RNA interference (RNAi) has recently been developed as a potent reverse genetics technique to analyze gene function with possible application in insect pest control (1).

In the silkmoth, *B. mori* (Lepidoptera), no potent RNAi response is induced following injection or feeding of dsRNA (2). This observation prompted us to evaluate factors that could contribute to the (lack of) RNAi efficiency in the silkmoth, such as:

**Expression pattern of basic intracellular RNAi factors**

Expression studies suggested that the absence of R2D2 expression, an essential co-factor of Dicer-2 and Ago-2, may play a role in the refractoriness of the systemic RNAi response in *Bombyx* (3). However, functional studies indicate that the intracellular RNAi machinery can work efficiently in the absence of R2D2 in silkmoth-derived Bm5 cells (4).

**Expression of dsRNA-degrading enzymes**

It was demonstrated that a non-specific DNA/RNA nuclease (“dsRNase”) has a broad expression in many different tissues and is capable both to degrade dsRNA intracellularly and to interfere with dsRNA-mediated gene silencing (5).

**DsRNA as (non-specific) “pathogen-activated molecular pattern” (PAMP)**

It was observed that injection of dsRNA into the hemolymph induces the expression of genes of the RNAi machinery (Dicer-2, Ago-2) and dsRNase in the midgut, while the expression of the innate immune Toll9-1 receptor was inhibited (6). Ectopic expression of Toll9-1 receptor in Bm5 cells was observed to modulate the response against the PAMPs dsRNA and lipopolysaccharide (LPS) with respect to the expression of the RNAi machinery and innate immunity genes (7).
Persistent RNA virus infection

It is hypothesized that persistent virus infection can severely affect the function of the RNAi machinery according to several different molecular mechanisms (8). Next-generation sequencing was used to evaluate the transcriptome and small RNA response during infection of silkmoth larvae with cytoplasmic polyhedrosis virus (CPV), characterized with a segmented dsRNA genome (Cypovirus, Reoviridae). Analysis reveals a unique response to dsRNA virus infection in the silkmoth, with no overlap with the classical innate immune pathways triggered by bacteria or fungi (9).


