

Transcriptomic analysis of the interaction geminivirus-tomato

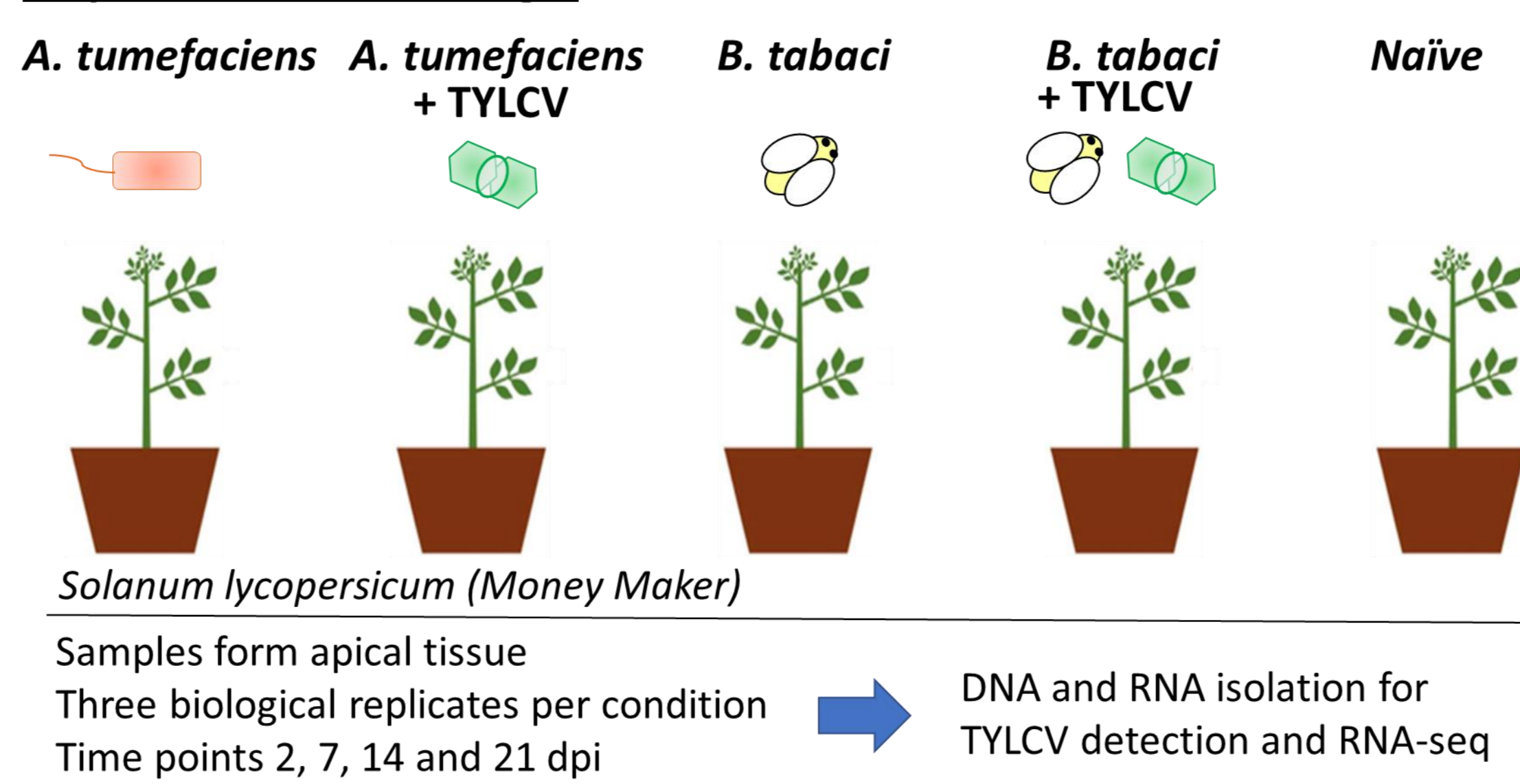
Beatriz Romero-Rodríguez¹, Marko Petek², Maja Zagorscak², Álvaro Piedra-Aguilera¹, Ana P. Luna¹, Kristina Gruden², Eduardo R. Bejarano¹ y Araceli G. Castillo¹.

¹ Área de Genética. Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", Universidad de Málaga-CSIC (IHSM-UMA-CSIC), Campus Teatinos, 29010 Málaga, Spain.
² Department of Biotechnology and Systems Biology, National Institute of Biology, Vecna pot 111, 1000 Ljubljana, Slovenia.

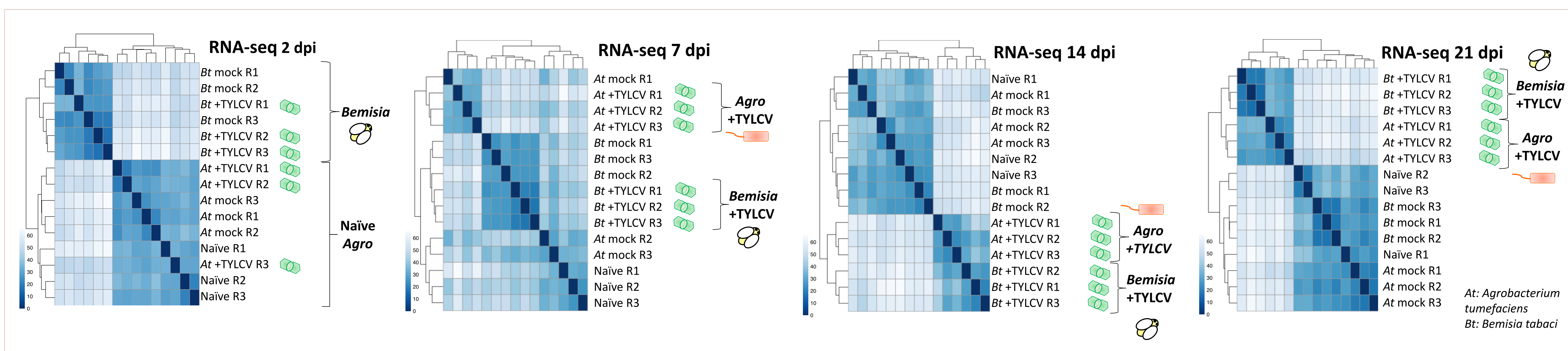
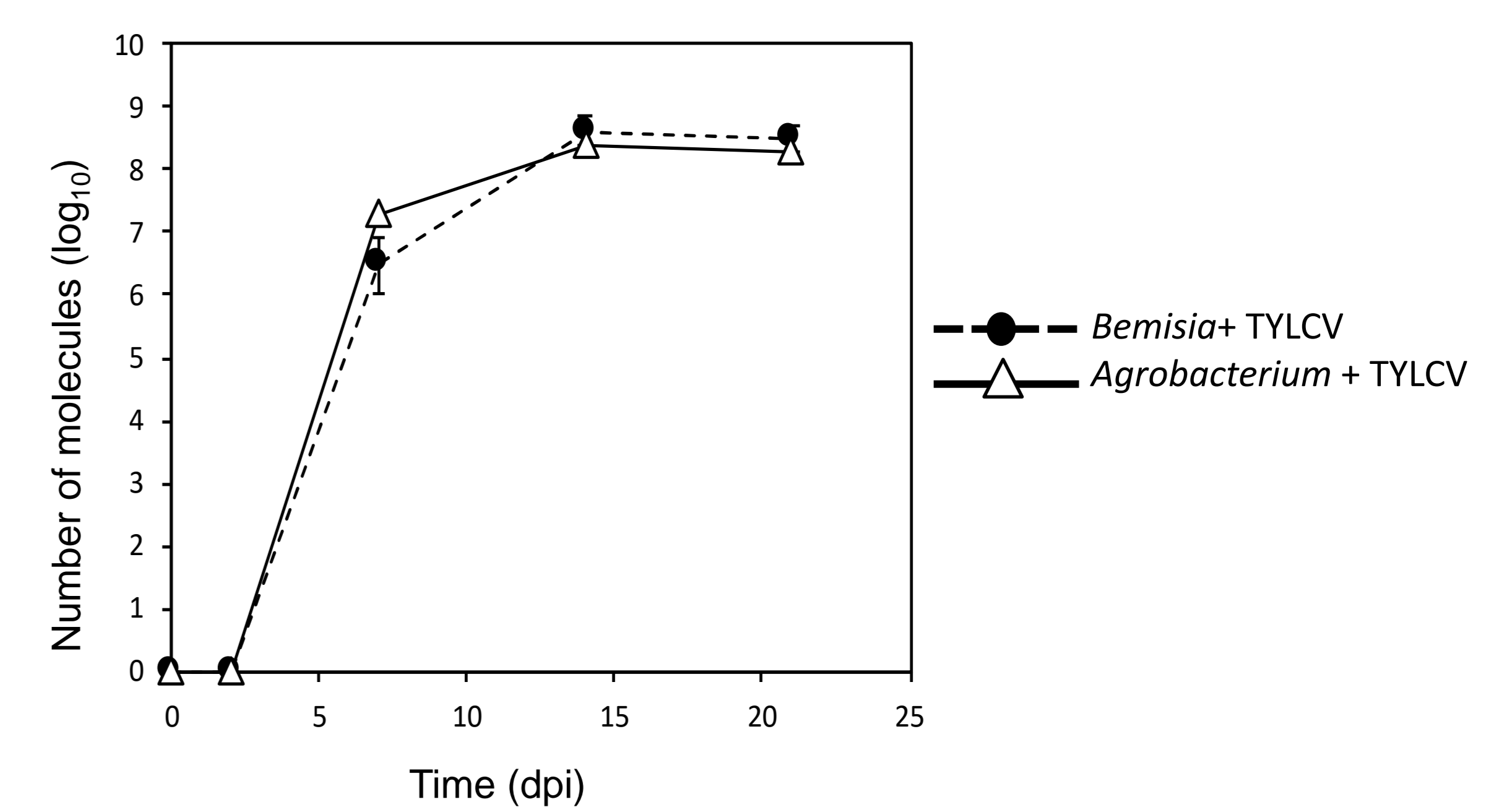
Introduction

Geminiviridae family is one of the main families of plant pathogenic viruses with large relevance as they cause great losses worldwide in commercial crops and crops destined to food production. Geminiviruses present a little single-stranded DNA genome and a capsid composed of two twin icosahedral parts. *Tomato Yellow Leaf Curl Virus* (TYLCV) belongs to the *Begomovirus* genus and is transmitted by the whitefly *Bemisia tabaci*. With only 6 viral proteins, this geminivirus must create a proper environment for viral replication, transcription and propagation. Behind the apparent simplicity of geminiviruses lies a complex network of molecular interactions with their host and even their natural vector, which induces a wide variety of transcriptional, post-transcriptional and chromatinic changes in both the plant and the geminivirus. In order to study these changes and decipher the effects of the transmission vector on the infection, we carried out a global approximation of the TYLCV-tomato interaction to generate integrated single-base resolution maps by NGS (next-generation sequencing) of the transcriptome, smallRNAome and methylome of the pathogen and the host. The transcriptome of the tomato-TYLCV interaction will be presented and discussed.

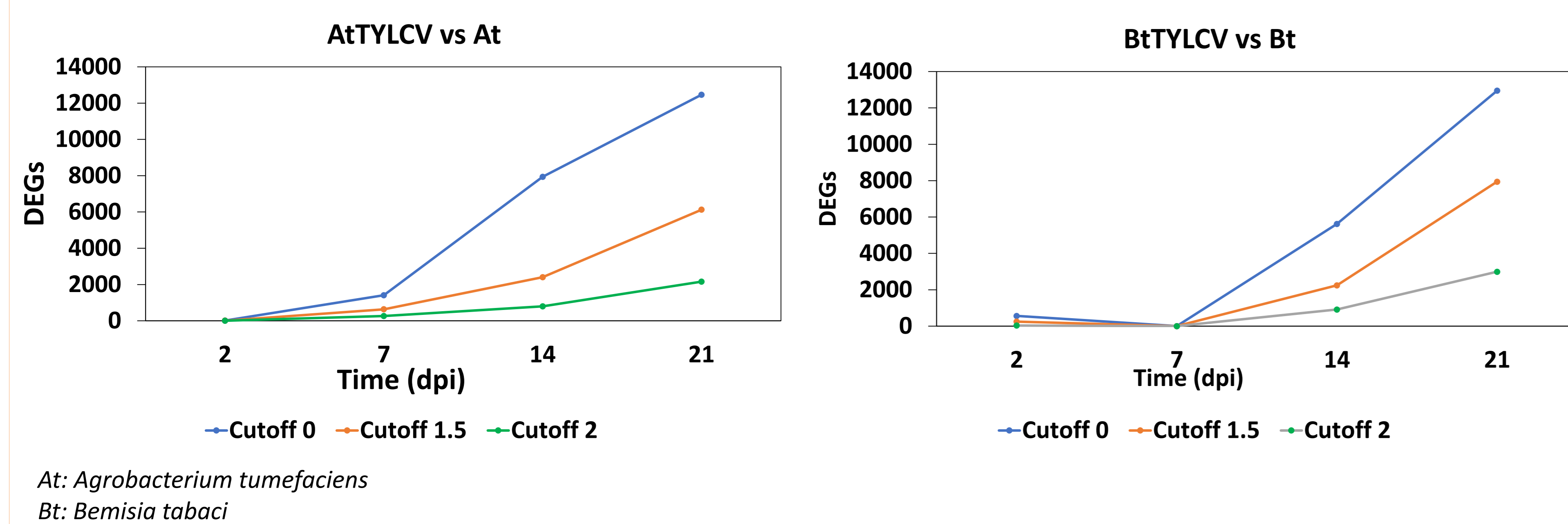
Experimental design



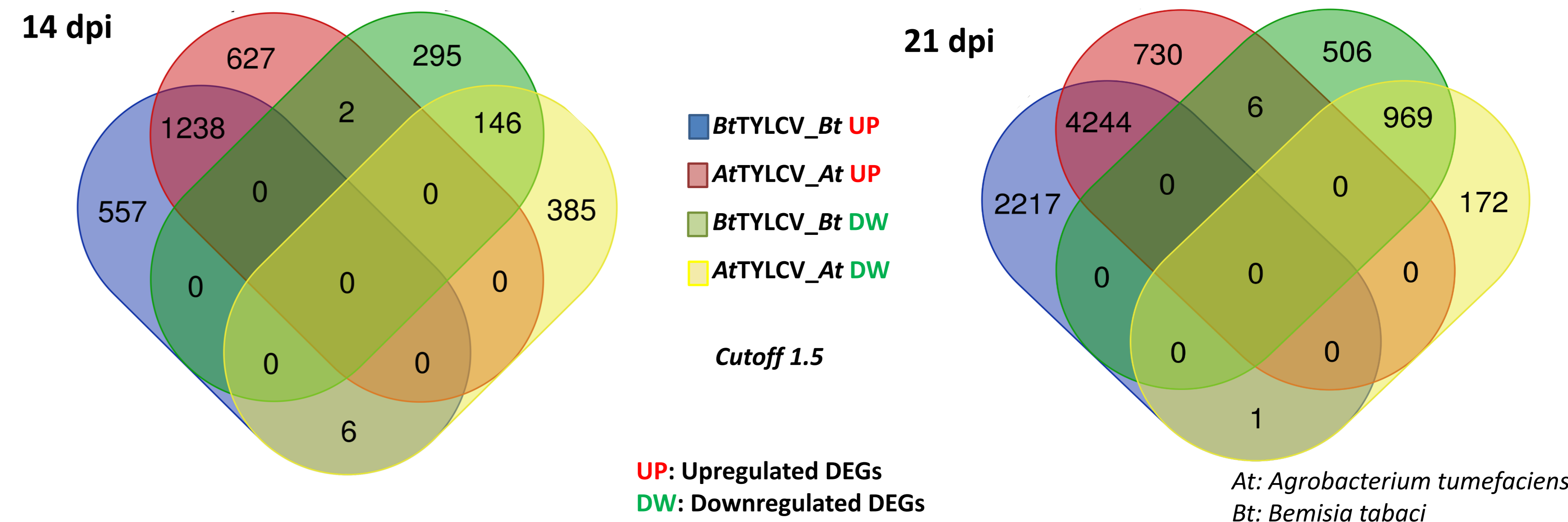
TYLCV detection in infected plants



Differentially expressed genes (DEGs) at each time



Differentially expressed genes (DEGs) at 14 and 21 dpi



Upregulated GO categories	S/ REF	At 14 dpi	At 21 dpi	Bt 14 dpi	Bt 21 dpi
Celular calcium ion homeostasis	19		12		12
Sequestering of calcium ion	7		6		7
Defense response	38		19		18
Response to stress	368	61	119	66	142
Innate immune response	21	7	13		13
Response to other organism	32	8		8	
Autophagy	21		11		14
Autophagy of mitochondrion	19		11		14
Autophagosome assembly	33		14		23
Cell death	53		19		22
Protein phosphorylation	269	29	64	27	75
Protein autophosphorylation	128	24	45	24	49
Intracellular signal transduction	335		87		125
Ras protein signal transduction	79		23		30
Protein ubiquitination	222		58		80
Transcription, DNA-templated	866		159		235
Intracellular protein transport	487		108		165
Cellular response to stimulus	825	66	197	68	275
Cellular response to DNA damage stimulus	219	25			65
Vesicle-mediated transport	361		75		123
MVB pathway	16		9		13
Translational termination and elongation	321			3	32

Downregulated GO categories	S/ REF	At 14 dpi	At 21 dpi	Bt 14 dpi	Bt 21 dpi
Photosynthesis	54	16	31		31
Carbohydrate metabolic process	326	15	29		33
Carbohydrate biosynthetic process	26	5	9	4	10
Gluconeogenesis	22	6	8		8
Cellular homeostasis	27	6	9		31
Response to stimulus	767	24	50		53
Response to light stimulus	70	10	25		25
Methylation	39				7
ncRNA metabolic process	224		22		29
tRNA metabolic process	68		15		17
Cellular response to oxidative stress	40		7		7
Reactive oxygen species metabolic process	37		8		8
Plastid organization	48	7	10		16
Chloroplast organization	37		7		14
Alcohol metabolic process	52	6	7		8
Cofactor metabolic process	237	12	28		31
Vesicle-mediated transport	361		1		1
Translational termination and elongation	321		33	13	40

Acknowledgement. This research was supported by a grant from the Spanish Ministerio de Ciencia y Tecnología (AGL2016-75819-C2-1-R, B. R. and A. P. were awarded a Predoctoral Fellowship from de Spanish Ministerio de Educación y Formación Profesional

