
	BC	051	1.1392	.964	-2.295	2.193
	ABC	-1.794	1.2594	.156	-4.275	.687
	Negative Control	4.323*	1.1775	.000	2.003	6.642
Negative Control	A (Enterobacter cloacae)	-2.357*	1.1145	.035	-4.552	161
	B (Klebsiella pneumoniae)	-1.744	1.1145	.119	-3.939	.452
	C (Kluyvera cryocrescens)	-3.214*	1.1145	.004	-5.409	-1.018
	AB	-3.284*	1.1145	.004	-5.479	-1.088
	AC	-2.674*	1.1145	.017	-4.869	478
	BC	-4.374*	1.1145	.000	-6.569	-2.178
	ABC	-6.117*	1.2372	.000	-8.554	-3.680
	Positive Control	-4.323*	1.1775	.000	-6.642	-2.003

Wet_Mass	A (Enterobacter	B (Klebsiella	.503	.3761	.182	237	1.244
	cloacae)	_pneumoniae)					
		C (Kluyvera	.317	.3761	.401	424	1.057
		cryocrescens)					
		AB	-1.590 [*]	.3761	.000	-2.331	849
		AC	-1.383*	.3761	.000	-2.124	643
		BC	-1.090*	.3761	.004	-1.831	349
		ABC	-1.077*	.4205	.011	-1.905	248
		Positive Control	-3.590*	.3989	.000	-4.376	-2.804
		Negative Control	553	.3903	.158	-1.322	.216
	B (Klebsiella	A (Enterobacter	503	.3761	.182	-1.244	.237
	pneumoniae)	cloacae)					
		C (Kluyvera	187	.3761	.620	927	.554
		cryocrescens)					
		AB	-2.093*	.3761	.000	-2.834	-1.353
		AC	-1.887*	.3761	.000	-2.627	-1.146
		BC	-1.593 [*]	.3761	.000	-2.334	853
		ABC	-1.580*	.4205	.000	-2.408	752
		Positive Control	-4.093*	.3989	.000	-4.879	-3.308
		Negative Control	-1.056*	.3903	.007	-1.825	287
	C (Kluyvera	A (Enterobacter	317	.3761	.401	-1.057	.424
	cryocrescens)	cloacae)					
		B (Klebsiella	.187	.3761	.620	554	.927
		pneumoniae)					
		AB	-1.907*	.3761	.000	-2.647	-1.166
		AC	-1.700*	.3761	.000	-2.441	959
		BC	-1.407*	.3761	.000	-2.147	666

	ABC	-1.393*	.4205	.001	-2.222	565
	Positive Control	-3.907*	.3989	.000	-4.692	-3.121
	Negative Control	869*	.3903	.027	-1.638	101
AB	A (Enterobacter	1.590*	.3761	.000	.849	2.331
	cloacae)					
	B (Klebsiella	2.093*	.3761	.000	1.353	2.834
	pneumoniae)					
	C (Kluyvera	1.907*	.3761	.000	1.166	2.647
	cryocrescens)					
	AC	.207	.3761	.583	534	.947
	BC	.500	.3761	.185	241	1.241
	ABC	.513	.4205	.223	315	1.342
	Positive Control	-2.000*	.3989	.000	-2.786	-1.214
	Negative Control	1.037*	.3903	.008	.268	1.806
AC	A (Enterobacter	1.383*	.3761	.000	.643	2.124
	cloacae)					
	B (Klebsiella	1.887*	.3761	.000	1.146	2.627
	pneumoniae)					
	C (Kluyvera	1.700*	.3761	.000	.959	2.441
	cryocrescens)					
	AB	207	.3761	.583	947	.534
	BC	.293	.3761	.436	447	1.034
	ABC	.307	.4205	.467	522	1.135
	Positive Control	-2.207*	.3989	.000	-2.992	-1.421
	Negative Control	.831*	.3903	.034	.062	1.599
BC	A (Enterobacter	1.090*	.3761	.004	.349	1.831
	cloacae)					

	B (Klebsiella	1.593*	.3761	.000	.853	2.334
	pneumoniae)					
	C (Kluyvera	1.407^{*}	.3761	.000	.666	2.147
	cryocrescens)					
	AB	500	.3761	.185	-1.241	.241
	AC	293	.3761	.436	-1.034	.447
	ABC	.013	.4205	.975	815	.842
	Positive Control	-2.500*	.3989	.000	-3.286	-1.714
	Negative Control	.537	.3903	.170	232	1.306
ABC	A (Enterobacter	1.077^{*}	.4205	.011	.248	1.905
	cloacae)					
	B (Klebsiella	1.580*	.4205	.000	.752	2.408
	pneumoniae)					
	C (Kluyvera	1.393*	.4205	.001	.565	2.222
	cryocrescens)					
	AB	513	.4205	.223	-1.342	.315
	AC	307	.4205	.467	-1.135	.522
	BC	013	.4205	.975	842	.815
	Positive Control	-2.513*	.4410	.000	-3.382	-1.645
	Negative Control	.524	.4332	.228	330	1.377
Positive Control	A (Enterobacter	3.590*	.3989	.000	2.804	4.376
	cloacae)					
	B (Klebsiella	4.093*	.3989	.000	3.308	4.879
	_pneumoniae)					
	C (Kluyvera	3.907*	.3989	.000	3.121	4.692
	cryocrescens)					
	AB	2.000^{*}	.3989	.000	1.214	2.786

		AC	2.207*	.3989	.000	1.421	2.992
		BC	2.500*	.3989	.000	1.714	3.286
		ABC	2.513*	.4410	.000	1.645	3.382
		Negative Control	3.037*	.4123	.000	2.225	3.849
	Negative Control	A (Enterobacter cloacae)	.553	.3903	.158	216	1.322
		B (Klebsiella pneumoniae)	1.056*	.3903	.007	.287	1.825
		C (Kluyvera cryocrescens)	.869*	.3903	.027	.101	1.638
		AB	-1.037*	.3903	.008	-1.806	268
		AC	831*	.3903	.034	-1.599	062
		BC	537	.3903	.170	-1.306	.232
		ABC	524	.4332	.228	-1.377	.330
		Positive Control	-3.037*	.4123	.000	-3.849	-2.225
Dry_Mass	A (Enterobacter cloacae)	B (Klebsiella pneumoniae)	.233	.1293	.072	021	.488
	,	C (Kluyvera cryocrescens)	.263*	.1293	.043	.009	.518
		AB	387*	.1293	.003	641	132
		AC	147	.1293	.258	401	.108
		BC	233	.1293	.072	488	.021
		ABC	180	.1445	.214	465	.105
		Positive Control	511*	.1371	.000	781	241
		Negative Control	.372*	.1341	.006	.107	.636
B (Klebsiella pneumoniae)	`	A (Enterobacter cloacae)	233	.1293	.072	488	.021

	C (Kluyvera	.030	.1293	.817	225	.285
	cryocrescens)					
	AB	620*	.1293	.000	875	365
	AC	380*	.1293	.004	635	125
	BC	467*	.1293	.000	721	212
	ABC	413*	.1445	.005	698	129
	Positive Control	744*	.1371	.000	-1.014	474
	Negative Control	.138	.1341	.304	126	.402
C (Kluyvera	A (Enterobacter	263*	.1293	.043	518	009
cryocrescens)	cloacae)					
	B (Klebsiella	030	.1293	.817	285	.225
	pneumoniae)					
	AB	650 [*]	.1293	.000	905	395
	AC	410*	.1293	.002	665	155
	BC	497*	.1293	.000	751	242
	ABC	443*	.1445	.002	728	159
	Positive Control	774*	.1371	.000	-1.044	504
	Negative Control	.108	.1341	.421	156	.372
AB	A (Enterobacter	.387*	.1293	.003	.132	.641
	cloacae)					
	B (Klebsiella	.620*	.1293	.000	.365	.875
	pneumoniae)					
	C (Kluyvera	.650*	.1293	.000	.395	.905
	cryocrescens)					
	AC	.240	.1293	.065	015	.495
	BC	.153	.1293	.237	101	.408
	ABC	.207	.1445	.154	078	.491

	Positive Control	124	.1371	.366	394	.146
	Negative Control	.758*	.1341	.000	.494	1.022
AC	A (Enterobacter	.147	.1293	.258	108	.401
	cloacae)					
	B (Klebsiella	.380*	.1293	.004	.125	.635
	pneumoniae)					
	C (Kluyvera	.410*	.1293	.002	.155	.665
	cryocrescens)					
	AB	240	.1293	.065	495	.015
	BC	087	.1293	.503	341	.168
	ABC	033	.1445	.818	318	.251
	Positive Control	364*	.1371	.008	634	094
	Negative Control	.518*	.1341	.000	.254	.782
BC	A (Enterobacter	.233	.1293	.072	021	.488
	cloacae)					
	B (Klebsiella	.467*	.1293	.000	.212	.721
	pneumoniae)					
	C (Kluyvera	.497*	.1293	.000	.242	.751
	cryocrescens)					
	AB	153	.1293	.237	408	.101
	AC	.087	.1293	.503	168	.341
	ABC	.053	.1445	.712	231	.338
	Positive Control	278*	.1371	.044	548	007
	Negative Control	.605*	.1341	.000	.341	.869
ABC	A (Enterobacter	.180	.1445	.214	105	.465
	cloacae)					

	B (Klebsiella	.413*	.1445	.005	.129	.698
	pneumoniae)					
	C (Kluyvera	.443*	.1445	.002	.159	.728
	cryocrescens)					
	AB	207	.1445	.154	491	.078
	AC	.033	.1445	.818	251	.318
	BC	053	.1445	.712	338	.231
	Positive Control	331*	.1516	.030	629	032
	Negative Control	.552*	.1489	.000	.258	.845
Positive Contro	l A (Enterobacter	.511*	.1371	.000	.241	.781
	cloacae)					
	B (Klebsiella	.744*	.1371	.000	.474	1.014
	pneumoniae)					
	C (Kluyvera	.774*	.1371	.000	.504	1.044
	cryocrescens)					
	AB	.124	.1371	.366	146	.394
	AC	.364*	.1371	.008	.094	.634
	BC	.278*	.1371	.044	.007	.548
	ABC	.331*	.1516	.030	.032	.629
	Negative Control	.882*	.1417	.000	.603	1.162
Negative Contr	ol A (Enterobacter	372*	.1341	.006	636	107
	cloacae)					
	B (Klebsiella	138	.1341	.304	402	.126
	pneumoniae)					
	C (Kluyvera	108	.1341	.421	372	.156
	cryocrescens)					
	AB	758*	.1341	.000	-1.022	494

AC	518*	.1341	.000	782	254
BC	605*	.1341	.000	869	341
ABC	552 [*]	.1489	.000	845	258
Positive Control	882*	.1417	.000	-1.162	603

Based on observed means.

The error term is Mean Square(Error) = .251.

IAA readings One Way ANOVA

Descriptives

Replicates

Replicates								
					95% Confidence Interval for			
			Std.		Mean			
	N	Mean	Deviation	Std. Error	Lower Bound	Upper Bound	Minimum	Maximum
Isolate 1	3	.157167	.0512334	.0295796	.029896	.284438	.1186	.2153
Isolate 2	3	.292100	.0229432	.0132463	.235106	.349094	.2659	.3086
Isolate 3	3	.274667	.0072501	.0041858	.256657	.292677	.2674	.2819
Isolate 4	3	.269100	.0617164	.0356320	.115788	.422412	.2125	.3349
Isolate 5	3	.238733	.0081144	.0046848	.218576	.258891	.2329	.2480
Isolate 6	3	.274067	.0688806	.0397683	.102958	.445176	.1963	.3274
Isolate 7	3	.228500	.0173491	.0100165	.185403	.271597	.2092	.2428
Isolate 8	3	.221033	.0166533	.0096148	.179664	.262402	.2077	.2397

^{*.} The mean difference is significant at the .05 level.

Isolate 9	3	.284033	.0474226	.0273795	.166229	.401838	.2295	.3156
Isolate 10	3	.199600	.0298878	.0172557	.125355	.273845	.1800	.2340
Isolate 11	3	.152300	.0130104	.0075115	.119980	.184620	.1390	.1650
Isolate 12	3	.192233	.0224068	.0129366	.136572	.247895	.1680	.2122
Isolate 13	3	.171667	.0257016	.0148388	.107820	.235513	.1440	.1948
Isolate 14	3	.185900	.0185548	.0107126	.139807	.231993	.1653	.2013
Isolate 15	3	.213467	.0373558	.0215674	.120670	.306264	.1916	.2566
Isolate 16	3	.214833	.0128165	.0073996	.182995	.246671	.2066	.2296
Isolate 17	3	.257900	.0108056	.0062386	.231058	.284742	.2473	.2689
Isolate 18	3	.231833	.0070010	.0040420	.214442	.249225	.2249	.2389
Isolate 19	3	.223233	.0728654	.0420689	.042226	.404241	.1737	.3069
Isolate 20	3	.226633	.0274201	.0158310	.158518	.294749	.2017	.2560
Total	60	.225450	.0499356	.0064467	.212550	.238350	.1186	.3349

ANOVA

Re	plicat	es
Ke	pncat	es

•	Sum of				
	Squares	df	Mean Square	F	Sig.
Between	.097	19	.005	4.088	.000
Groups					
Within Groups	.050	40	.001		
Total	.147	59			