

Graduate Student Research Day – Deadlines and Abstract Submission Guidelines

February 8, 2019, 5 PM: Submit abstracts by email to vmgrad@ucalgary.ca

February 15, 2019: Register on Eventbrite (<https://www.eventbrite.ca/e/graduate-student-research-day-tickets-54805409455>)

February 15, 2019: Announcement of abstract review results (decision on presentation format)

March 1, 2019, 8 AM: Submit your electronic posters (PPT format) to Multimedia by email to medphoto@ucalgary.ca (subject: VMS Poster) for printing. The OGE will pay for posters submitted to multimedia by this deadline

March 5, 2019, 5 PM: Submit oral presentation PowerPoint to vmgrad@ucalgary.ca

Abstracts should be submitted as a Word document with file name (Abstract-Last Name-First Name of the presenting student)

Please follow the example abstract format regarding font type, font size, capitalization, superscript, etc.). It is important to provide all required information (including research group name and 3 key words) as shown in the example abstract. If students are not unsure about their research group affiliations, please consult your supervisors. Abstracts (not including title, authors and affiliation) are limited to 200-250 words. Abstracts longer than this will be returned to the student and supervisor for revision

Example Abstract

Field application of Deep-amplicon sequencing approach to investigate nematode species composition and anthelmintic resistance-associated mutations

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Research group: Infection Biology

Key words: Drug resistance, GIN parasites, Deep-amplicon sequencing

Anthelmintic resistance is a global concern to producers and veterinarians, and the resistance on a pasture occur faster than new drugs are launched in the market. In addition to the limited-sensitivity of the methodologies used to diagnose resistance, there is still a poor understanding of genetics basis of resistance to develop accurate diagnosis tools. Under this perspective, molecular epidemiological studies on the different mutations underlying resistance can support these tests and provide information on how resistance arise and spread within and between populations, thus helping to design strategies to delay it. The Next-Generation deep amplicon sequencing has been used in microbiome and nemabiome studies. The approach has many advantages compared to other sequencing strategies, such as greater throughput, high sensitivity and an increasingly affordable cost. Deep-amplicon sequencing is a powerful approach as it allows for multiplexed sequencing from hundreds of samples in a single run. In this study, we show some field applications of Deep sequencing, as the Nemabiome and the investigation of some resistance-associated mutations in fecal samples obtained from farms in UK and Canada. The resulting data is reliable and accurate and can be used to quantify the parasite species composition, perform molecular epidemiology studies and investigate the occurrence of multiple resistance-associated mutations.