Modern Approaches for the Genetic Improvement of Rice, Wheat and Maize for Abiotic Constraints-Related Traits: a Comparative Overview (E. Benavente and E. Giménez)

Supplementary material: Methodology followed for the bibliometric and bibliographic analyses

The following table shows the search query terms and filtering fields used to perform the bibliographic database-based analyses for the three term categories considered in the review.

CATEGORY	Term used in Tables and Figures	Search query term	Search field ^a
CROP	rice	rice OR oryza	title
	wheat	wheat OR triticum	title
	maize	maize OR zea OR corn	title
TOOL/ APPROACH	QTL mapping	qtl OR "quantitative trait loc*"	topic
	GWAS	"Genome-wide associat*" OR GWAS	topic
	Genome selection	"Genom* selection" OR "Genom* predict*"	topic
	Gene expression b	"gene Express*" OR transcriptom*	topic
	Transcriptomics	transcriptom* OR "cDNA array"	topic
	Quantitative PCR	qPCR OR "quantitative PCR" OR "real time PCR"	topic
	RNA-seq	RNA-seq OR "NGS-based RNA sequencing"	topic
	Transgenesis	Transgen*	topic
	Gene editing	"Gene* editi*" OR TALENS or CRISPR	topic
	Mutagenesis	mutagenesis	topic
BREEDING TOPIC	(Any)		topic
	Drought tolerance, WUE	"water use" or "WUE" or "Drought toleran*"	topic
	Heat tolerance	thermotoleran* or "heat toleran*"	topic
	NUE	"Nitrogen use" or "N use" or NUE	topic

^a: The field named as 'topic' in the WOS database searches title, abstract, author keywords, and more. The equivalent field in the SCOPUS database is 'Article title, Abstract, Keywords'.

BIBLIOMETRIC ANALYSIS Based on searches in the WOS database

Figures 2, 4 and 6: Based on the number of records retrieved by combining search queries for [CROP] AND [TOOL/APPROACH].

Figures 3, 5 and 7: Based on the number of records retrieved by combining search queries for [CROP] AND [TOOL/APPROACH] AND [BREEDING TOPIC].

BIBLIOGRAPHIC ANALYSIS Based on searches in the WOS and SCOPUS databases

Tables 1 to 3: The records retrieved by each of the searches used for bibliometric analysis were sorted oldest first. Following in parallel the two chronological lists (in WOS and SCOPUS), the records were being manually revised by the authors until a document evidencing that the corresponding tool/approach was really used, and not merely mentioned, was found. For that purpose, the abstracts were accessed and checked, except when the title was descriptive enough to dispel any doubts. If the abstract was not helpful, the full document was downloaded to check the Materials and Methods section.

^b: Only used in the bibliographic search on the first documented evidence of gene expression analysis (Table 2)