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**BOOK OF ABSTRACTS**

- Agronomy
- Chemistry
- Technology
- Physiological effects
- Sustainability, climate changes

## Comparative characterization of resistance proteins in *Coffea* species

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### RATIONALE

Plants have evolved highly complex defense mechanisms to protect themselves from various pathogens. One of such mechanisms is activated when a given pathogen-derived molecule, called effector, is 'specifically recognized' by plant receptor proteins encoded by R genes. Understanding the role of R genes in plant defence is of utmost importance because the transference of particular R gene variants to susceptible individuals may confer resistance to specific pathogens. Dozens of thousands of R genes have been identified to date in hundreds of plant species and several tools are available to characterize R genes in a given sequence. The unprecedented power of next generation sequencing to produce genomic data has resulted in the release of entire genomes for dozens of plant species.

### METHODS

We have identified R genes present in the available whole reference genome sequences of *Coffea canephora*, *C. eugenioides*, and *C. arabica*, as implemented in DRAGO2 (<https://github.com/sequentiabiotech/DRAGO2-API>). Then we performed reciprocal BLAST searches using these R genes and their flanking regions to identify homology and paralogy across coffee species.

### RESULTS

The number of R genes found in the three coffee species ranged between 2345 for *C. canephora* and 5218 for *C. arabica*. Despite a basic analysis showed that the number of homologous proteins between species pairs ranged between 1350 (for the comparison *C. canephora*-*C. eugenioides*) and 1700 (for *C. eugenioides*-*C. arabica*), a deeper characterization of the genomic regions containing R genes provided additional details about the ancestry of these genes in the three species.

### CONCLUSIONS & PERSPECTIVES

Our results shed light into the molecular structure, distribution, and ancestry of R genes in *C. arabica*, *C. canephora*, and *C. eugenioides*. Using this knowledge, we aim to understand the molecular mechanisms underlying disease resistance in *Coffea* species.

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