PROTEIN PROFILE ANALYSIS OF THE FOAM PRODUCED BY THE NYMPH OF THE SPITTLEBUG Mahanarva spectabilis

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Mahanarva spectabilis, known as the spittlebug, is the primary insect pest causing damage to tropical forages, thereby adversely affecting cattle production and the dairy chain. Nymphs infest root regions, producing foam as a mechanism for environmental protection and defense against predators. Therefore, characterizing the chemical components present in the foam produced by this insect is crucial for developing a control strategy. To assess whether the host plant affects foam composition, grasses exhibiting different levels of resistance or susceptibility to spittlebug attack were subjected to infestation. The grass species *Pennisetum purpureum* cv. Pioneiro e cv Botucatu, *Brachiaria decumbens* cv. Basilisk, and B*rachiaria brizantha* cv. Marandu were propagated in 1 L pots containing a soil mixture and commercially available Plantmax substrate. Fourth and fifth instar *M. spectabilis* nymphs were collected from pastures located at Embrapa Dairy Cattle, Coronel Pacheco, MG, Brazil. The nymphs were kept on the plants covered with organza bags to prevent their escape, maintained at 25º C and 70% relative humidity until foam formation. Nymphs and foam were collected and stored at -80º C. Foam samples were concentrated using a speed vac. Protein samples containing 0,6 µg/µL were subjected to SDS-PAGE and LC/MS analysis. An aliquot of the foam proteins was initially separated by SDS-PAGE, and the bands were excised, quantified by densitometry, and subjected to trypsin cleavage to generate tryptic peptides. These peptides were analyzed using an LC/MS Ion Trap system for protein identification and sequencing. Another aliquot was analyzed using Gel-free and Label-free LCMS-based methods. Despite observing the presence of 8 major bands in the profiles, all were synthesized from a single contig, indicating the existence of post-transcriptional or post-translational regulatory mechanisms. Additionally, the relative abundance profiles varied between host plants. LC/MS analyses did not allow obtaining the N-terminal and C-terminal sequences, likely due to errors in the assembly of DNA sequences from the database. cDNA libraries will be used for sequencing and cloning of the coding regions (CDS). Finally, sequencing the N-terminal of proteins on the gel via LC/MS will enable determination of the regulatory mechanisms involved in foam protein synthesis with different molecular masses. This characterization will provide information for the development of strategies to control this insect pest

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