

ASSOCIATION BETWEEN *MAL DE RÍO CUARTO VIRUS* (MRCV) TITER AND TRANSMISSION EFFICIENCY BY 1st AND 3rd INSTAR NYMPHS OF *DELPHACODES KUSCHELI*

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MRCV causes the most important disease of maize in central Argentina. It is only transmitted by planthoppers (Hemiptera, *Delphacidae*) in a persistent propagative manner, being *D. kuscheli* the main vector species. Under controlled conditions, only 30% of MRCV-infected insects can actually transmit the virus. In turn, when MRCV is acquired by 1st instar nymphs (N1) the transmission frequency is higher than when acquired by 3rd instar (N3) nymphs. The aim of this work was to study the relation between N1 and N3 transmission efficiencies, and MRCV titer. Thirty *D. kuscheli* nymphs of each life stage were analyzed by 1:1 transmission tests (1 planthopper: 1 wheat seedling) with acquisition, latency and inoculation periods of 2, 17 and 1 day respectively. Absolute quantification of a fragment of MRCV segment 3 (MRCV-S3) in each planthopper was performed by qPCR in triplicate reactions using 1 ul of cDNA as a template and 200 nM of each primer in a final volume of 20 ul of SYBR Green. The Ct value obtained for each sample was extrapolated to a standard curve previously built from serial dilutions of a MRCV-S3 DNA fragment. Results were statistically analyzed by Mann-Whitney test. The N1 group showed higher transmission efficiency (60%) than N3 (28%). Regarding qPCR quantification, 20% and 26% of N1 and N3, respectively, resulted negative. All transmitting insects were positive and showed significantly higher viral titers than non-transmitting ones ($P < 0.003$ in N1 and $P < 0.013$ in N3). Our results showed that MRCV-transmitting planthoppers contained higher viral titers than non-transmitting ones, suggesting that successful transmission depends on a viral accumulation threshold. Thus, the higher transmission efficiency of N1 group might be explained by the greater number of individuals overcoming that threshold and consequently behaving as vectors. This work is relevant to better understand the mechanism underlying viral transmission and its epidemiological implications.

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