



Inducible NAD overproduction in Arabidopsis alters metabolic pools and gene expression correlated with increased salicylate content and resistance to Pst-AvrRpm1

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Plant development and function are underpinned by redox reactions that depend on co-factors such as nicotinamide adenine dinucleotide (NAD). NAD has recently been shown to be involved in several signalling pathways that are associated with stress tolerance or defence responses. However, the mechanisms by which NAD influences plant gene regulation, metabolism and physiology still remain unclear. Here, we took advantage of *Arabidopsis thaliana* lines that overexpressed the *nadC* gene from *E. coli*, which encodes the NAD biosynthesis enzyme quinolinate phosphoribosyltransferase (QPT). Upon incubation with quinolinate, these lines accumulated NAD and were thus used as inducible systems to determine the consequences of an increased NAD content in leaves. Metabolic profiling showed clear changes in several metabolites such as aspartate-derived amino acids and NAD-derived nicotinic acid. Large-scale transcriptomic analyses indicated that NAD promoted the induction of various pathogen-related genes such as the salicylic acid (SA)-responsive defence marker PR1. Extensive comparison with transcriptomic databases further showed that gene expression under high NAD content was similar to that obtained under biotic stress, eliciting conditions or SA treatment. Upon inoculation with the avirulent strain of *Pseudomonas syringae* pv. tomato Pst-AvrRpm1, the *nadC* lines showed enhanced resistance to bacteria infection and exhibited an ICS1-dependent build-up of both conjugated and free SA pools. We therefore concluded that higher NAD contents are beneficial for plant immunity by stimulating SA-dependent signalling and pathogen resistance.

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