Probiotics and competitive exclusion of pathogens in shrimp aquaculture

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Abstract

Probiotics, live microorganisms that, when administered in adequate amounts, confer a health benefit on the host, offer an alternative to antibiotics and have become popular among shrimp farmers for use in the regulation of pond water quality, promotion of shrimp growth and the prevention of disease. Most shrimp probiotics are selected for testing based on their ability to competitively exclude pathogens through bacterial antagonism assays, although the mechanisms of pathogen exclusion are rarely investigated. In this review, we provide a comprehensive overview of the mechanisms of competitive exclusion (interference and exploitation competition) by species screened and subsequently identified as shrimp probiotics based on their ability to inhibit the growth of pathogenic bacteria in vitro. We show that the current methods used to identify potential probiotics preferentially select for interference-based competitive mechanisms and may overlook the potential of many species to be considered a probiotic. Furthermore, we show that the efficiency of a probiotic in vivo may be improved by considering the suitability of competitive strategies to shrimp farming conditions. We highlight important limitations and future directions for the screening and identification of probiotics in shrimp aquaculture, to aid in the development of effective and sustainable microbial management strategies.

Key words: competitive exclusion, gut microbiome, microbial ecology, probiotics, shrimp aquaculture.

Introduction

Probiotics, defined as ‘live microorganisms that, when administered in adequate amounts, confer a health benefit on the host’ (Hill et al., 2014), are becoming increasingly popular antibiotic alternatives to promote growth and prevent disease in shrimp aquaculture. Whilst knowledge on their exact mechanisms of action is limited, there is strong evidence showing they are able to confer probiotic effects through the competitive exclusion of pathogenic bacteria, nutrient and enzymatic contribution to shrimp digestion, enhancement of the shrimp immune response and antiviral effects (Kumar et al., 2016; Hoseinifar et al., 2018; Li et al., 2018; Ringø, 2020). To date, approximately 20 genera of bacteria have been shown to have a probiotic effect in shrimp, although the majority of research has focused on Bacillus and lactic acid bacteria (LAB), such as Lactobacillus (Tables 1–3), due largely to their prevalence and successful application as probiotics in mammals and poultry. Probiotics can be administered orally with the feed (including bioencapsulation with live food vectors such as artemia; Immanuel, 2016), directly into the water as purified cultures or spores (Ringø, 2020), or within a fermented growth media, for example Bacillus subtilis E20-fermented soybean meal (Liu et al., 2009, 2010; Tseng et al., 2009; Tsai et al., 2019; Wang et al., 2019). Similarly, probiotics may be administered in combination with a complementary prebiotic, ‘a non-digestible food ingredient that beneficially affects the host by selectively stimulating the growth and/or activity of one or a limited number of bacteria in the colon’ (Gibson & Roberfroid, 1995), to form treatments known as 'symbiotics' (Schrezenmeir & de Vrese, 2001; Li et al., 2018).
Table 1  Lactic acid bacteria with a probiotic effect in shrimp aquaculture (For specific methods, see original papers)

| Genus       | Species     | Isolated from                           | Host (probiotic effect for)               | Inhibits (in vitro antagonism)                              | Method                     | Challenge test (in vivo) | Source of growth inhibition | References                              |
|-------------|-------------|-----------------------------------------|-------------------------------------------|------------------------------------------------------------|----------------------------|--------------------------|--------------------------|----------------------------------------|
| Enterococcus faecium NRW-2 | Commercial probiotics, guts of wild shrimp (Fenneropenaeus chinensis) and fish (Cheilomyctys stigmatias) | Litopenaeus vannamei | Vibrio harveyi, V. parahaemolyticus | Well-diffusion (CFCS) | V. parahaemolyticus | N/A | Sha et al. (2016a, 2016b, 2016c) | 1, 3, 4, 5 |
| Enterococcus faecium MC13 | Shrimp or fish intestines | Penaeus monodon | N/A | N/A | V. parahaemolyticus | N/A | Swain et al. (2009) | 1, 3 |
| Lactobacillus acidophilus 04 | Homemade curd | P. monodon | N/A | N/A | V. parahaemolyticus | N/A | Swakumar et al. (2012) | 3 |
| Lactobacillus acidophilus NCIM 2285 | Culture collection | F. indicus | V. alginolyticus | Cross-streak (LC), Culture (OD) with CFCS (pH neutralised) | V. alginolyticus | N/A | Aijitha et al. (2004) | 1, 3, 4, 6 |
| Lactobacillus acidophilus RS058 | Shrimp and common carp ponds | L. vannamei | N/A | N/A | V. parahaemolyticus | N/A | Wang and Gu (2010) | 1, 5 |
| Lactobacillus bulgaricus E20 | Digestive tracts of L. vannamei | L. vannamei | V. parahaemolyticus | Agar diffusion (LC) | V. parahaemolyticus | N/A | Roomiani et al. (2018) | 2, 3, 5 |
| Lactobacillus bulgaricus NCIM 2056, NCIM2057 | Culture collection | F. indicus | V. alginolyticus | Cross-streak (LC), Culture (OD) with CFCS (pH neutralised) | V. alginolyticus | N/A | Aijitha et al. (2004) | 1, 3, 4, 6 |
| Lactobacillus fermentum LW2 | Lake water | L. vannamei | N/A | N/A | V. alginolyticus | N/A | Wang et al. (2019) | 6 |
| Lactobacillus pentosus BD6 | Pigeon faeces | L. vannamei | N/A | N/A | V. alginolyticus | N/A | Wang et al. (2019) | 5, 6 |
| Lactobacillus plantarum AS13 | Digestive tracts of L. vannamei | L. vannamei | V. vulnificus, V. raf TERANUS and V. campbellii | Well-diffusion (CS) | V. vulnificus, V. raf TERANUS, V. campbellii | N/A | Zheng and Wang (2017) | 1, 3, 6 |
| Lactobacillus pentosus HC-2 | Commercial probiotics, guts of wild shrimp (F. chinensis) and fish (C. stigmatias) | L. vannamei | V. harveyi, V. parahaemolyticus | Well-diffusion (CFCS) | V. parahaemolyticus | Up-regulated expression of luxS | Sha et al. (2016a, 2016b, 2016c) | 1, 3, 4, 5 |
| Lactobacillus plantarum | Digestive tracts of juvenile | L. vannamei | V. harveyi | Well-diffusion (LC) | V. harveyi, V. alginolyticus | N/A | Vieira et al. (2007, 2016), Ramirez et al. (2017) | 2, 3, 4, 6 |
| Lactobacillus plantarum 7-40 (NTU102) | Korean-style cabbage pickles | L. vannamei | N/A | N/A | V. alginolyticus | N/A | Chu et al. (2007) | 3, 5 |
| Lactobacillus plantarum MRO3.12 | Digestive tracts of wild shrimp (M. brevipinnis, P. megueri X) and cultured | L. vannamei | V. harveyi | Double layer (LC), Culture with CFCS (pH neutralised, catalaseterated), Co-culture | V. harveyi | Exclude potential antibacterial effect caused by a pH decrease and/or production of hydrogen peroxide | Kongrum and Hongsattarakul (2012) | 1 – 6 |
### Table 1 (continued)

| Genus | Species | Isolated from | Host (probiotic effect for) | Inhibits (in vitro antagonism) | Method† | Challenge test (in vivo) | Source of growth inhibition | References | Probiotic effects‡ |
|-------|---------|---------------|----------------------------|-------------------------------|---------|-------------------------|-----------------------------|------------|-------------------|
| **plantarum T8, T13** | L. vannamei | hepatopancreas | L. vannamei | *V. parahaemolyticus* | Well-diffusion (CFCS, pH neutralised and catalase treated) | *V. parahaemolyticus* | Exclude potential antibacterial effect caused by a pH decrease and/or production of hydrogen peroxide | Nguyen et al. (2018b) | 1, 3 |
| **plantarum MTCC no. 1407** | Culture collection | M. rosenbergii | Digestive tracts of healthy L. vannamei | *A. hydrophila, Pseudomonas fluorescens* | Well-diffusion (LC), Disc-diffusion (CFCS) | *A. hydrophila* | N/A | Dash et al. (2014, 2016) | 1, 3, 4, 5, 6, 8 |
| **plantarum SGLAB01** | Culture collection | L. vannamei | Staphylococcus aureus, Aerococcus viridans, Bacillus megaterium, B. subtilis, *V. parahaemolyticus*, *V. harveyi*, and *Escherichia coli* | | Culture (OD) with *V. parahaemolyticus*. N/A, excluding the | N/A | *V. parahaemolyticus* | Chomwong et al. (2018) | 3, 5 |
| **sp AMET1506** | Cured | L. vannamei, P. monodon | E. coli, *V. chalaraea*, *V. parahaemolyticus*, *Salmonella sp.* and *Shigella sp.* | Disc-diffusion (CFCS, pH neutralised) | *V. harveyi* | N/A, excluding the potential inhibitory effect of acid production on *V. parahaemolyticus* | Karthik et al. (2014) | 1, 3 |
| **Lactococcus lactis D1813** | Culture collection (OD) with *V. parahaemolyticus*. N/A, excluding the | *V. parahaemolyticus* | *V. parahaemolyticus* | *V. parahaemolyticus* | Cross-streak (LC), Culture (OD) with *V. parahaemolyticus* | N/A, excluding the potential inhibitory effect of acid production | Ajitha et al. (2004) | 3, 4 |
| **Lactococcus lactis subsp. cremoris NCIM 2179** | Culture collection (OD) with *V. parahaemolyticus*. N/A, excluding the | *V. parahaemolyticus* | *V. parahaemolyticus* | *V. parahaemolyticus* | Cross-streak (LC), Culture (OD) with *V. parahaemolyticus* | N/A, excluding the potential inhibitory effect of acid production | Ajitha et al. (2004) | 3, 4 |
| **Lactococcus lactis subsp. lactis** | Culture collection (OD) with *V. parahaemolyticus*. N/A, excluding the | *V. parahaemolyticus* | *V. parahaemolyticus* | *V. parahaemolyticus* | Cross-streak (LC), Culture (OD) with *V. parahaemolyticus* | N/A, excluding the potential inhibitory effect of acid production | Ajitha et al. (2004) | 3, 4 |
| **Pediococcus acidilactici/GY2** | Gut of *M. rosenbergii* | Intestine of healthy L. vannamei | *V. anguillarum*, *V. harveyi* | | N/A | *V. anguillarum*, *V. parahaemolyticus* | N/A | Adel et al. (2017a), Won et al. (2020) | 1–7 |
| **Pediococcus pentosaceus** | Gut of *M. rosenbergii* | Intestine of healthy L. vannamei | | | N/A | *V. anguillarum*, *V. parahaemolyticus* | N/A | Swain et al. (2009) | 3 (V. harveyi only) |
| **Pediococcus acidilactici/GY2** | Gut of *M. rosenbergii* | Intestine of healthy L. vannamei | | | N/A | *V. anguillarum*, *V. parahaemolyticus* | N/A | Swain et al. (2009) | 3 (V. harveyi only) |
| **Streptococcus cremoris NCIM 2285** | Culture collection (OD) with *V. parahaemolyticus*. N/A, excluding the | *V. parahaemolyticus* | *V. parahaemolyticus* | *V. parahaemolyticus* | Agar diffusion (LC) | *A. hydrophila* | N/A | Miao et al. (2020) | 1, 3, 5 |
| | | | | | | | | |}

*Bolded text indicates potential inhibitory effects.*
### Table 1 (continued)

| Genus | Species | Isolated from | Host (probiotic effect for) | Inhibits (in vitro antagonism) | Method† | Challenge test (in vivo) | Source of growth inhibition | References | Probiotic effects‡ |
|-------|---------|---------------|-----------------------------|-------------------------------|---------|-------------------------|-----------------------------|------------|-------------------|
| *Phocae* PI80 | Intestine of *P. indicus* | *P. monodon* | *V. parahaemolyticus, V. vulnificus, V. anguillicaudatus, V. fischeri, A. hydrophila and Listeria monocytogenes* | Cross-streak (LC), Culture (OD) with CFCS (pH neutralised) Double layer (LC), Well diffusion (unspecified) | V. harveyi | Detection of bacteriocin activity (Tricine SDS-PAGE electrophoresis). Bacteriocin (phocaecin PI80) characterised by Satish Kumar and Arul (2009) | Effect of acid production | Swain et al. (2009), Kanmani et al. (2010) | 1, 3 |

†Method: Double layer (CS, LC): Probiotic cultured on agar medium. Colonies killed by exposure to chloroform (culture supernatant; CS) or left and used as live cultures (LC). Pathogen cultured in liquid media, mixed (seeded) with soft agar and poured over the probiotic plate. Incubated and inhibition of pathogen growth recorded. Cross-streak (CS, LC): Probiotic and pathogen streaked perpendicular to each other on plates (LC). Alternatively, probiotic streaked on plate, incubated and growth scraped. Remaining bacteria killed by exposure to chloroform (CS). Pathogenic strain streaked perpendicular to probiotic. Growth inhibition observed as linear clear zones. Co-culture (LC): Both probiotic and pathogen cultured together in liquid media (broth). Samples withdrawn, serially diluted and plated to determine viable cell counts (growth enumerated on agar). Culture (CS, CFCS): Pathogen cultured in liquid media (broth) with probiotic CS or cell free culture supernatant (CFCS). Growth and bacteriolytic activity measured using optical density (OD) or samples withdrawn, serially diluted and plated to determine viable pathogen count. Disc-diffusion (CFCS, LC): Discs impregnated with CFCS or LC of probiotics positioned on top of lawn cultures of pathogenic bacteria. Incubated and then clear zones of inhibition around the disc measured. Wells-diffusion (CFCS, LC): Pathogen suspensions spread evenly over agar plate (lawn culture). Wells punched into solidified agar and filled with CFCS or LC of probiotic. Incubated and (clear) zones of inhibition around the wells measured. Agar diffusion (LC): Pathogen spread onto agar plate (lawn culture). Small amounts of probiotic LC smeared or spotted over lawn culture. Zones of inhibition surrounding the plaques of probiotic culture measured. Co-culture (F): Both probiotic and pathogen (expressing green fluorescent protein (GFP)) cultured together in liquid media (broth). Fluorescence (F) signal generated by GFP-expressing cells used to quantify the bacterial growth.

‡Probiotic effect: (1) Increased growth (including weight gain), (2) increased survival (no pathogen challenge), (3) increased survival (pathogen challenge), (4) decreased pathogen counts (including presumptive *Vibrio* sp.), (5) immunomodulatory effect, (6) increased digestive efficiency (including digestive enzyme activity, feed conversion ratio, feed efficiency or protein efficiency ratio), (7) morphological changes in intestines (including increased villi height and number of folds/revines), and (8) improved water quality (including reduction in presumptive pathogen counts).
Table 2: Bacillus species with a probiotic effect in shrimp aquaculture (For specific methods see original papers)

| Genus   | Species     | Isolated from | Host (probiotic effect loc) | Inhibits (in vitro antagonism) | Method | Challenge test (in vivo) | Source of growth inhibition | Reference | Probiotic effects |
|---------|-------------|---------------|-----------------------------|--------------------------------|--------|-------------------------|-----------------------------|-----------|------------------|
| Bacillus| subtilis MTCC 121 | Culture collection | Macrobrachium rosenbergii | N/A | N/A | N/A | N/A | Karthik et al. (2018), Lud-Villaseñor et al. (2011) | 1, 2, 4, 6 |
|         | amyloyliquefaciens | Digestive tracts of adult Litopenaeus vannamei | Vibrio campbellii, V. vulnificus, V. parahaemolyticus, V. harveyi | Double layer (CS), Well-diffusion (LC) | N/A | N/A | N/A | N/A | N/A |
|         | aquaries SH5 | Gastrointestinal tract (GIT) of wild shrimp | L. vannamei | N/A | N/A | N/A | N/A | N/A | N/A | N/A | Nigo et al. (2016), Nguyen et al. (2018a, 2020), Tepasamondex et al. (2019), Wee et al. (2018) | 1, 5, 10 |
|         | aryabhatta/TBRC8450 | Sediment from shrimp farm | L. vannamei | V. harveyi, V. parahaemolyticus | Agar diffusion (LC) | V. harveyi | N/A | N/A | N/A | N/A | Ravi et al. (2007) | 3 |
|         | cereus M. rosenbergii | Gut of healthy M. rosenbergii | P. monodon | V. harveyi, V. vulnificus, Vibrio spp. | Well diffusion (LC) | V. harveyi, Vibrio spp. | N/A | N/A | N/A | N/A | Vidal et al. (2018) | 4, 11 |
|         | cereus Seawater, sediment and gut content of healthy fish (Lates calcarifer) | Gut of L. vannamei | L. vannamei | V. harveyi | Disc-diffusion (LC) | V. harveyi | N/A | Detection of bacteriocin activity (SDS-PAGE electrophoresis) | Mansih et al. (2016) | 3, 5 |
|         | cereus Intestine of juvenile L. vannamei | Gut of wild P. monodon | L. vannamei | N/A | N/A | V. parahaemolyticus, V. alginaeolyticus | N/A | N/A | N/A | N/A | Chandran et al. (2014, 2017) | 1, 2, 5, 6 |
|         | cereus Gut of wild P. monodon | P. monodon | P. monodon | V. harveyi, Staphylococcus aureus, Escherichia coli, Bacillus subtilis, Aeromonas hydrophila | Well-diffusion (CFCS) | N/A | N/A | N/A | N/A | Raghuram et al. (2016) | 5 |
|         | coagulans | Gut of wild P. monodon | P. monodon | V. parahaemolyticus | N/A | V. parahaemolyticus | N/A | N/A | N/A | N/A | Raghuram et al. (2016) | 1, 3, 5, 6, 7, 12 |
|         | coagulans (ATCC 7050) | Culture collection | L. vannamei | N/A | N/A | V. parahaemolyticus | N/A | N/A | N/A | N/A | Armos et al. (2019) | 3 |
|         | coagulans | Culture collection | L. vannamei | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | Karthik et al. (2018) | 1, 2, 4, 6 |
|         | coagulans (MTCC 2302) | Gut of healthy M. rosenbergii | P. monodon | V. parahaemolyticus | N/A | N/A | N/A | N/A | N/A | N/A | Wang and Guo (2010), Wang et al. (2012) | 1, 2, 5, 6 |
|         | coagulans (MTCC 1105) | Shrimp and common carp ponds | L. vannamei | N/A | N/A | N/A | N/A | N/A | N/A | N/A | Zhou et al. (2009), Lud-Villaseñor et al. (2011) | 2, 6 |
|         | coagulans SCB168 endophyticus | Shrimp pond sediment | L. vannamei | N/A | N/A | N/A | N/A | N/A | N/A | N/A | Raghuram et al. (2016) | 5 |
|         | finorus | Gut of wild P. monodon | P. monodon | V. parahaemolyticus | N/A | N/A | N/A | N/A | N/A | N/A | Cai et al. (2019) | 2, 3, 4, 5, 6, 8, 9 |
|         | flexus LD-1 | Pond waters/sediments | L. vannamei | V. parahaemolyticus, V. alginaeolyticus | Double layer (LC) | V. harveyi | N/A | N/A | N/A | N/A | Guo et al. (2009) | 2 |
|         | fusiformis | Fermented solution | L. vannamei, P. monodon | Streptococcus iniae, Photobacterium damselae subsp. piscicida | Co-culture (LC) | N/A | N/A | N/A | N/A | Li et al. (2007) | 4, 5 |
|         | Ichthio Formis | Shrimp pond sediment | L. vannamei | N/A | N/A | N/A | N/A | N/A | Selected for its ability to secrete extracellular | N/A | N/A | N/A | N/A |
| Genus | Species | Isolated from | Host (probiotic effect for) | Inhibits (in vitro antagonism) | Method† | Challenge test (in vivo) | Source of growth inhibition | Reference | Probiotic effect‡ |
|-------|---------|----------------|-----------------------------|-------------------------------|---------|-------------------------|----------------------------|-----------|------------------|
| *licheniformis* | Culture collection | Macrobrachium rosenbergi | V. harveyi, V. vishnisucci | Double layer (CS) | N/A | N/A | N/A | Kumar et al. (2013) | 1, 5, 3 |
| *licheniformis* C6GB-232 | L. vannamei intest ine | L. vannamei | V. harveyi | Double layer (CS) | N/A | N/A | N/A | Franco et al. (2017) | 1, 5, 9 |
| *licheniformis* DAH81 | Gut of Feneropenaeus indicus | F. indicus | V. paraaemolyticus | N-Acylated homoserine lactone (AHL)-lactonase bioassay, biofilm development assay | N/A | Production of AHL-lactonase, shown to inhibit V. paraaemolyticus biofilm formation | | Vinoj et al. (2014) | 3, 4 |
| *licheniformis* LS-1 | Pond waters/sediments | L. vannamei | V. harveyi, V. vishnisucci | Double layer (LC) | N/A | N/A | N/A | Cai et al. (2019) | 1, 2, 3, 4, 5, 6, 8, 9 |
| *pollaci um* | N/A | L. vannamei | N/A | N/A | N/A | N/A | N/A | Gomos et al. (2011) | 9 |
| *OI* | L. vannamei intestine | L. vannamei | N/A | N/A | N/A | WSSV | N/A | Li et al. (2009) | 3, 4, 5 |
| *PC465* | Intestine of *P. chinensis* | L. vannamei | N/A | N/A | N/A | WSSV | N/A | Chai et al. (2016) | 1, 2, 3, 5, 6, 7, 12 |
| *sp.* | Mangrove sediment | N/A | N/A | N/A | N/A | N/A | N/A | Baneyjee et al. (2010) | 1, 2, 4, 8 |
| *sp.* MJA1.1, MJA2.1 | Fish mucus of tilapia (Drelichromis sp.) | L. vannamei | N/A | N/A | N/A | N/A | N/A | Lin et al. (2004) | 6 |
| *sp.* MK22 | Salt-pan sediment | P. monodon | V. paraaemolyticus, V. harveyi | Well-diffusion (unspecified) | V. paraaemolyticus | N/A | N/A | Doroteo et al. (2018) | 2, 9 |
| *sp.* NFMI-C | Open cultures of the microalgae Chaetoceros muelleri | M. rosenbergii | N/A | N/A | V. campbelli | Inhibition of acylhomoserine lactones (AHL) quorum sensing by AHL degradation | N/A | Ashokkumar and Mayawu (2014), Ashokkumar et al. (2016) | 1, 2, 3, 4, 6 |
| *sp.* NL110 | M. rosenbergii/larvae | M. rosenbergii | A. hydrophila, V. paraaemolyticus, V. vishnisucci, V. harveyi, E. coli, Salmo nella Newport, S. typhi | Well-diffusion (LC), Cross-streak (CS) | N/A | N/A | N/A | Rahman et al. (2010) | 1, 2, 5, 8 |
| *sp.* P11 | GIT of P. monodon broodstock | P. monodon | V. harveyi, E. coli | Agar diffusion (LC) | V. harveyi | 18 antibiotics undetected in CFCS (screening test kit). | Utsawannakul et al. (2011), Sapcharoen and Rengpipat (2013) | 1, 2, 3, 6 |
| *sp.* P64 | Homogenised wild | L. vannamei | V. harveyi | Agar diffusion (LC) | V. harveyi | N/A | N/A | Gullian et al. (2004) | 5, 1, 3 |
| *sp.* S11 | GIT of P. monodon broodstock | P. monodon | V. harveyi, V. paraaemolyticus | Agar diffusion (LC) | V. harveyi | 18 antibiotics undetected in CFCS (screening test kit). | Rengpipat et al. (1998, 2000, 2003), Powedchagun et al. (2011), Sapcharoen and Rengpipat (2013) | 1, 2, 3, 5 |
| *sp.* | Juvenile M. rosenbergii gut | M. rosenbergii | A. hydrophila, V. paraaemolyticus | Double layer (CS) | A. hydrophila | N/A | N/A | Keyami et al. (2012) | 1, 2, 3, 6 |
| Genus | Species | Isolated from | Host (probiotic effect for) | Inhibits (in vitro antagonism) | Method | Challenge test (in vivo) | Source of growth inhibition | Reference | Probiotic effects‡ |
|-------|---------|---------------|-----------------------------|-------------------------------|--------|-------------------------|---------------------------|-----------|-------------------|
| *subtilis* | N/A | *L. vannamei* | N/A | N/A | N/A | N/A | N/A | Keysami and Mohammadpour (2013) | **1, 9** |
| *subtilis* (IPA-5.51) | *L. vannamei* | *L. vannamei* | V. alginolyticus | Well diffusion (CFCS, LC) | N/A | N/A | N/A | Interaminene et al. (2018) | **1** |
| *subtilis BT23* | Shrimp culture ponds | *P. monodon* | V. harveyi, V. anguillarum, V. vallnicus, V. damselfa | Well-diffusion (CFCS), Coculture (LC with V. harveyi), Culture with CFCS (V. harveyi, OD) | N/A | V. harveyi | N/A | Vaseeharan and Ramasamy (2003) | **3** |
| *subtilis SI2* | Natto (fermented soybeans) | *L. vannamei* | A. hydrophila | Disc-diffusion (CFCS) | V. alginolyticus | N/A | N/A | Liu et al. (2009, 2010), Tseng et al. (2009), Tsai et al. (2019), Wang et al. (2019) | **1, 2, 3, 5, 6, 9** |
| *subtilis SI2* | *L. vannamei* digestive content | *L. vannamei* | A. hydrophila, Aeromonas sobria, Aeromonas caviae, Aeromonas hydrophila, V. anguillarum, V. vallnicus, V. alginolyticus, V. harveyi, V. parahaemolyticus | Well-diffusion (LC, CFCS) | V. harveyi | N/A | N/A | Liu et al. (2014) | **1, 2, 3, 5** |
| *subtilis SH23* | Gut of white-leg shrimp | *L. vannamei* | V. parahaemolyticus, V. vallnicus | Well-diffusion (unspecified) | N/A | N/A | N/A | Nguyen et al. (2020) | **5** |
| *subtilis UTM 126* | GIT of adult *L. vannamei* | *L. vannamei* | V. alginolyticus, V. parahaemolyticus, V. harveyi | Disc-diffusion (CFCS) (pH neutralised), Well-diffusion (CFCS) | V. harveyi, V. parahaemolyticus | N/A | N/A | Balcazar and Rque-Luna (2007), Balcazar et al. (2007) | **3, 1, 6, 2** |
| *subtilis WB60* | Intestine of juvenile Japanese eel | *L. vannamei* | N/A | Agar diffusion (LC) | V. parahaemolyticus | N/A | N/A | Won et al. (2020) | **1, 6, 3, 5, 7** |
| *tequilensis* | Digestive tracts of adult | *L. vannamei* | V. campbellii, V. vallnicus, V. parahaemolyticus, V. harveyi | Double layer (C), Well-diffusion (L,C) | N/A | N/A | N/A | Luis-Villasenor et al. (2011) | **1, 2** |
| *theuringiensis* | GIT of *L. vannamei* | *L. vannamei* | V. harveyi | Disc-diffusion (L,C) | V. harveyi | N/A | N/A | Mastoh et al. (2016) | **3, 5** |
| *theuringiensis GS-8-3TD2* | *P. monodon* intestine | *P. monodon* | V. mimicus | Disc-diffusion (L,C) | V. mimicus | N/A | N/A | Mastoh et al. (2016) | **1, 3** |
Table 2 (continued)

| Genus Species | Isolated from | Host (probiotic effect for) | Inhibits (in vitro antagonism) | Method† | Challenge test (in vivo) | Source of growth inhibition | Reference | Probiotic effects‡ |
|---------------|---------------|-----------------------------|--------------------------------|---------|-------------------------|-----------------------------|-----------|---------------------|
| *M. rosenbergii* intestine | *M. rosenbergii* | *Pseudomonas aeruginosa* | Well-diffusion (CFCS) | Antimicrobial activity of CFCS not lost after treatment with enzymes (pepsin, catalase, lipase and α-amylase) and surfactants (Sodium dodecyl sulphate and Tween 80). Heat (37°C – 121°C) and pH (2-9) stable. Gas Chromatography-Mass Spectrometry (GC-MS) of CFCS revealed 15 bioactive compounds. The main compound produced was 2, 6, 10-Trimethyltridecane. | Anyanwu and Ariole (2019), Ariol and Anyanwu (2020) | 3, 12 |

†Method: Double layer (CS, LC): Probiotic cultured on agar medium. Colonies killed by exposure to chloroform (culture supernatant; CS) or left and used as live cultures (LC). Pathogen cultured in liquid media, mixed (seeded) with soft agar and poured over the probiotic plate. Incubated and inhibition of pathogen growth recorded. Cross-streak (CS, LC): Probiotic and pathogen streaked perpendicular to each other on plates (LC). Alternatively, probiotic streaked on plate, incubated and growth scraped. Remaining bacteria killed by exposure to chloroform (CS). Pathogenic strain streaked perpendicular to probiotic. Growth inhibition observed as linear clear zones. Co-culture (LC): Both probiotic and pathogen cultured together in liquid media (broth). Samples withdrawn, serially diluted and plated to determine viable cell counts (growth enumerated on agar). Culture (CS, CFCS): Pathogen cultured in liquid media (broth) with probiotic CS or cell free culture supernatant (CFCS). Growth and bacteriocin activity measured using optical density (OD) or samples withdrawn, serially diluted and plated to determine viable pathogen count. Disc-diffusion (CFCS, LC): Discs impregnated with CFCS or LC of probiotics positioned on top of lawn cultures of pathogenic bacteria. Incubated and clear zones of inhibition around the disc measured. Well-diffusion (CFCS, LC): Pathogen suspensions spread evenly over agar plate (lawn culture). Wells punched into solidified agar and filled with CFCS or LC of probiotic. Incubated and (clear) zones of inhibition around the wells measured. Agar diffusion (LC): pathogen spread onto agar plate (lawn culture). Small amounts of probiotic LC smeared or spotted over lawn culture. Zones of inhibition surrounding the plaques of probiotic culture measured. Co-culture (F): Both probiotic and pathogen (expressing green fluorescent protein (GFP)) cultured together in liquid media (broth). Fluorescence (F) signal generated by GFP-expressing cells used to quantify the bacterial growth.

‡Probiotic effect: (1) Increased growth (including weight gain), (2) increased survival (no pathogen challenge), (3) increased survival (pathogen challenge), (4) decreased pathogen counts (including presumptive Vibrio sp.), (5) immunomodulatory effect, (6) increased in digestive efficiency (including digestive enzyme activity, feed conversion ratio, feed efficiency or protein efficiency ratio), (7) morphological changes in intestines (including increased villi height and number of folds/revines), (8) improved water quality (including reduction in presumptive pathogen counts), (9) increased survival (stress test), (10) improved pigmentation, (11) prevention of weight loss during pathogen challenge and (12) improved antioxidant activity.
## Table 3: Bacterial species with a probiotic effect in shrimp aquaculture (for specific methods see original papers)

| Genus | Species | Isolated from | Host (probiotic effect for) | Inhibits (in vitro antagonism) | Method | Challenge test (in vivo) | Source of growth inhibition | References | Probiotic effects |
|-------|---------|---------------|-----------------------------|-------------------------------|--------|------------------------|-----------------------------|------------|-----------------|
| Alteromonas | sp. BY-9 | Coastal waters | Penaeus monodon | Vibrio harveyi | N/A | N/A | N/A | N/A | Haryanti et al. (2001) 1, 2, 4 |
| Arthrobacter | sp. CWA | Guts of L. vannamei | L. vannamei | N/A | N/A | N/A | N/A | Xue et al. (2014) 1, 2, 5 |
| XE-7 | P. cheniensis | L. vannamei | N/A | N/A | N/A | N/A | N/A | Li et al. (2009) 3, 8 |
| Clostridium | butyricum | L. vannamei culture water | N/A | N/A | N/A | N/A | N/A | Xue et al. (2016) 3, 4, 5 |
| butyricum | Zhongke Biotic Co., Ltd, China | | | | | | | Li et al. (2008) 1, 7, 9 |
| butyricum | L. sp. CW9 | Guts of L. vannamei | N/A | N/A | N/A | N/A | N/A | Xia et al. (2014) 1–29 |
| Enterobacter | butyricum | XE-7 | L. vannamei | Vibrio parahaemolyticus | Disc-diffusion (method unspecified) | V. parahaemolyticus | N/A | Li et al. (2019a,b) 1, 3, 5, 6 |
| Phaeobacter | aquamaris | Water column of L. vannamei | N/A | N/A | N/A | N/A | N/A | Wang et al. (2016) 2 |
| Pseudoalteromonas | sp. CD22, sp. CD18 | Water column of L. vannamei | N/A | N/A | N/A | N/A | N/A | Xue et al. (2018) 1, 2, 3, 4, 5, 6, 7, 10 |
| Pseudomonas | aeruginosa | Gastrointestinal tract (GIT) of adult L. vannamei | N/A | N/A | N/A | N/A | N/A | Wang et al. (2018) 3, 4 |
| sp. NC201 | Marine (intertidal) | V. nigripulchritudo, V. harveyi | Agar diffusion (method unspecified), Co-culture (F) | V. nigripulchritudo | N/A | N/A | N/A | Patterson et al. (2014), Sorensen et al. (2018) 2, 3, 5, 9 |
| aeruginosa | SLV22 | Gastrointestinal tract (GIT) of adult L. vannamei | N/A | N/A | N/A | N/A | N/A | Balcells et al. (2007) 1, 2, 3, 6 |
| sp. PS102 | Brackish water | N/A | N/A | N/A | N/A | N/A | N/A | Vijayan et al. (2006) N/A |
| Pseudomonas | alkalisolvens | Intensive shrimp cultivation pond water | N/A | N/A | N/A | N/A | N/A | Rattanaudcha et al. (2007, 2010, 2011) 3 |
| sp. W3 | Marine (intertidal) | V. nigripulchritudo, V. harveyi | Well diffusion (LS, CFCS), Culture (CS, CFCS with live and heat-killed V. harveyi: OD) | V. nigripulchritudo | N/A | N/A | N/A | Franco et al. (2016) 1, 3, 5, 6, 9 |
| Psychrobacter | sp. 17-1 | Gastrointestinal tract (GIT) of healthy L. vannamei | N/A | N/A | N/A | N/A | N/A | Wang and Gu (2010) 1, 5 |
| Rhodopseudomonas | palustris GH642 | Shrimp and common carp ponds | N/A | N/A | N/A | N/A | N/A | Kurita et al. (2003) N/A |
Table 3 (continued)

| Genus          | Species                  | Isolated from                                      | Host (probiotic effect) | Inhibits (in vitro antagonism) | Method                          | Challenge test (in vivo) | Source of growth inhibition | References                  | Probiotic effects |
|----------------|--------------------------|----------------------------------------------------|-------------------------|-------------------------------|---------------------------------|----------------------------|-----------------------------|----------------|----------------------|
| Roseobacter    | gelatinosus SL-V03       | GT of adult L. vannamei                            | L. vannamei             | V. parahaemolyticus           | Well-diffusion (CFCS)           | V. parahaemolyticus         | N/A                         | Balcázar et al. (2007) | 1, 2, 3, 6          |
| Streptomyces   | haliae degradans         | Mangrove sediment                                  | P. monodon              | N/A                           | N/A                             | N/A                        | N/A                         | Aftabuddin et al. (2013)| 1, 8               |
|                | rubra/avocanulinae M56  | Coastal sediment                                    | P. monodon              | V. harveyi                    | Cross-streak (CS)               | V. harveyi                 | N/A                         | Augustine et al. (2016)| 2, 4               |
| sp.            |                          | Shrimp pond sediment                                | P. monodon              | N/A                           | N/A                             | N/A                        | N/A                         | Das et al. (2006)        | 1, 4, 8             |
| sp. CLS-28     |                          |                                                    |                         | V. harveyi                    | Cross-streak (CS)               | V. harveyi                 | N/A                         | Das et al. (2010)        | 1, 4, 3, 6          |
| sp. CLS-39, sp. CLS-45 |                | Shrimp pond sediment                                | P. monodon              | V. harveyi                    | Cross-streak (CS)               | V. harveyi                 | N/A                         | Das et al. (2010)        | 1, 2                |
| Vibrio         | algicidolyticus UTM 102  | GIT of adult L. vannamei                            | L. vannamei             | V. parahaemolyticus           | Well-diffusion (LC)             | V. parahaemolyticus         | N/A                         | Balcázar et al. (2007) | 1, 3, 6             |
|                | sp.                      | Marine sediment                                     | L. vannamei             | V. harveyi                    | Well-diffusion (LC)             | V. parahaemolyticus         | N/A                         | Bernal et al. (2015)    | 1, 4               |
|                |                          | Marine sediment                                     | L. vannamei             | V. harveyi                    | Well-diffusion (LC)             | V. parahaemolyticus         | N/A                         | Bernal et al. (2015)    | 1, 3               |
|                |                          | Marine (inter tidal)                                | L. styliartris          | V. nigripulchitudo, V. harveyi| Diffusion agar assay (method unspecified) | N/A                        | N/A                         | Pham et al. (2014)       | 2, 5               |
| sp. N17        |                          |                                                    |                         | V. parahaemolyticus           | Well-diffusion (LC)             | N/A                        | N/A                         | Rahiman et al. (2010)    | 1, 2, 5, 8          |
| sp. R117       |                          |                                                    |                         | V. parahaemolyticus           | Well-diffusion (LC)             | N/A                        | N/A                         | Guillian et al. (2004)   | 1, 3               |
| sp. P62, sp. P63 | Homogenised wild L. vannamei |                                      | L. vannamei             | V. harveyi                    | Cross-streak (CS)               | V. harveyi                 | N/A                         | Guillian et al. (2004)   | 1, 3               |
| sp. P62, sp. P63 | Homogenised wild L. vannamei |                                      | L. vannamei             | V. harveyi                    | Agar diffusion (LC)             | V. harveyi                 | N/A                         | Guillian et al. (2004)   | 1, 3               |

†Method: Double layer (CS, LC): Probiotic cultured on agar medium. Colonies killed by exposure to chloroform (culture supernatant, CS) or left and used as live cultures (LC). Pathogen cultured in liquid media, mixed (seeded) with soft agar and poured over the probiotic plate. Incubated and inhibition of pathogen growth recorded. Cross-streak (CS, LC): Probiotic and pathogen streaked perpendicular to each other on plates (LC). Alternatively, probiotic streaked on plate, incubated and growth scraped. Remaining bacteria killed by exposure to chloroform (CS). Pathogenic strain streaked perpendicular to probiotic. Growth inhibition observed as linear clear zones. Co-culture (LC): Both probiotic and pathogen cultured together in liquid media (broth). Samples withdrawn, serially diluted and plated to determine viable cell counts (growth enumerated on agar). Culture (CS, LC): Probiotic cultured in liquid media (broth) with probiotic CS or cell free culture supernatant (CFCS). Growth and bacteriolytic activity measured using optical density (OD) or samples withdrawn, serially diluted and plated to determine viable pathogen count. Disc-diffusion (CFCS, LC): Discs impregnated with CFCS or LC of probiotics positioned on top of lawn cultures of pathogenic bacteria. Incubated and then clear zones of inhibition around the disc measured. Well-diffusion (CFCS, LC): Pathogen suspensions spread evenly over agar plate (lawn culture). Wells punched into solidified agar and filled with CFCS or LC of probiotic. Incubated and (clear) zones of inhibition around the wells measured. Agar diffusion (LC): probiotic spread onto agar plate (lawn culture). Small amounts of probiotic LC smeared or spotted over lawn culture. Zones of inhibition surrounding the plaques of probiotic culture measured. Co-culture (F): Both probiotic and pathogen (expressing green fluorescent protein (GFP)) cultured together in liquid media (broth). Fluorescence (F) signal generated by GFP-expressing cells used to quantify the bacterial growth.

‡Probiotic effect: (1) Increased growth (including weight gain), (2) increased survival (no probiotic challenge), (3) increased survival (pathogen challenge), (4) decreased pathogen counts (including presumptive Vibrio sp.), (5) immunomodulatory effect, (6) increased in digestive efficiency (including digestive enzyme activity, feed conversion ratio, feed efficiency or protein efficiency ratio), (7) morphological changes in intestines (including increased villi height and number of fold/styline), (8) improved water quality (including reduction in presumptive pathogen counts), (9) increased survival (stress test) and (10) improved antioxidant activity.
Probiotic species are often isolated from the intestines of shrimp and the surrounding water or sediment of their environment (examples are shown in Tables 1–3). However, they have also been isolated from fruit waste filtrates (Nurliana et al., 2020), curd (Karthik et al., 2014), fermented soybeans ‘Natto’ (Liu et al., 2010), fermented pickles (Zokaeifar et al., 2012a,b) and the intestines of other species. For example, in the case of the latter, shrimp probiotic Lactobacillus species have been isolated from the digestive tracts of chickens (Phianphak et al., 1999) and fish (Sha et al., 2016a; Doroteo et al., 2018). Commercial probiotic treatments, which largely contain LAB and Bacillus spp., have also been tested for their probiotic effects in shrimp (Ringo, 2020). Lack of strict regulations regarding commercial probiotics intended for aquaculture in some regions, however, has raised concerns regarding the reliability of the labelling of such treatments. As an example to illustrate this, Vargas-Albores et al. (2016) detected both additional and different bacterial species in the commercial probiotic Eco-AQUAPROTEC (Eco Technology Solutions, Australia) to those reported for the product by the manufacturer. Furthermore, it is also the case that commercial probiotics often contain more than one microbial species, as well as feed additives such crude protein and fibre, and enzymes such as proteases, amylases, cellulase, xylanase and beta-glucanases. This, in turn, often makes it difficult to attribute probiotic effects to any individual species or component of the formulation to be able to characterise their underlying effect mechanisms. In this review, we focus on shrimp probiotic treatments containing a single species, including those isolated from commercial products to better understand competitive exclusion mechanisms in shrimp probiotics. For an extensive list of commercial and multi-species probiotics that have been investigated, we refer the reader to the recent paper by Ringo (2020).

Prior to in vivo testing, a number of criteria are considered by researchers during the screening and selection of potential probiotic species in shrimp aquaculture. For example, ease of culture, bio-safety (including haemolytic activity and antibiotic susceptibility) and their ability to produce extracellular enzymes and competitively exclude pathogens. However, after isolation, potential probiotics are more often than not selected for based on the competitive exclusion principle (that species competing for the same limited resources cannot co-exist; Volterra, 1928; Gause, 1932; Hardin, 1960; Levin, 1970), through bacterial antagonism assays, in which pathogens are exposed directly (co-culture) or indirectly (extracellular products) to candidate bacteria (Tables 1–3). If they show a significant inhibitory effect against the pathogenic bacteria and are presumed to be safe to the host organism (the presence of safety-related virulence factors such as haemolytic activity (Chang et al., 2000) and chitinase production (Defoirdt et al., 2010; Frederiksen et al., 2013) are often not determined prior to in vivo testing), then they are generally applied as an experimental treatment to test for probiotic effects. However, few studies have attempted to identify the underlying mechanisms involved in bacterial growth inhibition, or considered the wider competitive strategies employed and how this relates to the efficiency and mechanism of probiotic action in vivo. Although antagonism assays offer a limited representation of the diverse and complex interactions between probiotics and their associated host, microbial community and environmental factors, characterisation of these mechanisms is nonetheless necessary to ensure that probiotic use in shrimp aquaculture is both effective and sustainable. Furthermore, considering the rise of antimicrobial resistance (which is predicted to result in 10 million deaths by 2050 if the current trend continues; Meade et al., 2020), the potential insights gained from such investigations extend far beyond the field of probiotics in shrimp aquaculture given that these probiotic species produce antimicrobial substances that have not yet been identified and which make them ideal candidates for bioprosppecting for novel antimicrobial therapeutics. Here, after introducing the competitive exclusion principle and how it works through exploitation and interference competition, we provide a comprehensive overview of the mechanisms of competitive exclusion by species that have been screened and subsequently identified as probiotic based on their ability to inhibit the growth of pathogenic bacteria in vitro. We then go on to discuss how our current understanding of the mechanisms of competitive exclusion could be used to improve the selection and application of probiotics. Finally, we highlight important considerations and future directions for the selection and application of probiotics, with the aim to aid best practise in the development of effective microbial management strategies in shrimp aquaculture.

**Competitive exclusion of pathogenic bacteria**

Competitive exclusion is where co-occurring bacterial species in the same ecological niche compete for limited resources (nutrients and space) through two competitive strategies: exploitation and interference competition. Exploitation competition is indirect, characterised by rapid resource consumption (restricting supply to competitors and investing in growth), whereas interference competition occurs when one organism directly harms another, for example, through the production of antimicrobial compounds.

Exploitation competition includes mechanisms that increase, relative to the competitors, the rate at which nutrients are captured and utilised. Nutrient capture can be improved by the secretion of extracellular molecules that...
break down complex macromolecules thus making nutrients more readily accessible. These extracellular excretion molecules include proteases (Bachmann et al., 2011) and iron-chelating siderophores that access insoluble iron (Kümmel et al., 2015). These mechanisms can be considered co-operative traits, as the ‘public goods’ produced are accessible to all and may benefit a population (Morris et al., 2012). Not all members of that population necessarily invest resources in the production of the compounds and the bacteria producing materials for enabling nutrient capture are vulnerable to inter- and intra-specific competition from social ‘cheaters’, who save resources and invest them in growth. For example, some bacteria can utilise heterologous siderophores, allowing them to save energy on production costs and reduce the accessibility of iron to the siderophore producing species (Khan et al., 2006). The extent to which cheating occurs, however, appears to be dependent on environmental and social context (Ghoul et al., 2014). Niehus et al. (2017) argue that although siderophores can be public goods (when all cells have the same receptors), they should be considered a competitive phenotype. Certainly, species able to produce ‘private’ siderophores with higher iron binding affinities have an advantage over lower-affinity siderophore producing organisms (Weaver & Kolter, 2004; Joshi et al., 2006). The efficiency and speed with which microorganisms utilise nutrients can provide another competitive advantage. Optimal allocation of resources can maximise growth rates (Flamholz et al., 2013; Bosdriesz et al., 2015; Hui et al., 2015). For example, switching between metabolic strategies depending on substrate availability, such as from the higher ATP-yielding respiration process to fermentation, even when glucose is available in excess, to maximise growth rates. This phenomenon, termed ‘overflow metabolism’ (Neijssel & Tempest, 1976; Molenaar et al., 2009), has been observed in a number of fast-growing bacterial and fungal species including Saccharomyces cerevisiae, Escherichia coli and Bacillus subtilis (van Dijken et al., 1993; Vemuri et al., 2006; Sonenshein, 2007; Molenaar et al., 2009; Basan et al., 2015; LaCroix et al., 2015). Whilst this mechanism may appear counter-intuitive, an increasing growth rate is the result of a trade-off between energy yield and synthesis rate of alternative pathways; fermentation requiring more carbon flux but being more proteome efficient (requires fewer proteins) than respiration, thereby allowing more resources to invest in growth (Molenaar et al., 2009; Basan et al., 2015).

Exploitation competition for space can be achieved through rapid colonisation of uninhabited niches, or through competing with populations that are already established. The production of adhesins and receptors that bind to specific surface features can provide a competitive advantage for the colonisation of unoccupied niches, as well as prevent displacement by invaders (Schluter et al., 2015). For example, after adherence to human epithelial cells, some Lactobacillus species produce extracellular glycoproteins, preventing pathogen attachment (Horie et al., 2002; Golowczyc et al., 2007; Johnson-henry et al., 2007). Furthermore, attachment, whilst decreasing mobility, is critical for biofilm formation (surface-attached microbial communities; Hall-Stoodley et al., 2004). The expansion of adhesive cells in biofilms can also aid the removal of non-adhesive cells from the population (Schluter et al., 2015). Cell aggregation of the same genotype can also provide another competitive advantage by sharing resources, such as plasmin conferring antibiotic resistance (Savage et al., 2013), limiting exposure to social ‘cheaters’ (West et al., 2007; Smukalla et al., 2008; Queller et al., 2011; Drescher et al., 2014), and increasing tolerance to antimicrobials (Olsen, 2015). However, there is strong competition within these biofilms (Xavier & Foster, 2007; Davies & Marques, 2009), in which nutrients become limited regionally (Stewart & Franklin, 2008; Kim et al., 2014). On the other hand, to compete with biofilm formation, many species produce molecules that can actively stimulate dispersal of other species (without killing them), such as rhamnolipid and cis-2-decenoic acid (Irie et al., 2005; Davies & Marques, 2009), within established biofilms. Alternatively, some species can disrupt biofilm formation. For example, Pseudomonas aeruginosa PsDAHP1 (isolated from the Indian prawn Fenneropenaeus indicus) has been found to antagonise the ability of Vibrio parahaemolyticus to form biofilms in zebrafish gills and intestine, resulting in a much looser architecture and possibly making them more susceptible to antimicrobials (Vinoj et al., 2015).

Interference competition typically involves the production of antimicrobials, which range from strain-specific bacteriocins (ribosomally synthesised antimicrobial peptides; Yang et al., 2014), to broad-spectrum antibiotics such as the quinolones (Aldred et al., 2014). Investigation into the functional role of sub-inhibitory concentrations of antimicrobials has revealed their multifaceted nature (Fajardo & Martinez, 2008), with involvements in signalling (Davies et al., 2006; Linares et al., 2007; Romero et al., 2011), inhibition of quorum sensing (Hong et al., 2012; Algburi et al., 2017) and kin recognition (Wall, 2016). Nevertheless, there is substantial experimental evidence to support the hypothesis that antibiotics are primarily used as weapons (Abrudan et al., 2015; Cornforth & Foster, 2015). It is plausible that some species have evolved to use certain antimicrobials solely as weapons, whereas others have multiple functions. Interference competition also includes contact-dependent mechanisms such as Type V and Type VI secretion systems. The contact-dependent growth inhibition system (CDI) is a Type V system, first recognised in Escherichia coli (Aoki et al., 2005), in which...
polymorphic protein toxins (growth inhibitory signals) are delivered into the cytoplasm of the target cell displaying complementary receptors, mediating killing unless the recipient bacterium produces a corresponding antidote (Aoki et al., 2005, 2010; Anderson et al., 2012; Nikolakakis et al., 2012). For example, the CdiA-CTEC869 tRNase toxin from enterohemorrhagic *E. coli* EC869 obstructs protein synthesis and thus inhibits growth by specifically cleaving transfer RNAs of recipient cells (Jones et al., 2017). Recently, Garcia et al. (2016) have shown that, in *Burkholderia thailandensis*, gene expression and phenotypic changes that promote community-associated behaviours, such as biofilm formation, occur in immune (self) recipients in response to the CDI toxin. Their results suggest that the CDI system may have two functions, challenging heterospecific (non-immune) bacteria and promoting conspecific (immune) bacteria. Similarly, type VI secretion systems deliver effectors (substrates) directly into the cytoplasm of recipient cells (Gianfelli et al., 2016) resulting in death (Hood et al., 2010; MacIntyre et al., 2010; Schwarz et al., 2010; Murdoch et al., 2011; Russell et al., 2014). Interestingly, the usefulness of this system appears to be highly dynamic, with some species (such as *Vibrio cholerae*) employing highly offensive (non-directional) strategies (Basler et al., 2012), while others, such as *P. aeruginosa*, orientate the machinery towards a perceived threat in a ‘tit-for-tat’ response (Basler et al., 2013; Le Roux et al., 2015). Furthermore, cell lysis via Type VI secretion systems may facilitate horizontal gene transfer, as DNA from the target cell may also be transferred into the attacking cell, potentially conferring benefits in the form of new genes, such as those conferring antimicrobial resistance, to the new host and providing a competitive advantage (Borgeaud et al., 2015).

**Probiotic bacteria**

Considering the relative importance of bacterial antagonism assays for the screening of potential probiotics in shrimp aquaculture, investigations into the underly- ing mechanisms are limited. In the following sections, we discuss our current understanding of the mechanisms of pathogenic growth inhibition, *in vitro*, for individual strains within each genus of bacteria that has been identified as shrimp probiotic (Tables 1-3). We then go on to discuss the implications of the use of antagonism assays in probiotic screening, and how we can improve their efficiency and sustainability, *in vivo*, based on our current understanding of the mechanisms of competitive exclusion. We also highlight some of the key limitations and future directions for the methods used to identify probiotics in shrimp aquaculture.

**Lactic acid bacteria (LAB)**

Lactic acid bacteria produce many antibacterial substances including lactic acid, acetic acid, hydrogen peroxide and bacteriocins (Mokoena, 2017; Ringo et al., 2020) that suppress growth of competing bacteria (Nes et al., 2011; Reis et al., 2012; Alvarez-Sieiro et al., 2016). Many LAB have been identified as shrimp probiotics due to their ability to inhibit the growth of several pathogenic *Vibrio* species, *Aeromonas hydrophila* and *Pseudomonas fluorescens* through well and disc diffusion assays (Table 1), suggesting these species produce extracellular compounds with antimicrobial properties. The mechanisms of growth inhibition for LAB remain largely uncharacterised, but some studies have used catalase-treated and/or pH-neutralised cell-free culture supernatants (CFCs) to test for antagonistic activity and determine whether or not the source of growth inhibition was due to the effect of hydrogen peroxide and/or organic acid production, respectively (see Table 1). Kongnum and Hongpattarakere (2012) found that hydrogen peroxide was a major agent contributing to the antibacterial effect of *Lactobacillus plantarum* MRO3.12. Interestingly, Sgibnev and Kremleva (2017) found that hydrogen peroxide produced by probiotic vaginal lactobacilli were effective in increasing sensitivity to antibiotics, suggesting that hydrogen peroxide producing LAB in combination with antibiotic-producing species may be more effective for pathogenic growth inhibition. The antimicrobial activity of LAB shrimp probiotic *Streptococcus phocae* PI80 has been shown to be due to the production of the bacteriocin Phocacin PI80, which inhibits the growth of a range of Gram-positive and Gram-negative bacteria, including *Listeria monocytogenes*, *Vibrio* spp., *Aeromonas hydrophila* and *Pseudomonas aeruginosa* (Satish Kumar & Arul, 2009). The authors of this work suggest that Phocacin PI80 increases the permeability of sensitive cells through pore formation in the cytoplasmic membrane, as it was shown to induce potassium ion leakage in the tested indicator strains: *E. coli*, *Listeria monocytogenes* and *V. parahaemolyticus* (Satish Kumar & Arul, 2009).

Lactic acid bacteria have also been shown capable of inhibiting the adhesion of pathogenic bacteria to the intestinal mucosa of shrimp. For example, *Lactobacillus pentosus* HC-2 and *Enterococcus faecium* NRW-2 have been shown to adhere to crude intestinal shrimp mucus, suggesting that these strains may compete against pathogens such as *Vibrio* spp. for adherence sites in the intestinal mucus (Sha et al., 2016c). The authors used fluorescent imaging to subsequently confirm that *L. pentosus* HC-2 was able to competitively exclude *V. parahaemolyticus* E1 in the intestine of the Whiteleg shrimp *Litopenaeus vannamei*. *L. pentosus* HC-2 was also shown to increase the level of transcription of the luxS gene in response to
V. parahaemolyticus E1, suggesting it may play an important role in improving its adherence to the gut of L. vannamei and in turn competitively exclude the adhesion of V. parahaemolyticus E1. These authors also reported that heat-killed L. pentosus HC-2 cells upregulated the expression of toxicity-related factors in V. parahaemolyticus E1 and suggested that shrimp fed a diet containing the intracellular components of L. pentosus HC-2 may result in an increase in the risk of infection by Vibrio spp. This hypothesis, however, was not then tested. Collectively, these findings illustrate the importance of understanding the underlying probiont-pathogen interactions, determining strain specific characteristics, and not extrapolating from related strains or even species. They also highlight that community analyses alone (for example through the use of 16S sequencing) are limited for assessments seeking to identify putative interactions.

Lactic acid bacteria are Generally Recognised as Safe (GRAS) by the USA Food and Drug Administration (US FDA) and currently have a wide range of applications in the human food chain, primarily in the manufacturing of fermented food products such as yogurt, cheese and alcoholic beverages. Similarly, the European Food Safety Agency (EFSA) includes many LAB species (belonging to the genera Lactobacillus, Lactococcus, Pediococcus, Streptococcus) in the Qualified Presumption of Safety (QPS) list, meaning that, except for enterococci which no longer has QPS status, a demonstration of their safety only requires confirmation of the absence of determinants of resistance to antibiotics of human and veterinary clinical significance (EFSA BIOHAZ Panel, 2020). This would suggest that the use of LAB, with the exception of Enterococcus faecium, as probiotics is unlikely to have any significant potential health concern for human consumption of treated shrimp. There may, however, be safety concerns based on antibiotic resistance and virulence factors for multiple genus of LAB. This, in turn, highlights that a more thorough risk assessment may be required when considering the application of LAB as probiotics in shrimp aquaculture (Muñoz-Atienza et al., 2013; Sharma et al., 2016).

**Bacillus**

The genus Bacillus, like LAB, includes representatives that are defined as GRAS by the US FDA, but which, for the EFSA QPS qualification, are modified to include ‘absence of food poisoning toxins, absence of surfactant activities, absence of enterotoxic activities’ (EFSA BIOHAZ Panel, 2020). Therefore, Bacillus species would also seem to be ideal candidates for animals destined for human consumption, and indeed, they currently have a range of applications in food processing. Bacillus species also need to show an ‘absence of acquired genes for antimicrobial resistance’ before introduction into the food chain (EFSA BIOHAZ Panel, 2020). The large majority of probiotics in shrimp aquaculture belong to the genus Bacillus, but their safety for use in shrimp aquaculture should not be presumed, and this should be the case with all isolates. For example, Guo et al. (2009) found that addition of Bacillus cereus biovar toyoi to cultures of the giant tiger prawn Penaeus monodon culture resulted in near total mass mortality. Similarly, Bacillus subtilis and B. cereus have been reported to cause bacterial white spot syndrome in cultured P. monodon (Wang et al., 2000) and bacterial white patch disease in L. vannamei, respectively (Velmurugan et al., 2015). This highlights the importance of thorough testing of probiotic candidates, and not simply extrapolating from related species or strains. Ngo et al. (2016) have shown that Bacillus strains isolated from shrimp intestines exhibit resistance to clinically relevant antibiotics, highlighting the importance of antibiotic susceptibility screening when evaluating shrimp probiotics. Bacillus produce a diverse array of over 20 different types of antimicrobial compounds (including polypeptide antibiotics, bacteriocins and lipopeptides), with a wide variety of activities ranging from antibacterial and antifungal, to anticancer and antiviral (Martirani et al., 2002; Stein, 2005; Sutyk et al., 2008; Smitha & Bhat, 2012; Mondol et al., 2013; Cochrane & Vederas, 2016). Recently, genome mining of Bacillus spp. has successfully guided the identification and characterisation of novel antimicrobial metabolites (Yang et al., 2016; Zhao & Kuipers, 2016), highlighting their competitive potential. Many studies investigating Bacillus species as potential probiotics in shrimp aquaculture (Soltani et al., 2019) demonstrate antagonistic growth inhibition of shrimp, fish and human pathogens (Table 2). Most of these studies suggest that Bacillus species produce diffusible extracellular antimicrobials, through the inhibition of pathogens as assessed using the agar or well diffusion techniques and CFCs diffusion assays (Table 2). More specifically, the production of proteinaceous antibacterial substances (bacteriocins or bacteriocin-like inhibitory substances; BLIS, Zokaeifar et al., 2012a,b; Masitoh et al., 2016), antimicrobial polypeptides (AMPs; Cheng et al., 2017; Cheng et al., 2020) and antimicrobial lipopeptides (Lee et al., 2016) have all been identified as a source of inhibition.

Recently, (Gao et al., 2017) reported that Bacillus pumilus H2 produces an anti-Vibrio substance, structurally identical to amicoumacin A, that has been shown to inhibit the growth of 29 Vibrio strains by disrupting cell membranes and leading to cell lysis (Itoh et al., 1981). No extracellular antimicrobial activity, however, was detected in B. subtilis BS11 and Bacillus sp. P11 when using an antimicrobial residue screening test kit (Powedchagun et al., 2011; Utsiwannakul et al., 2011) but this method tests only for ‘18 known standard antibiotics’ (Utsiwannakul et al., 2011). Tseng
et al (2009) found that B. subtilis E20, isolated from the gut of L. vannamei, had no inhibitory effect against eight fish and shrimp pathogens and was only weakly inhibitory against A. hydrophila (Tseng et al., 2009). Nevertheless, the authors found that a B. subtilis E20 supplemented diet increased resistance of L. vannamei to Vibrio alginolyticus. These results may be due to a variety of reasons, including an increased immune capability of the shrimp. Importantly, however, it helps illustrate that the disc diffusion method (using CFCS) alone may not capture the ability of B. subtilis E20 to inhibit growth using exploitation competition mechanisms. Illustrating this further, Luis-Villaseñor et al. (2015) showed that Bacillus strains, isolated from the intestinal tract of shrimp, can adhere to intestinal mucus and gastric mucin of L. vannamei, which may then confer an ability to exclude pathogens by competing for binding sites, as well as producing antimicrobial compounds. Similarly, Bacillus licheniformis DAHBl, isolated from F. indicus, has been shown to invest in exploitation mechanisms, producing a quorum-quenching N-hexanoyl-L-homoserine lactone (AHL)-lactonase (AiiA) able to inhibit vibrio biofilm development and colonisation of shrimp intestines (Vinoj et al., 2014). More recent work has shown that B. cereus BP-MB RG/1b, isolated from the gut of a healthy giant freshwater prawn (Macrobrachium rosenbergii), is able to ablate both AHL signal molecules and quorum sensing in A. hydrophila (Wee et al., 2018). Further effects relating to quorum sensing have been demonstrated. For example, Bacillus sp. NFMI-C has been shown to degrade N-hexanoyl-L-homoserine lactone (HHL) molecules (also produced by A. hydrophila) in co-culture, which subsequently increased the survival of M. rosenbergii larvae when challenged with Vibrio campbellii, whose virulence is regulated by AHL quorum sensing (Pande et al., 2013, 2015). Bacillus spp. are known to produce intracellular lactonases, one of the two major classes of AHL-inactivating enzymes, that act by hydrolysing the lactone ring and are capable of inactivating a wide range of AHLs (Dong et al., 2007; Pande et al., 2015). The growth of V. campbellii was not affected by culture with Bacillus sp. NFMI-C or its CFCS, nor was the growth of the shrimp larvae affected when treated with Bacillus sp. NFMI-C. This would suggest that the probiotic effect was likely due to the ability of this isolate to degrade AHL through the production of lactase. This is of particular interest in the management of Vibrio spp. in shrimp aquaculture, whose ubiquitous and abundant presence in the shrimp gut (Holt et al., 2020) plays an important role in the health of the animal, and not just in disease. Vibrio is the most dominant genus in the early development of P. monodon (Anghthong et al., 2020) and dominates in the gastrointestinal tract regardless of environment or life stage (Mongkol et al., 2018). Probiotics that are theoretically able to prevent the onset of disease that have limited effects on the microbial diversity of ecologically important genera warrant further investigation.

**Vibrio**

Cordero et al. (2012) showed that marine Vibrio populations are organised into socially cohesive units, in which interference competition is greater between (rather than within) ecologically defined populations. These findings suggest that the inhibitory activities of Vibrio species are strain-specific. The results from this study also indicate that low intra-population antagonism may result from fast allelic turnover and rapid loss and acquisition of genes. Therefore, considering virulence or antibiotic resistance of clinical importance, the use of Vibrio species in shrimp aquaculture may be unwise. Furthermore, these authors suggested that the antagonistic interactions investigated were due to small molecules and not proteins such as bacteriocins. Nevertheless, several vibriocins (bacteriocins produced by the genus Vibrio; Wahba, 1965; McCall & Sizemore, 1979; Sugita et al., 1997; Shehane & Sizemore, 2002) and bacteriocin-like inhibitory substances (Prasad et al., 2005; Carraturo et al., 2006) involved in inter-strain and inter-species inhibition have been described. Several Vibrio species investigated for their probiotic potential in shrimp (Table 3) have been shown to produce diffusible extracellular antimicrobials, able to inhibit the growth of fish, shrimp and human pathogens (Gullian et al., 2004; Balcázar et al., 2007; Rahiman et al., 2010; Pham et al., 2014). These studies suggest that some Vibrio isolates may be good probiotics. The lack of QPS qualification, however, would suggest that there is currently not enough literature supporting the use of Vibrio species in animals intended for the food chain. Furthermore, it has been shown that the bacteriophage Vibrio harveyi myovirus like (Munro et al., 2003) and V. harveyi siphophage 1 (Khemayan et al., 2012) are able to confer and increase virulence of V. harveyi to shrimp, respectively. This is of concern when using uncharacterised Vibrio species in shrimp aquaculture (Table 3), as virulence may be easily acquired or transferred.

**Pseudomonas**

Pseudomonas spp. are known to produce a range of bioactive compounds, such as bacteriocins, pyocin, phenazine, quinoline and quinolone (Isnansetyo & Kamei, 2009; Preetha et al., 2010), and have been shown to antagonise the growth of several shrimp pathogens (Table 3). Pseudomonas aeruginosa, Pseudomonas synxantha (Van Hai et al., 2007) and Pseudomonas aestu marina SLV22 (Balcázar et al., 2007) produce diffusible extracellular antimicrobials that can inhibit the growth of several Vibrio pathogens; however, only few studies have characterised these
compounds. The anti-Vibrio activity of *P. aeruginosa* 1-2, however, has been suggested to be attributed to a low molecular weight, non-proteinaceous antimicrobial compound, possibly pyocyanin (Chythanya *et al*., 2002), that is a well-described virulence factor associated with disease in patients with cystic fibrosis (Jeffries *et al*., 2016). If this is indeed the case, then it would raise safety concerns regarding use of this species in the food chain. *Pseudomonas* sp. W3, isolated from intensive shrimp pond water (Rattanachuay *et al*., 2007), has been shown to produce proteolytic enzymes and lysozyme (N-acetylmuramidase; Rattanachuay *et al*., 2010) and 2-heptyl-4-quinolone (HHQ) with anti-Vibrio activity (Rattanachuay *et al*., 2011). Interestingly, *Pseudomonas* sp. W3 appears to have lost its ability to convert HHQ to PQS (2-heptyl-3-hydroxy-4(1H)-quinolone; Diggle *et al*., 2006, 2007), a quorum sensing molecule involved in the production of iron-scaping compounds (Diggle *et al*., 2007; Rattanachuay *et al*., 2011). Nevertheless, Reen *et al*., (2011) demonstrated strong antibacterial activity of HHQ against *Vibrio fischeri* and *Vibrio vulnificus*. The authors reported that this compound was bacteriostatic, in addition to reducing mobility and interfering with pellicle and biofilm activity in *B. subtilis*. This may raise concerns surrounding the efficiency of this species for use as probiotic treatment, particularly in combination with *Aeromonas* strains, isolated from the hindgut of healthy *L. vannamei*, and shown to display antagonistic activity against pathogenic *V. parahaemolyticus* (Wang *et al*., 2018). The antagonistic effect was abolished when the CFCS (for both species) was treated with catalase, suggesting that the inhibition was likely the result of hydrogen peroxide production. The two most predominant proteins isolated from the CFCS of CDM8 and CDA22 (identified by MALDI-TOF/TOF mass spectrometry), shared high similarity to a TonB-dependent receptor (TBDRs) and an antibacterial protein (L-lysine 6-oxidase) of *Pseudoalteromonas flavipulchra* JG1, respectively. TBDRs play a fundamental role in nutrient uptake, including iron-siderophore complexes (Moeck & Coulton, 1998), whilst the antimicrobial activity of L-lysine 6-oxidase has been attributed to its generation of hydrogen peroxide. In *Pseudoalteromonas tunicate*, the hydrogen peroxide generated by the lysine oxidase AlpP is involved in biofilm killing (Mai-Prochnow *et al*., 2008). Interestingly, *Pseudoalteromonas* sp. CDM8 displayed weak antagonistic activity against *Pseudoalteromonas* sp. CDA22 and a noncooperative effect were observed for shrimp when fed with a combination of CDM8 and CDA22, highlighting the importance of investigating probiotic relationships in multi-strain/species treatments. Theoretically, similar species that occupy the same ecological niche within the shrimp gut will have likely developed strategies to compete with [competitively exclude] each other, suggesting that multi-strain probiotics would be better targeted to a wide range of niches.

**Pseudoalteromonas**

*Pseudoalteromonas* spp. isolated from the marine intertidal areas of New Caledonia have shown growth inhibition activity against *Vibrio nigrisulphuritudo* and *V. harveyi*, through the production of diffusible antimicrobials (Pham *et al*., 2014). The antimicrobial compounds were not characterised in this study, but the authors noted that the isolates were coloured, and that pigmented species belonging to the *Pseudoalteromonas* genus are known to produce a variety of bioactive compounds (Bowman, 2007). Similarly, yellow colony-forming *Pseudoalteromonas* spp. CDM8 and CDA22 have been isolated from the hindgut of healthy *L. vannamei*, and shown to display antagonistic activity against pathogenic *V. parahaemolyticus* (Wang *et al*., 2018). The antagonistic effect was abolished when the CFCS (for both species) was treated with catalase, suggesting that the inhibition was likely the result of hydrogen peroxide production. The two most predominant proteins isolated from the CFCS of CDM8 and CDA22 (identified by MALDI-TOF/TOF mass spectrometry), shared high similarity to a TonB-dependent receptor (TBDRs) and an antibacterial protein (L-lysine 6-oxidase) of *Pseudoalteromonas flavipulchra* JG1, respectively. TBDRs play a fundamental role in nutrient uptake, including iron-siderophore complexes (Moeck & Coulton, 1998), whilst the antimicrobial activity of L-lysine 6-oxidase has been attributed to its generation of hydrogen peroxide. In *Pseudoalteromonas tunicate*, the hydrogen peroxide generated by the lysine oxidase AlpP is involved in biofilm killing (Mai-Prochnow *et al*., 2008). Interestingly, *Pseudoalteromonas* sp. CDM8 displayed weak antagonistic activity against *Pseudoalteromonas* sp. CDA22 and a noncooperative effect were observed for shrimp when fed with a combination of CDM8 and CDA22, highlighting the importance of investigating probiotic relationships in multi-strain/species treatments. Theoretically, similar species that occupy the same ecological niche within the shrimp gut will have likely developed strategies to compete with [competitively exclude] each other, suggesting that multi-strain probiotics would be better targeted to a wide range of niches.

**Paenibacillus**

Two isolates from the genus *Paenibacillus*, *P. polymyxa* (formerly recognised as *Bacillus polymyxa*) and an unassigned *Paenibacillus* spp., have shown probiotic effects in *L. vannamei* (Amoah *et al*., 2020) and *P. monodon* (Ravi *et al*., 2007), respectively. *P. polymyxa* are able to produce a variety of bioactive compounds, including lipopeptide biosurfactants able to disrupt biofilms (Quinn *et al*., 2012). Even in their sporulated state, they can produce fusaricidins, AMPs and polymyxins due to the activity of non-ribosomal peptide synthetase systems (Shaheen *et al*., 2011; Grady *et al*., 2016). *Paenibacillus* spp. was shown to inhibit the growth of *Vibrio* species (including *V. harveyi*) when co-cultured using the well diffusion method, suggesting
that it is able to produce diffusible extracellular antimicrobials; however, the mechanism of antagonism was not investigated further.

**Streptomyces**
Species belonging to the genus *Streptomyces* produce a substantial number of bioactive compounds (over 7630; Bérdy, 2005) including antimicrobial, antifungal, anti-cancer agents (Bérdy, 2005; Kim et al., 2008; Wang et al., 2013; Zothanpuia et al., 2017) and are good candidates for potential use as probiotics in aquaculture (Das et al., 2010; Tan et al., 2016). *Streptomyces* spp. N7 and RL8 isolated from marine sediment both have antagonistic activity against pathogenic *Vibrio* spp. (Bernal et al., 2015). *Streptomyces* sp. N7 improved haemocyte counts, growth parameters and *Vibrio* counts in the shrimp hepatopancreas, but it also increased *Vibrio* counts in the rearing water and reduced the SOD activity. Furthermore, there was no difference in the survival rate of the treated shrimp when challenged with *V. parahaemolyticus*. Again, this highlights the importance of thorough testing of probiotic candidates, and not extrapolating from related species or strains. Interestingly, when *Streptomyces* spp. N7 and RL8 were combined, the negative effects on water *Vibrio* counts and survival rates were not counteracted by *Streptomyces* sp. RL8, albeit SOD activity returned to the level of that in the control group. This illustrates the importance of considering both the individual and the combined functional traits of probiotic candidates. Bernal et al. (2015) also showed that these strains are likely to adhere to the gut of their host, allowing them to competitively inhibit *Vibrio* spp. *in vitro*, in addition to the production of antimicrobials. Similarly, *Streptomyces* isolates and *Streptomyces rubrolavendula* biogranules (filamentous aggregation of cells) have demonstrated the ability to inhibit the growth of *Vibrio* sp. in co-culture (Das et al., 2006, 2010; Augustine et al., 2016); however, the mechanisms were not investigated.

**Clostridium**
*Clostridium butyricum* is the only member of the genus *Clostridium* tested as a probiotic in shrimp aquaculture (Table 3) and it shows several probiotic effects in shrimp, as it does in humans and other animals (Kanai et al., 2015; Zhao et al., 2017) including fish (Pan et al., 2008; Gao et al., 2013). The competitive exclusion mechanisms, however, have not been investigated (Table 3).

**Psychrobacter**
Few studies have been conducted on the use of *Psychrobacter* spp. as potential probiotics in aquaculture, and only *Psychrobacter* sp. 17-1 has been reported as a probiotic for shrimp (Table 3). Screening of this isolate by the double layer method has suggested that it is able to produce extracellular antimicrobials, but the mechanism of antagonism against *V. harveyi* and *Aeromonas* sp. has not been investigated (Franco et al., 2016).

**Using competitive exclusion principles to enhance disease resistance**
Despite the majority of probiotics in shrimp aquaculture being screened and selected for further testing based on their ability to antagonise bacterial shrimp pathogens *in vitro*, from the studies reported upon it is clear that relatively little is known about the mechanisms by which this growth inhibition occurs. Furthermore, the investment of energy into interference mechanisms (the production of extracellular antimicrobials) by shrimp probiotics suggests that they may be useful targets for bioprospecting for novel antimicrobial therapeutics. In the following sections, we discuss the implications and limitations of the use of antagonism assays to screen for potential probiotics.

**Competitive exclusion principles and life strategies**
Interference competition has been shown to improve species fitness (Rao et al., 2005; Shank et al., 2011) and stimulate biodiversity (Czárán et al., 2002; Little et al., 2008; Hibbing et al., 2010). However, the energy investment involved in antimicrobial production generally results in slower growth rates and reduced rates of reproduction (Case & Gilpin, 1974; Little et al., 2008). Closely related and co-occurring species can employ fundamentally different competitive strategies. To illustrate this, Patin et al. (2016) have shown that for two co-occurring marine Actinomycete species, *Salinispora arenicola* invests in interference competition via the production of antibiotics at the expense of growth, whereas *Salinispora tropica* invests in growth and exploitation competition. Copiotrophic species invest in rapid growth and are selected for in environments that are nutrient rich, whereas oligotrophic microbes are selected for in resource-poor environments (Koch, 2001; Roller & Schmidt, 2015). Roller and Schmidt (2015) defined a conceptual model proposing innate differences in growth efficiency, progeny per unit of resource utilised, between copiotrophic and oligotrophic microbial species and suggested that selection for efficiency based on resource availability and quality is a primary driver of microbial community composition. However, this model does not account for resources that are invested in interference competition mechanisms and may therefore result in population persistence regardless of the growth rate or efficiency. Furthermore, whilst this model shares many of the
underlying principles of r/K selection – the selection of combinations of traits in an organism that trade-off between quantity and quality of offspring – it does not consider environmental factors beyond resource availability. Thus, the use of functional traits to understand processes that influence community structure, such as the competitor/stress-tolerator/ruderal (CSR) theory (Grime & Pierce, 2012) are more applicable to developing microbial management strategies. The theory links community function and environmental conditions by classifying traits as Competitive (C; neighbours seek to capture the same unit of resource), Ruderal (R; assisting in re-establishment of population after disturbance) or Stress tolerant (S; tolerance of resource shortage, as opposed to resource competition) and proposes that prevailing traits will be a result of resource investment trade-off in such traits that confer an adaptive advantage to environmental disturbance and stress. Whilst the CSR theory was originally developed to explain plant communities, it has been successfully applied to soil microbial communities (Wood et al., 2018). Using Grime’s CSR theory, fast growing species investing in exploitation competition mechanisms (Ruderal life strategists) are selected for in disturbed environments that are not resource-limited, whereas slower growing species investing in interference mechanisms (competitive life strategists) are selected for in undisturbed environments where resources are not limiting (Wood et al., 2018).

Considerations for the selection of shrimp probiotics

Most probiotics used in shrimp aquaculture appear to be competitive life strategists, as they are often selected for based on their ability to produce extracellular antimicrobials. Due to the nature of shrimp aquaculture, in which ponds are disturbed by chemical treatments, weather events and disease, these probiotics may not always be the most effective choice. Rather, certain environmental conditions and disturbances are likely to favour the proliferation of ruderal life strategists. To compensate for this, frequent treatment may be necessary to establish the probiotic (competitive life strategist) within the microbial community at the required abundance and achieve the desired effects. This may in turn impact the microbial community structure of the system and further favour ruderal life strategists that invest in exploitation mechanisms. Improper use of probiotic treatments may potentially lead to conditions which favour pathogenic invasion, for example by using species that compete with indigenous beneficial species, or alter the overall structure or function of the community (Long & Azam, 2001; Pérez-Gutiérrez et al., 2013). Therefore, elucidating the mechanisms underlying growth efficiency and competitive strategies employed by potentially probiotic and pathogenic species, as well as understanding their optimal environmental conditions, are needed to develop the most effective microbial management strategies to both prevent and treat disease. For example, tailoring treatments so that they contain species, or strains, that can competitively exclude specific pathogens using multiple mechanisms will increase the likelihood of successful pathogen exclusion; particularly if the pathogen becomes resistant to a mechanism, or there is a new (or opportunistic) pathogenic invasion. Patin et al. (2016) designed a workflow that aims to determine whether interference or exploitation competition is employed by using a series of simple inhibition assays. Following a direct challenge (co-culture) assay, a cell-free agar (and disc) diffusion assay determines if the antagonistic activity can be attributed to a diffusible molecule and thus is indicative of antimicrobial production. A negative result suggests the production of non-diffusible growth inhibitors, indicating an exploitation mechanism is at work. In this case, the assay is followed with a supplement assay in which the direct challenge assay is repeated with media supplemented by specific nutrients, such as iron. Applying this workflow provides a simple and cost-effective way to assess the competitive strategy likely employed by probiotic species in vivo, although future studies should consider the extent to which in vitro models (mechanisms of antagonism) are accurate representations of their interactions with pathogens, and other competitors, in vivo. Making this distinction is of importance when considering the type (i.e. desired characteristics) of probiotic to apply to specific conditions; for example, to improve disease resistance before a pathogenic invasion, or in response to an environmental disturbance, such as disease. Theoretically, competitive life strategists would be more suited to prophylactic treatment, as they are selected for in undisturbed environments, whilst ruderal life strategists would be best applied to reduce the severity of disease, as they are selected for in disturbed environments. This also highlights the importance of applying ecological theory to develop effective probiotics for disease prevention in shrimp aquaculture.

Potential probiotic identification based on the use of limited methods, such as cell-free extracts or diffusion assays exclusively, is selective of interference-based competition strategies due to the antimicrobial (and diffusible) properties of the extracellular metabolites. The culture conditions of potential probiotics may not stimulate inhibitory compound production (Long & Azam, 2001), or increase the activity of the compound (Rattanachuay et al., 2011). Furthermore, the inhibitory effect of cell-free supernatants and resistance of pathogens may be incorrectly determined due to insufficient concentrations in assays such as the disc-diffusion method (Smith, 2006; Van Hai et al., 2007). The limitations of culture-based probiotic selection...
methods, combined with the current focus on the ability of probiotic species to inhibit the growth of *Vibrio* species (Table 3), may overlook the capability of many putative probiotic species for shrimp aquaculture. Whilst pathogenic *Vibrio* species are undoubtedly an important target for potential probiotics to antagonise, screening based on *in vitro* growth inhibition of a limited number of specific pathogens (i.e. *Vibrio*) may be inadvertently polarising the type (i.e. competitive strategy) of shrimp probiotics available. Therefore, closer attention to characterising the underlying mechanisms by which probiotics inhibit the growth of these pathogens in vitro, combined with our increasing understanding of their effects *in vivo*, will enable us to better evaluate and develop our screening and selection methods. Probiotic treatment is able to alter the microbial community structure in the shrimp gut and confer resistance to pathogens such as *V. parahaemolyticus*, as is the case for *Bacillus aryabhatai* TBRC8450 treatment in *L. vannamei* (Tepaamornedech *et al.*, 2019). Probiotics targeted specifically at *Vibrio* spp. may increase the risk of disease in the event of an invasion by another species that the probiotic cannot inhibit, doing so by lowering the probability that other members of that community provide antagonistic traits. Stimulation of the shrimp immune response by such probiotics should, theoretically, mitigate some of these effects. However, it remains to be tested that a probiotic with such effects is able to enhance resistance to multiple pathogens. Rather, the current trend is to identify novel probiotics, which, without focusing on the underlying mechanisms, will continue to create a ‘never-ending story’ in this field (Ringø *et al.*, 2016). We suggest, therefore, that emphasis should be placed on the development of complementary, culture-independent, methods of potential probiotic identification and characterisation. With the increasing affordability of sequencing approaches, whole genome sequencing of probiotic species would benefit our understanding of the potential mechanisms of probiotic effects and allow us to make more informed decisions about the suitability of such species. Furthermore, metagenomic, transcriptomic, and metatranscriptomic studies, complemented by proteomics, would allow for more thorough investigation, assessment and development of probiotic treatments in shrimp aquaculture.

**Conclusions and future perspectives**

Probiotics in shrimp aquaculture are often screened and selected for *in vivo* testing based on their ability to competitively exclude pathogens *in vitro*. Few studies have attempted to identify the underlying mechanisms involved in bacterial growth inhibition; however, they collectively illustrate the importance of understanding the underlying probiont-pathogen interactions, determining strain specific characteristics and not extrapolating from related strains or even species. This is particularly important to consider when assessing the safety and suitability of a probiotic species for use in animals intended for human consumption, and consideration should be given to investigating the potential impact of probiotic treatment on the virulence of pathogens. The application of complementary sequencing approaches such as whole-genome sequencing of probiotic species will aid this assessment. The antagonism assays employed to screen for probiotics in shrimp aquaculture use a limited number of pathogens (i.e. *Vibrio*) and preferentially select for interference-based mechanisms, which may overlook the probiotic potential of many species and possibly increase the risk of pathogen invasion. To address this, future work should focus on expanding probiotic screening methods (including the development of culture-independent approaches) to include more species that use exploitation-based mechanisms and pathogens with distinct mechanisms of pathogenesis. Tailoring treatments so that they contain species, or strains, that can competitively exclude specific pathogens using multiple mechanisms will increase the likelihood of successful pathogen exclusion; particularly if the pathogen becomes resistant to a mechanism, or there is a new (or opportunistic) pathogenic invasion. The impact of probiotic treatment on the shrimp gut microbiota and disease resistance should also be carefully considered as not to reduce the abundance of other ecologically important species. Special consideration should be given to identifying and testing probiotics that are able to prevent the onset of disease with limited effects on the microbial community structure and function. Furthermore, the efficiency of treatment may be improved by considering the competitive life strategy of the probiotic species. Future studies should investigate this by validating the competitive strategies used *in vivo*, and designing pathogen challenge trials that compare the effects of probiotic administration, prior to and at the onset of disease or other such environmental disturbances, on the shrimp gut microbiome and disease resistance.

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