

CHAPTER I

INTRODUCTION

1.1 Background

Probiotics are defined as “live microorganisms that, when administered in adequate amounts, confer a health benefit on the host” (Hill et al., 2014). It is now recognized that probiotics are a component of the diet of livestock, including pigs, because of the benefits they can confer at all stages of production. These benefits include improved performance, disease mitigation, increased product quality, and reduced environmental pollution (Barba-Vidal, Martín-Orúe, & Castillejos, 2019). Thus, it is important to explore new bacterial isolates as potential probiotics.

The isolates in this study were obtained from the intestine of a locally-farmed pig. Previously, a study by Rini (2014) explored the possibility using several bacterial isolates taken from piglet intestines as probiotic candidates. In that study, a difference in the phenotype of resistance to lincomycin was reported, despite the two isolates having the same source. The piglet which the isolates were derived from had been raised with traditional methods and had not been given antibiotics. Hence, this study is a follow-up to that study, aiming to explain the discrepancy in AMR phenotype by genotyping.

1.2 Research Question

Why is there a difference in the phenotype between two bacteria of the same species isolated from the same organism?

1.3 Aim of Study

The general aim of this study is to genotype of 2 *Pediococcus pentosaceus* isolates (D32 and H29) obtained from piglet intestines in order to understand the differences in phenotype in regards to antibiotic resistance. The specific aims of this study are as follows:

1. General characterization of *P. pentosaceus* D32 and H29;
2. Whole-genome sequencing of *P. pentosaceus* D32 and H29;
3. Genotyping antibiotic resistance traits through bioinformatic analysis in *P. pentosaceus* D32 and H29.

