AWET Scholarship Thesis Abstract – Olivia Kelly

The rapid escalation of anthelmintic resistance (AR) poses a major threat to the productivity and sustainability of the Australian sheep industry. Gastrointestinal nematodes (GINs) such as *Trichostrongylus colubriformis* and *Teladorsagia circumcincta* are among the most pathogenic parasites of small ruminants, with widespread resistance now reported across multiple anthelmintic classes. Levamisole (LEV) remains one of the few effective compounds available and is used in combination drenches to manage mixed-species GIN infections. However, emerging reports of LEV resistance are cause for significant concern. The single nucleotide polymorphism (SNP) S168T within the acr-8 exon 4 region has been functionally validated in *Haemonchus contortus* as a marker of LEV resistance, providing a valuable molecular target for surveillance. This study aimed to establish a proof of concept for the molecular detection of the S168T SNP in *Tri. colubriformis* and *Tel. circumcincta* populations using metabarcoding and next-generation sequencing. Across 200 mixed-larval samples collected from New South Wales sheep flocks, the average frequency of the S168T mutation was 34.64% in *Tel. circumcincta* and 24.34% in *Tri. colubriformis*. These results provide the first molecular evidence of LEV resistance alleles in *Tel. circumcincta* and *Tri. colubriformis* in Australia. By integrating real-time parasite monitoring with SNP-based screening, resistance alleles can be detected at low frequencies before phenotypic drug failure occurs. This approach provides a foundation for improved anthelmintic stewardship and highlights the need for further research to define the threshold at which genotypic resistance translates to phenotypic drug failure. Overall, this work supports a proactive transition in AR management, shifting from reactive treatment to evidence-based prevention.