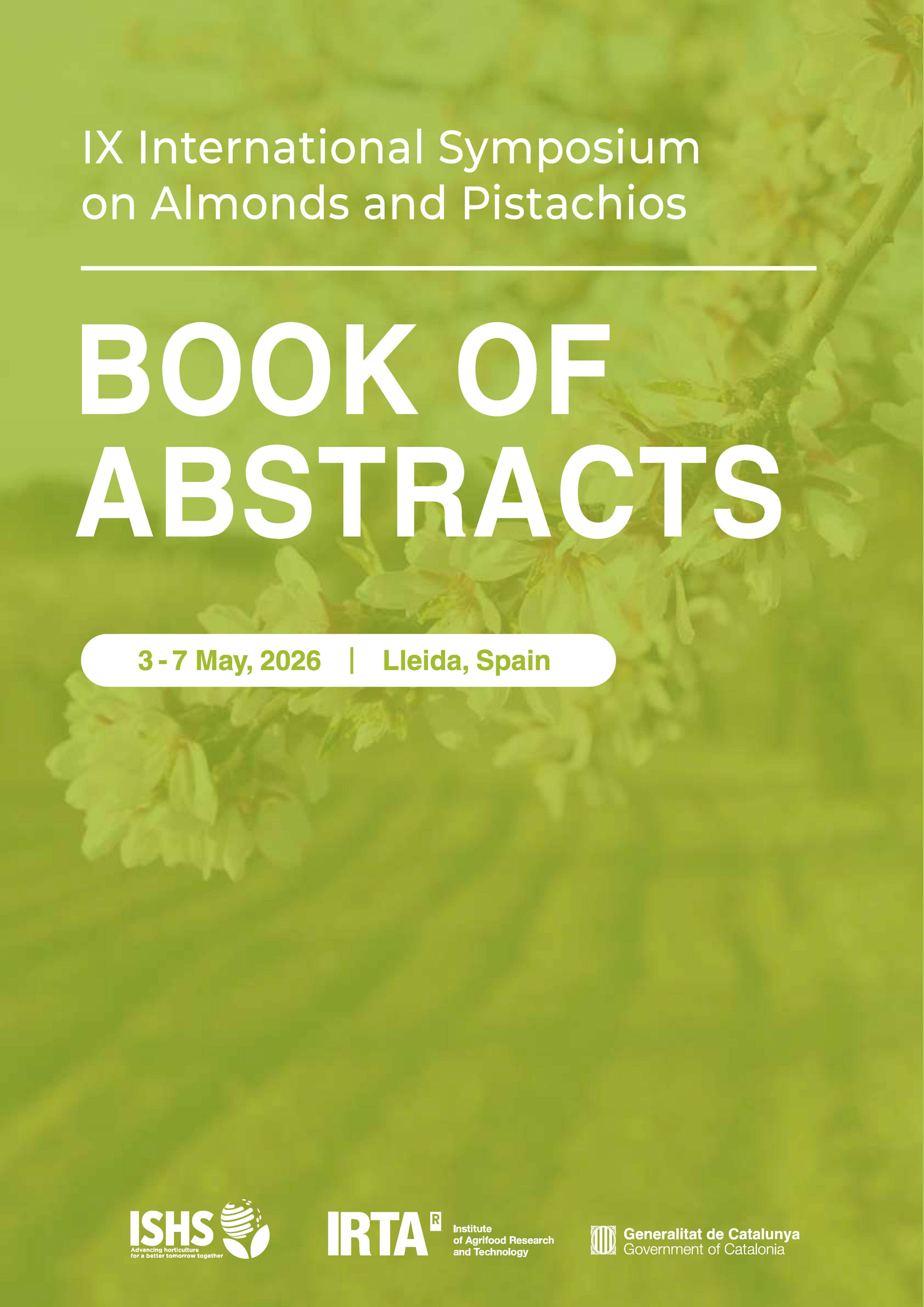

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BOOK OF ABSTRACTS

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Exploring Almond R-Genes for Enhanced Pathogen Defense

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Resistance (R) genes are central to plant immunity, primarily encoding leucine-rich repeat-containing proteins that detect pathogen effectors and activate defense mechanisms. Due to their structural complexity and repetitive domains, accurate annotation of these genes remains a challenge, especially in large plant genomes. In *Prunus dulcis* (almond), we performed a thorough manual curation of R genes to overcome limitations in automated annotation. This effort combined outputs from three annotation pipelines, comparative genomics with related species, and transcriptomic data from short- and long-read RNA sequencing across multiple tissues. Hidden Markov Models were also employed to identify conserved domains such as TIR, NBS, and LRR. We identified 1,064 high-confidence R genes, organized into five subfamilies and 25 structural subgroups. Over one-third of gene models required correction relative to the V3 reference genome. Notably, we report the discovery of a novel LRR-WD40 subfamily in higher plants, offering new perspectives on NBS domain evolution. Expression profiling across six almond tissues revealed widespread transcriptional activity, including in regions previously annotated as pseudogenes. This curated gene set provides a robust foundation for functional studies and supports breeding efforts aimed at enhancing disease resistance in almond and related species.