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Short Report

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Pre-symptomatic biophysical profiling as a candidate approach for early screening of cowpea mild mottle virus tolerance in common bean

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Abstract

Cowpea mild mottle virus (*Carlavirus vignae*, CPMMV) is an emerging pathogen impacting common bean (*Phaseolus vulgaris* L.) production. While genetic tolerance protects yield, it allows systemic viral replication, demanding rapid, non-destructive tools for early diagnostic screening. This study characterized the chronological biophysical alterations in the photosynthetic apparatus of near-isogenic common bean lines under early CPMMV stress. Two cultivars with contrasting responses to CPMMV — BRSFC401RMD (susceptible) and BRSFC420RMD (tolerant) — were evaluated. High-sensitivity RT-qPCR detected systemic viral loads in stems and roots of the susceptible cultivar by 3 days after inoculation (DAI), long before any macroscopic symptoms emerged. Simultaneously, OJIP chlorophyll *a* fluorescence profiling captured immediate pre-symptomatic photosynthetic disruptions by 1 DAI. The susceptible cultivar exhibited a marked and consistent reduction in maximum fluorescence (*F_m*) as early as 1 DAI, accompanied by more variable changes in electron acceptor pool size (*Area*) and

thermal dissipation yield ($\Phi D0$). Conversely, the tolerant cultivar preserved photosystem II structural integrity (Fm/Fo and Fv/Fo) ratios) across evaluation seasons. Correlation matrix analysis at 10 DAI suggested that these early biophysical shifts reflect internal kinetic realignments that precede visual cell damage or biomass reduction. This rapid screening approach is a promising, non-destructive candidate tool for early-stage phenotyping in breeding programs under controlled or partially controlled environments and warrants further validation across a broader panel of genotypes.

Keywords: *Carlavirus vignae*, CPMMV, *Bemisia tabaci*, OJIP transient, diagnostic screening, phenotypic tolerance.

Common bean (*Phaseolus vulgaris* L.) is a vital socio-economic crop in tropical agriculture, representing a primary dietary protein source in developing nations (Brigide et al. 2014; Martins et al. 2016; Yi et al. 2016). Managing viral diseases remains a primary bottleneck for stable production. Cowpea mild mottle virus (*Carlavirus vignae*, CPMMV), transmitted rapidly by the whitefly *Bemisia tabaci* in a non-circulative manner, has shifted from a secondary disease to a major biotic stress affecting common bean production (Lamas et al. 2017; Souza et al. 2018). Integrated Pest Management (IPM) frameworks emphasize strict vector control thresholds. However, because *B. tabaci* is a highly efficient supervector (Gilbertson et al. 2015), standard density thresholds fail when local viral inoculum is high. A pyramided cultivar with natural tolerance protects grain yields but allows active systemic viral replication (Silva et al. 2022). Since non-circulative transmission lacks a latent period, rapid secondary spread may occur before visual leaf wrinkling or mosaic symptoms become apparent. Early diagnostic screening protocols in controlled environments can potentially help accelerate elite genotype selection and optimize management choices.

Viral infections trigger energy-intensive host defense mechanisms that directly affect chloroplast function (Zhao et al. 2016). To establish systemic infection, viruses disrupt photosynthesis-dependent defense pathways, targeting chloroplast structures and inducing early non-stomatal limitations, such as electron transport inhibition and photosystem II (PSII) disassembly (Bhattacharyya & Chakraborty 2018). Chlorophyll *a* fluorescence monitoring offers a sensitive, non-destructive tool to track these sub-lethal biophysical modifications before macroscopic chlorosis or necrosis materializes. This study characterized the chronological biophysical alterations induced by CPMMV in near-isogenic common bean lines to determine if dark-adapted OJIP fluorescence parameters can serve as reliable indicators for pre-symptomatic genotype screening.

Early detection of CPMMV on common bean plants was evaluated using two different approaches: molecular analysis by RT-PCR and RT-qPCR, or PSII kinetic performance using the OJIP protocol. Experiments used two contrasting common bean cultivars: BRSFC401RMD (BGMV-resistant/CPMMV-susceptible; "401") (Faria et al. 2016) and BRSFC420RMD (pyramided with natural CPMMV-tolerance; "420") (Silva et al. 2022). Plants were inoculated 7 days after sowing (DAS) either using a mechanical sap rubbing protocol (primary leaves treated with crude leaf extract in 0.1 M phosphate buffer), as described (Silva et al. 2022) or by biological vector transmission (viruliferous *B. tabaci* MEAM1 confined in clip cages for a 6-h inoculation access period). Control groups were mock-inoculated (with phosphate buffer only or exposure to non-viruliferous *B. tabaci*). Plants were kept isolated under vector-free conditions to ensure physical handling stress was equivalent between inoculated and control plants.

Systemic viral accumulation was monitored via conventional RT-PCR and high-sensitivity quantitative real-time PCR (RT-qPCR) using coat-protein-specific primers (CPMMV-cpF/R) (Table S1), tracking accumulation in stems, roots, and uninoculated foliage at 3, 5, and 10 days after inoculation (DAI), with 3 biological replicates per treatment. Amplifications and readings were evaluated on an ABI QuantStudio 7 (Applied

Biosystems) using appropriate qPCR reagents: Real-Time Q-PCR 2X master mix for Probe (Ampliqon), TaqMan 20X assays containing primers and probes specific for the Carlavirus cDNA (CP-CPMMV) and the endogenous bean gene (*PVT197*) (Table S1), and cDNA at 50 ng/uL. The results, expressed as threshold cycles (CT), were analyzed using DataAssist™ software (Thermo Fisher). For relative quantification, the sample with the lowest viral load was used as the reference for comparison with other samples positive for the virus. Non-inoculated control plants were tested in parallel and consistently returned negative results, confirming assay specificity. Molecular confirmation of systemic infection (conventional RT-PCR and RT-qPCR) was conducted exclusively in the susceptible cultivar (BRSFC401RMD), used as the reference host to establish the temporal kinetics of CPMMV replication and systemic movement, since the absence of tolerance mechanisms in this cultivar allows the earliest and most complete infection scenario to be captured. These temporal kinetics are assumed to serve as a qualitative reference for interpreting the biophysical changes captured by OJIP in the tolerant cultivar as well, in which the molecular response to CPMMV is expected to be slower or more restricted because of the genetic mechanisms underlying tolerance.

PSII kinetic performance was monitored in a randomized block design under a two-way factorial scheme (2 x 2, infected/non-infected per cultivar) with eight replicates, using exclusively mechanically inoculated plants to standardize infection timing and dose across treatments, a requirement for precise comparison at the evaluated time points. Evaluations spanned two greenhouse trials capturing microclimatic shifts: Experiment 1 (September–October 2022; higher mean temperatures/lower humidity) and Experiment 2 (March 2023; lower mean temperatures/higher humidity) (Figure 1). Dark-adapted (30 min) OJIP fluorescence transients were captured at 0, 1, 3, 5, and 10 DAI on uninoculated primary leaves opposite the inoculation site using a portable FluorPen FP-100 fluorometer, as described by Strasser et al. (2010) and Campos et al. 2021 (Table S2). Macroscopic disease severity (1–5 visual scale, Silva et al. 2024) and final whole-

plant biomass were recorded destructively at 20 DAI to determine final phenotypic outcomes.

Data were subjected to two-way factorial analysis of variance (ANOVA, 2 x 2 scheme), and means were compared using the Tukey HSD test ($p \leq 0.05$) for RT-qPCR relative expression data and for OJIP fluorescence parameters. Pearson correlation coefficients were calculated between OJIP parameters, plant weight, and disease severity. All statistical analyses were performed in R software (version 4.3.1) and AgroR package (Shimizu et al., 2025).

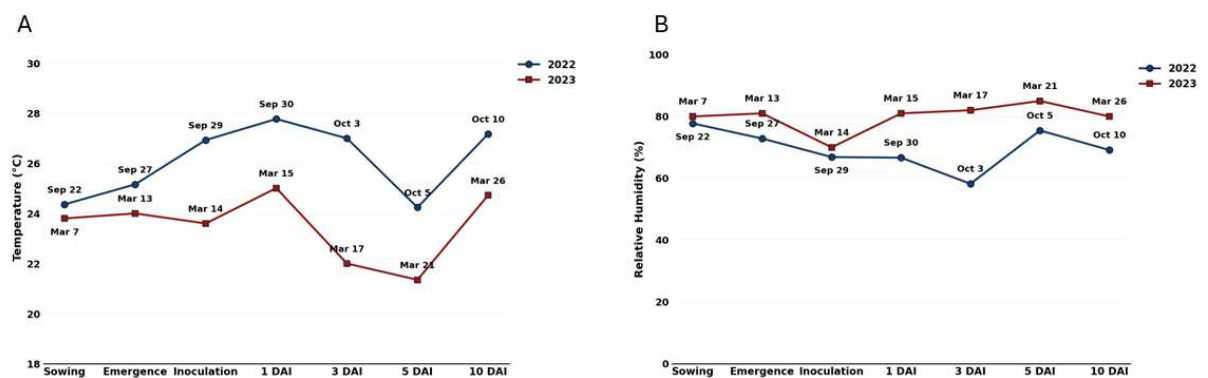


Figure 1. Average daily temperature (A) and relative humidity (B) in the screenhouse during experiments measuring the performance of photosystem II in common bean (*Phaseolus vulgaris*) plants mechanically inoculated with cowpea mild mottle virus (*Carlavirus vignae*, CPMMV) in 2022 and 2023. The labels for the averages indicate the dates (day/month) on which the steps (described on the x-axis) occurred. DAI: days after virus inoculation.

Molecular analyses demonstrated a clear diagnostic window during early incubation. Conventional RT-PCR did not reveal systemic viral bands at 3 DAI, with clear amplification appearing only by 5 DAI across both mechanical and biological cohorts (Table 1). In contrast, high-sensitivity RT-qPCR detected significant accumulation of the CPMMV coat protein gene in both stem and root tissues by 3 DAI, showing no statistical

variance between the inoculation methods or tissues (Figure 2). Crucially, all plants remained entirely asymptomatic up to 10 DAI, confirming that high viral transcription and systemic movement occur well before structural leaf deformation begins.

Table 1. Detection of *Carlavirus vignae* (cowpea mild mottle virus, CPMMV) on different parts of mechanically (rubbing the leaf with a CPMMV crude extract) or biologically (by the insect vector whitefly, *Bemisia tabaci*) inoculated common bean (*Phaseolus vulgaris*) plants cv. BRSFC401RMD at 3, 5 and 10 days post-inoculation, by RT-PCR.

Part of the plant	Type of inoculation	Days after inoculation		
		3	5	10
Stem	mechanical	-	+	+
	biological	-	+	+
Root	mechanical	-	+	+
	biological	-	+	+
Opposite leaf	mechanical	-	-	+
	biological	-	-	+
First trifoliolate leaf	mechanical	NA	NA	+
	biological	NA	NA	+

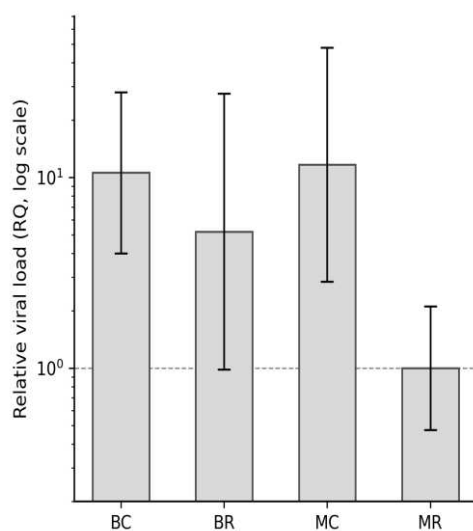


Figure 2. Relative viral RNA accumulation of the *Carlavirus vignae* (cowpea mild mottle virus, CPMMV) coat protein gene on stems and roots of common bean (*Phaseolus*

vulgaris) cv. BRSFC401RMD 3 days after mechanical (rubbing the leaf with a CPMMV crude extract) or biological (by the whitefly *Bemisia tabaci* vector) inoculation, using quantitative RT-qPCR, and normalized to the common bean endogenous reference gene *PvT197*. The mechanically inoculated root sample (MR) was used as the reference sample (calibrator) for relative quantification. BC: Biological inoculation of stems; BR: Biological inoculation of roots; MC: Mechanical inoculation of stems; MR: Mechanical inoculation of roots. Means are not significantly different at $p < 0.005$.

Among the OJIP parameters evaluated, maximum fluorescence (F_m) showed the most consistent response to early viral replication. Initial fluorescence F_o , reflecting the structural layout of the light-harvesting antenna complex, increased in infected tissues, though with a less uniform pattern across experiments. In Experiment 1, conducted under higher mean temperatures and lower relative humidity, this F_o elevation appeared in tolerant plants by 3 DAI, while remaining lower in infected susceptible cohorts before increasing by 10 DAI (Figure 3A). In Experiment 2, conducted under lower mean temperatures and higher relative humidity, the F_o increase occurred uniformly in both cultivars by 1 DAI (Figure 3B). These distinct patterns suggest that varying environmental conditions may modulate virus-host interaction kinetics, potentially altering the speed of systemic viral movement or enzymatic lipid peroxidation within thylakoid membranes; however, the current experimental design could not disentangle the relative contributions of temperature, humidity, and other seasonal factors.

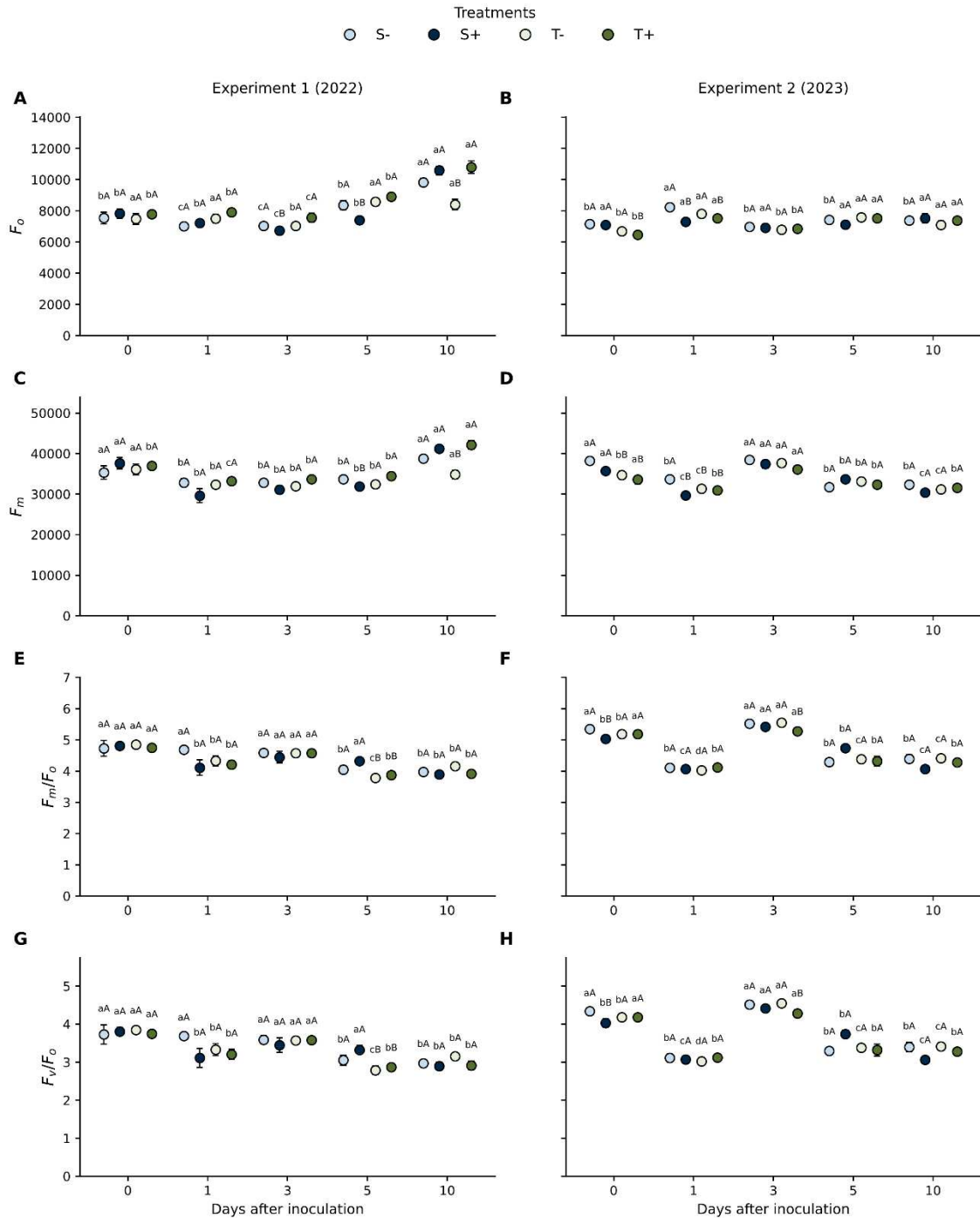


Figure 3. Biophysical parameters measured to monitor photosystem II performance in common bean (*Phaseolus vulgaris*) plants mechanically inoculated with *Carlavirus vignae* (cowpea mild mottle virus, CPMMV) at 5 time points (0, 1, 3, 5, and 10 days after inoculation) using the OJIP protocol. A and B) F_o : initial fluorescence; C and D) F_m : maximum fluorescence; E and F) F_m/F_o : ratio between open and closed reaction centers; G and H) F_v/F_o : ratio between variable fluorescence and initial fluorescence. Treatments: CPMMV-inoculated (T+) and non-inoculated (T-) common bean cultivar BRSFC420RMD, tolerant to CPMMV; CPMMV-inoculated (S+) and non-inoculated (S-) common bean cultivar BRSFC401RMD, susceptible to CPMMV. Means followed by the same letter (lowercase comparing days within a treatment and uppercase comparing treatments within a day) do not differ significantly by the Tukey HSD test ($p \leq 0.05$).

Experiment 1 (Sep-Oct 2022): A, C, E and G. Experiment 2 (March 2023): B, D, F and H.

Maximum fluorescence (F_m), representing the maximum fluorescence yield when all PSII reaction centers are closed, decreased by 1 DAI in the infected groups across both seasons (Figure 3C, D). In Experiment 1, infected tolerant plants exhibited a localized rebound in F_m at 10 DAI (Figure 3C). Rather than representing a permanent yield benefit, this transient rebound highlights a homeostatic adjustment that allows tolerant plants to preserve basal electron transport under thermal stress. This dynamic adjustment was absent in Experiment 2 (Figure 3D), possibly because the environmental conditions of that run lowered the host's basal metabolic demand and slowed viral multiplication, reducing physiological divergence between treatments.

The F_m/F_o ratio reflects changes in the fluorescence response between the minimum and maximum fluorescence states of PSII. The susceptible cultivar "401" showed declines in this ratio, which became clearly evident by 10 DAI in Experiment 2 (Figure 3F). The tolerant cultivar "420", in turn, showed a punctual and transient divergence at 3 DAI in Experiment 2 (Figure 3F, H), but maintained F_m/F_o and F_v/F_o ratios comparable to non-infected plants for most of the evaluation period, suggesting that tolerance is associated with a faster recovery of PSII photochemical performance rather than the complete absence of initial perturbation.

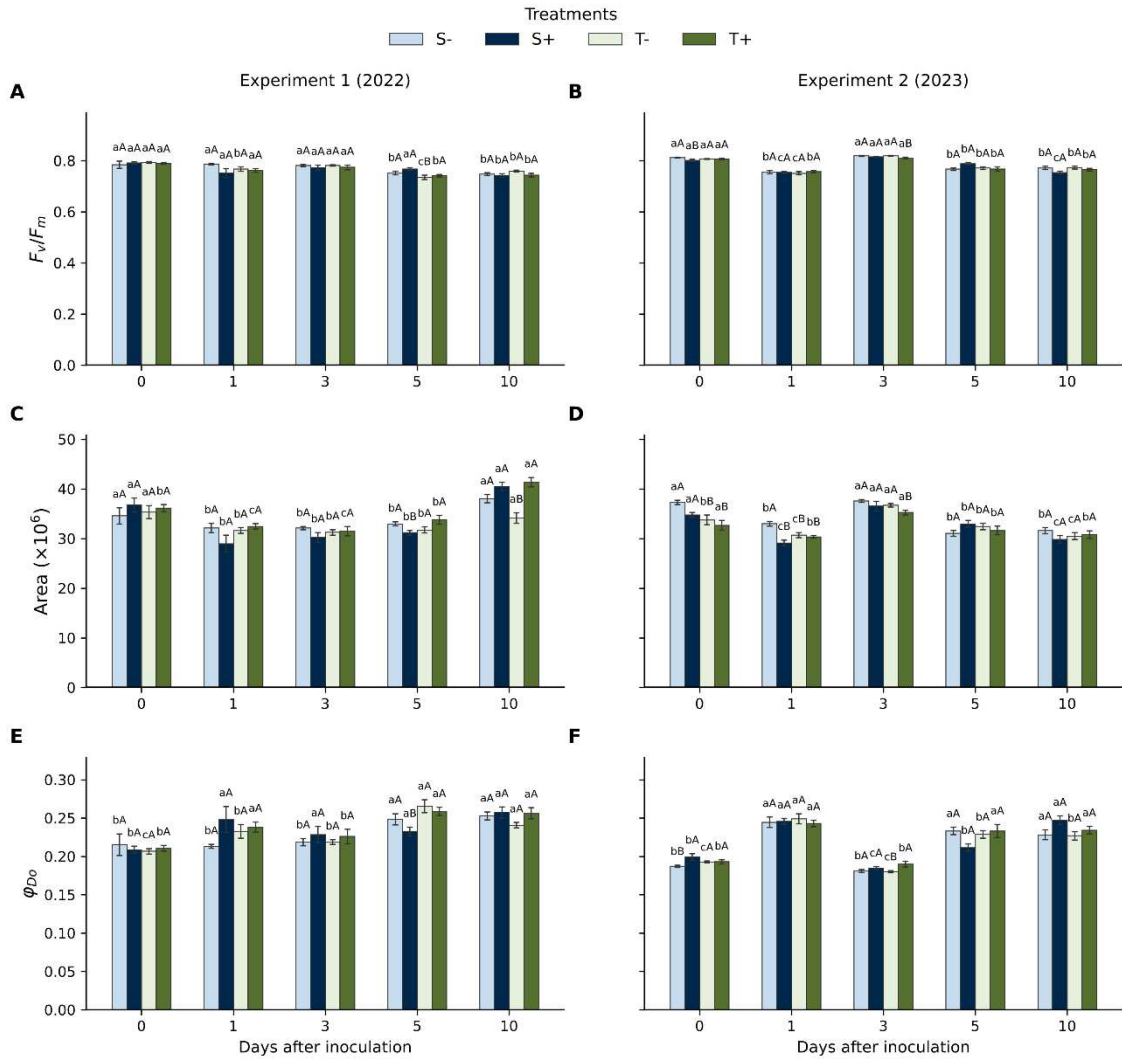


Figure 4. Biophysical parameters measured to monitor the photosystem II performance in common bean (*Phaseolus vulgaris*) plants mechanically inoculated with *Carlavirus vignae* (cowpea mild mottle virus, CPMMV) at 5 time points (0, 1, 3, 5, and 10 days after inoculation) using the OJIP protocol. A and B) F_v/F_m : ratio of variable fluorescence to maximum fluorescence; C and D) Area above the OJIP curve; and E and F) Φ_{Do} : quantum yield of energy dissipation, representing the fraction of absorbed photons dissipated as heat rather than used in photochemistry. Treatments: CPMMV-inoculated (T+) and non-inoculated (T-) common bean cultivar BRSFC420RMD, tolerant to CPMMV; CPMMV-inoculated (S+) and non-inoculated (S-) common bean cultivar BRSFC401RMD, susceptible to CPMMV. Means followed by the same letter (lowercase comparing days within a treatment and uppercase comparing treatments within a day) do not differ significantly by the Tukey HSD test ($p \leq 0.05$). Experiment 1 (Sep-Oct 2022): A, C and E. Experiment 2 (March 2023): B, D and F.

The complementary active area above the induction curve, *Area*, tracks the downstream electron acceptor pool size. CPMMV-driven stress contracted the *Area* in the susceptible cultivar, which became statistically detectable from 5 DAI onward in

Experiment 1 (Figure 4C), suggesting suppression of electron transport through the plastoquinone pool. Similarly, the quantum yield for thermal dissipation $\Phi D0$ increased significantly in infected susceptible plants from 5 DAI onward in Experiment 1 (Figure 4E). Although this pattern suggests that energy absorbed by the antenna could not be fully directed to photochemistry, being partially dissipated as heat, the absence of significant differences at the earlier time points (1 and 3 DAI) indicates that this response develops more gradually than immediately.

Correlation matrix analysis at 10 DAI (Figure 5) showed that agronomic traits (plant weight and disease severity, data not shown) presented no statistical correlation with the internal OJIP biophysical parameters, with coefficients remaining close to zero. This lack of correlation is expected at this stage of the experiment, since OJIP parameters and final agronomic outcomes capture physiological processes on distinct time scales: the former reflects immediate changes in the photosynthetic electron transport chain, whereas the latter results from cumulative damage over time. This dissociation reinforces the interpretation that OJIP parameters function as an early, independent indicator of physiological stress, registering cellular stress long before it results in visible tissue damage or biomass loss, rather than as a direct substitute for conventional agronomic measurements, which remain necessary to validate the final impact on yield. Among the parameters derived directly from the same raw fluorescence data, a near-perfect negative correlation was also observed between the maximum quantum yield Fv/Fm and thermal dissipation $\Phi D0$ ($r = -0.9997$, $p < 0.01$), a relationship mathematically expected from the JIP-test definition $\Phi D0 = 1 - Fv/Fm$, and therefore should not be interpreted as independent evidence of biophysical coordination.

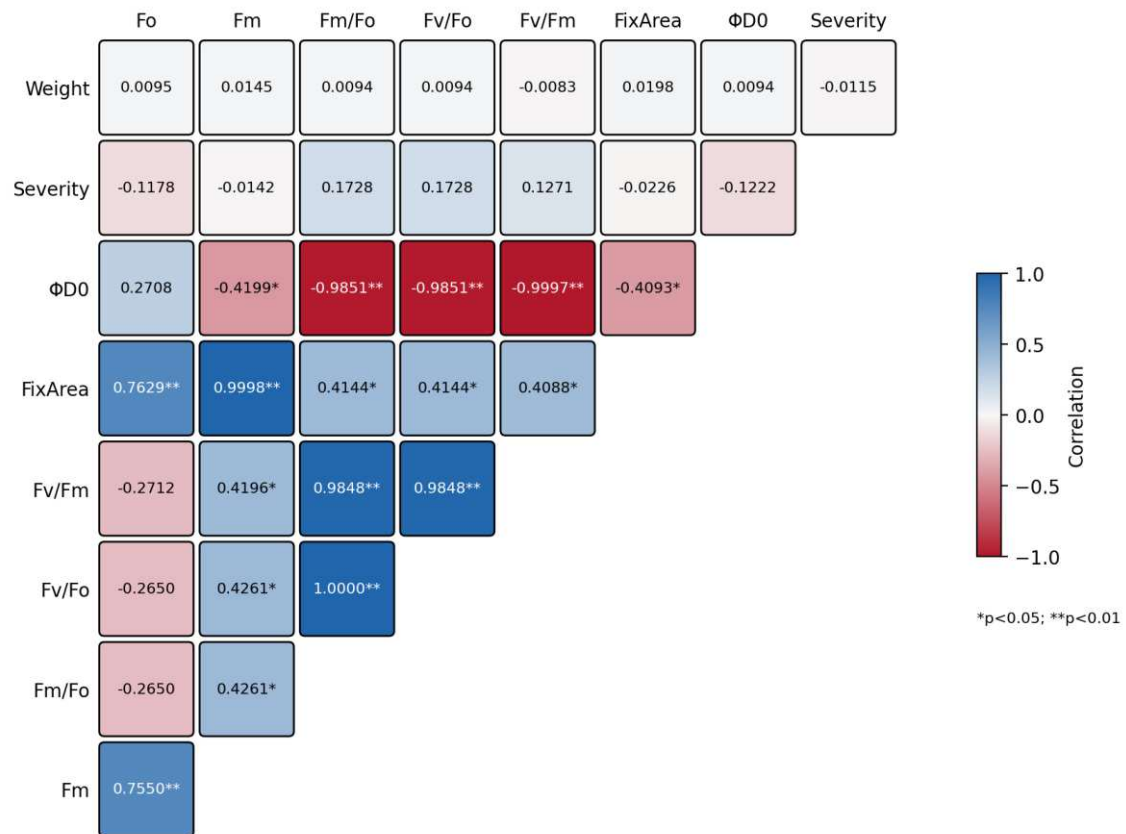


Figure 5. Correlation between OJIP parameters, plant weight and disease severity in common bean (*Phaseolus vulgaris*) plants, obtained on the 10th day after inoculation with *Carlavirus vignae* (cowpea mild mottle virus, CPMMV). Numbers followed by * or ** indicate correlation significance at $p \leq 0.05$ or $p \leq 0.01$, respectively. Note that Fv/Fo and Fm/Fo, as well as Fv/Fm and $\Phi D0$, are mathematically related parameters ($Fv/Fo = Fm/Fo - 1$; $\Phi D0 = 1 - Fv/Fm$); their near-identical or near-perfect correlation coefficients with other variables reflect this formulaic relationship rather than independent biological associations.

In conclusion, high-sensitivity RT-qPCR identifies systemic CPMMV in the susceptible common bean cultivar by 3 DAI. Among the OJIP parameters evaluated, maximum fluorescence (*Fm*) showed the earliest and most consistent response, with detectable contraction as early as 1 DAI in susceptible genotypes, preceding both the systemic detection of viral RNA at 3 DAI and the onset of visible symptoms. Complementary changes, such as increased thermal dissipation ($\Phi D0$), became statistically detectable at somewhat later stages (from 5 DAI onward). The tolerant cultivar 420 showed greater stability in PSII-related parameters, such as Fm/Fo and Fv/Fo, under viral pressure across distinct environmental seasons. Consequently, dark-

adapted OJIP fluorescence parameters — particularly *Fm* — represent a promising, non-destructive approach for early-stage physiological phenotyping before macroscopic disease expression, warranting further validation across a broader panel of common bean genotypes.

Authors' contributions

PVP (principal investigator), MLJ, WRR and LJMC developed the conceptualization of this research. WRR, ALF, MCM and LJMC carried out the experimental design, setup, conduct and evaluation of the experiments. ALF and MCM conducted sample collection, preparation and RT-PCR. PAMRV validated quantitative PCR viral load quantification. LJMC and ALF performed data analysis and graph designs. PVP, ALF and LJMC performed manuscript writing. All authors reviewed the article and revised it critically for important intellectual content.

Data availability statement

The datasets generated during and/or analyzed during the current study are available in the Figshare repository, at <https://doi.org/10.6084/m9.figshare.34050246>.

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compliance with Brazilian biodiversity legislation and registered in SisGen under code ABDA1C2.

Supplementary Data

Table S1. Primers used in the PCR and qPCR reactions for CPMMV detection in common bean (*Phaseolus vulgaris*).

Table S2. Biophysical parameter formulas and definitions for chlorophyll a fluorescence analysis adapted from Strasser et al. (2000) and Campos et al. (2021).

Conflict of interest

The authors declare no competing interests.

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