














ORIGINAL RESEARCH ARTICLE

Crop Breeding & Genetics

Rank-based data synthesis of common bean on-farm trials across four Central American countries

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Abstract

Location-specific information is required to support decision making in crop variety management, especially under increasingly challenging climate conditions. Data synthesis can aggregate data from individual trials to produce information that supports decision making in plant breeding programs, extension services, and of farmers. Data from on-farm trials using the novel approach of triadic comparison of technologies (tricot) are increasingly available, from which more insights could be gained using a data synthesis approach. The objective of our study was to present the applicability of a rank-based data synthesis approach to several datasets from tricot trials

Abbreviations: AIC, Akaike information criteria; AOA, area of applicability; DAP, daily accumulated precipitation; DI, dissimilarity index; DP, daily precipitation; DSRF, daily solar radiation flux; tricot, triadic comparison of technologies.

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to generate location-specific information supporting decision making in crop variety management. Our study focuses on tricot data from 14 trials of common bean (*Phaseolus vulgaris* L.) performed between 2015 and 2018 across four countries in Central America (Costa Rica, El Salvador, Honduras, and Nicaragua). The combined data of 17 common bean genotypes were rank aggregated and analyzed with the Plackett–Luce model. Model-based recursive partitioning was used to assess the influence of spatially explicit environmental covariates on the performance of common bean genotypes. Location-specific performance was predicted for the three main growing seasons in Central America. We demonstrate how the rank-based data synthesis methodology allows integrating tricot trial data from heterogenous sources to provide location-specific information to support decision making in crop variety management. Maps of genotype performance can support decision making in crop variety evaluation such as variety recommendations to farmers and variety release processes.

1 | INTRODUCTION

Reliable location-specific information supports better decision making in crop variety management especially under increasing climate variability. On-farm trial data are expensive to obtain and limited by different factors such as institutional reach into certain areas, availability of seeds, staff, and other resources. It is possible to aggregate data from individual trials to gain insights into variety performance at broader temporal and spatial scales. This can help to gain insights on using varieties across broader areas as climates shift and to avoid simplistic assumptions about variety environmental adaptation based on rough adaptation zonation approaches. Data synthesis is needed for this and can lead to new insights into a genotype \times environment interaction under real farming conditions, as trial data can be combined with environmental data, which is increasingly available. Novel data synthesis approaches can extract information from crop variety evaluations to support critical decision making in crop variety management (Brown et al., 2020). In their review, Brown et al. (2020) have proposed rank-based methods as a way forward in data synthesis because it allows for flexible aggregation of heterogenous data collected using different measurement scales. Rank-aggregation methods have been proposed for the meta-analysis of data from crop genetic resources evaluations by Simko and Pechenick (2010) and Simko and Linacre (2010) with further developments by Simko et al. (2012). This involves converting numerical data to relative ranks and applying a statistical model suitable to ranking data such as the Plackett–Luce model (Luce, 1959; Plackett, 1975).

Rank aggregation as a data synthesis method involves no data conversion if ranking data are analyzed, which are collected in on-farm trials, such as the triadic comparison of

technologies (tricot) and comparable formats (Coe, 2002; van Etten, Beza, et al., 2019). The tricot approach involves farmers participating as citizen scientists evaluating sets of three genotypes in their own farms (van Etten, Beza, et al., 2019). Farmers grow the varieties in small trial plots and rank the varieties accordingly to different traits such as yield, disease resistance, market value, and the overall performance of the genotypes (van Etten, Beza, et al., 2019). The use of rankings implies an inherent loss of information when compared to measurements in a continuous scale using specialized instruments (Coe, 2002). However, collecting data in ranking format allows the participation of a larger number of farmers and a reduction in the costs of the experiments compared with other participatory methods (Coe, 2002; van Etten et al., 2020). Since the data are in ranking format, it should be analyzed with an appropriate statistical model such as the Plackett–Luce model (Luce, 1959; Plackett, 1975). The tricot approach is increasingly used for different crops by several organizations in Africa and Latin America producing considerable volumes of data. van Etten, de Sousa, Aguilar, et al. (2019) applied the Plackett–Luce model to analyze the variety performance of red common bean (*Phaseolus vulgaris* L.) varieties in Nicaragua. That analysis determined the influence of environmental factors on variety performance using model-based recursive partitioning in combination with the Plackett–Luce model (Turner et al., 2020; Zeileis et al., 2008). The current study explores combining data from several trials executed by different organizations in multiple locations following a data synthesis strategy as described in Brown et al. (2020). Applying a data synthesis approach to tricot data overcomes some of the limitations for data synthesis identified by Brown et al. (2020) such as incompatible data formats, scales, and experimental designs. Still, aggregating tricot data drawn from trials established by different

organizations requires effort. Several elements can be adopted from the existing work on tricot, but an additional investment is required especially when characterizing uncertainty of model predictions, complementing the Plackett–Luce tree model. In this paper, we describe this new approach and apply it to a dataset on common bean from Central America.

Here, our main objective is to present the applicability of a rank-based data synthesis approach to several datasets from tricot trials to generate location-specific information supporting decision making in crop variety management. The proposed approach is demonstrated with red common bean genotypes, which were evaluated by four teams of five different organizations in a series of tricot trials in four countries in Central America (Costa Rica, El Salvador, Honduras, and Nicaragua).

The specific objectives are to (a) integrate data from tricot trials produced by different organizations at different locations and seasons, (b) identify the environmental factors affecting the performance of the evaluated genotypes, (c) predict the best performing genotypes for each main planting season in the study region, and (d) assess the uncertainty and applicability of model predictions.

2 | MATERIALS AND METHODS

2.1 | Tricot trial data

We obtained data from 14 on-farm trials across Central America (Figure 1). Each trial is a set of incomplete blocks located on farms that test a set of genotypes in a single area and within the same agricultural season. The trials were executed by four teams of five different organizations working in the field across four Central American countries. Key characteristics of the datasets are provided in Table 1. All trials followed the tricot citizen science approach described by van Etten, Beza, et al. (2019). This consists of an incomplete block design with blocks of size three, the use of ranking as a farmer-centric data collection approach, and the intensive use of digital tools to streamline the process. Each tricot plot is an incomplete block set of three red common bean genotypes, which were grown and evaluated by farmer citizen scientists. Genotypes include both released varieties and experimental lines. Packages of bean seeds were delivered to farmers without disclosing the names of the genotypes; bags with the genotypes were labeled as A, B, and C. Each farmer assessed the three genotypes and provided feedback by ranking the genotypes. Farmers evaluated plant foliage, plant height, reaction to pests and diseases, drought tolerance, yield, market value, and taste and also gave their overall judgment considering all the traits. In our work, we analyzed the ranking data generated from the overall performance of the genotypes. The data collection card used is provided in Supplemental Figure S1. Each organization col-

Core Ideas

- We aggregate data from trials established by different organizations across different seasons and locations.
- We generate location-specific insights on genotype performance and environmental interaction.
- We characterize uncertainty of model predictions using Shannon's entropy and area of applicability assessment.

lected the data and then uploaded it to the ClimMob digital platform (van Etten et al., 2017).

The use of the ClimMob digital platform helped to standardize the data, making it compatible to be aggregated. However, the datasets still required some data curation before aggregating them to conduct the data synthesis. One important data preparation step involved checking variety names across datasets. In Central America, the same genotypes are generally released under distinct variety names in different countries (Rosas, Beaver, Beebe, et al., 2004). To allow data aggregation, the genotype names were translated into experimental line names (Table 2). The resulting dataset revealed partial overlap in the varieties tested across the different trials, but we removed genotypes that were tested only in one trial to avoid highly unbalanced comparisons across trials. This reduced the number of genotypes from 27 to 17. The data were aggregated using a rank-aggregation approach (Turner et al., 2020). Data were prepared with the R package *gosset* (de Sousa et al., 2022) for their use in the R package *PlackettLuce* (Turner et al., 2020).

In most of the cases, trial plots had geographic coordinates, as these were part of the tricot data collecting process. In cases when the geographic coordinates were not registered, we assigned the median value of geographic coordinates of remaining plots in the same community where the trial was conducted. Each trial plot data point should include the planting and harvest dates. To identify outliers of planting dates, we set a threshold of 40 d above or below the median of each trial and replaced the outliers by the median planting date of the corresponding trial. We also identified outliers for the length of the growing period, with 60 d as the lower limit and 120 d as the upper limit and discarded any data point outside these limits.

2.2 | Environmental data

The main abiotic limiting factors for common bean production are drought, heat stress, and low soil fertility

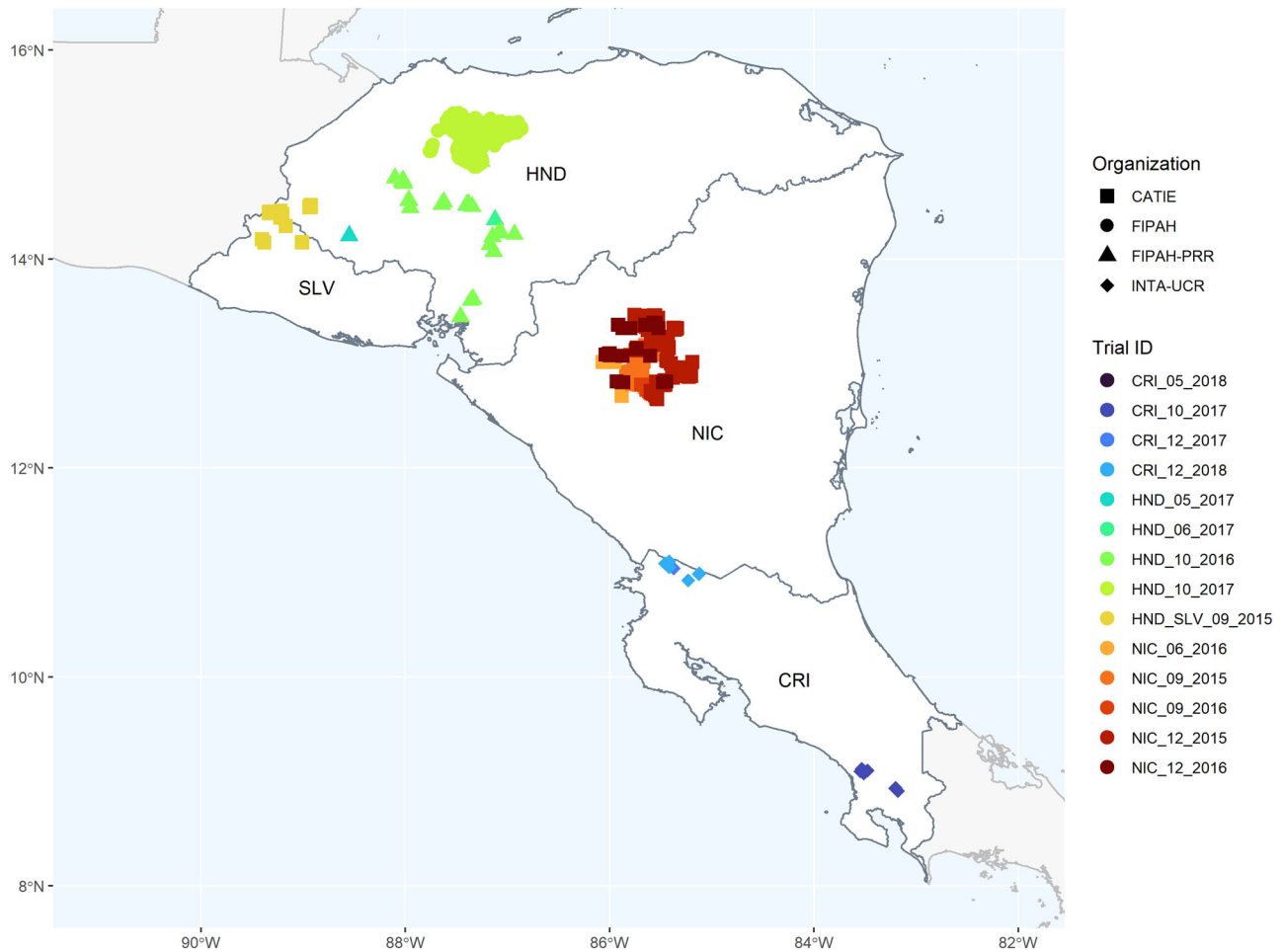


FIGURE 1 Location of tricort trials (identified by Trial ID) in Costa Rica (CRI), El Salvador (SLV), Honduras (HND), and Nicaragua (NIC). Symbol shapes indicate the organization that established and managed the trials

TABLE 1 Trial identifiers, managing organization, country, average planting date, and sample size of plots by trial

Trial ID	Organization ^a	Country	Planting date ^b	<i>n</i> ^c
CRI_05_2018	INTA-UCR	Costa Rica	21 May 2018	14
CRI_10_2017	INTA-UCR	Costa Rica	19 Oct. 2017	46
CRI_12_2017	INTA-UCR	Costa Rica	8 Dec. 2017	41
CRI_12_2018	INTA-UCR	Costa Rica	15 Dec. 2018	23
HND_05_2017	FIPAH-PRR	Honduras	22 May 2017	87
HND_06_2017	FIPAH-PRR	Honduras	5 June 2017	17
HND_10_2016	FIPAH-PRR	Honduras	16 Oct. 2016	37
HND_10_2017	FIPAH	Honduras	20 Sep. 2017	714
HND_SLV_09_2015	CATIE	Honduras-El Salvador	24 Sep. 2015	31
NIC_06_2016	CATIE	Nicaragua	22 June 2016	59
NIC_09_2015	CATIE	Nicaragua	23 Sep. 2015	178
NIC_09_2016	CATIE	Nicaragua	17 Sep. 2016	33
NIC_12_2015	CATIE	Nicaragua	16 Dec. 2015	484
NIC_12_2016	CATIE	Nicaragua	27 Dec. 2016	107

^aINTA, Instituto Nacional de Innovación y Transferencia en Tecnología Agropecuaria, Costa Rica; UCR, Universidad de Costa Rica; CATIE, Centro Agronómico Tropical de Investigación y Enseñanza; FIPAH, Fundación para la Investigación Participativa con Agricultores de Honduras; PRR, Programa de Reconstrucción Rural-Honduras.

^bMedian.

^cNumber of plots in each trial.

TABLE 2 Experimental line names and variety names used in each country after variety release along with references used to make the translation for red common bean genotypes evaluated in tricot trials in Central America

Experimental name	Variety name (Country)	Reference
429 DFSZ 15094-39-4	INTA Ferroso (NIC)	Llano et al. (2013)
703-SM 15216-11-4-VB	Chepe (HND)	J. C. Rosas, personal communication, 11 Feb. 2022
ALS 0532-6	Tolupan Rojo (HND)	Feed the Future Legume Innovation Lab and USDA (2018)
BCR 122-74	Experimental line	J. C. Rosas, personal communication, 11 May 2020
BFS 47	Experimental line	J. C. Rosas, personal communication, 11 May 2020
BRT 103-182	Experimental line	J. C. Rosas, personal communication, 11 May 2020
EAP 9508-93	Cedron (HND)	PRR-FIPAH (2019)
EAP 9510-77	Amadeus 77 (HND); INTA Rojo (NIC); Cabécar (CRI); CENTA Sand Andrés (SLV); IDIAP R3 (PAN)	Rosas, Beaver, Beebe, et al. (2004)
IBC 301-204	INTA Centro Sur (NIC); Paraisito Mejorado 1 (HND)	Feed the Future Legume Innovation Lab and USDA (2018); Rosas and Escoto (2011)
IBC 302-29	Paraisito Mejorado 2 Don Rey (HND)	Feed the Future Legume Innovation Lab and USDA (2018)
IBC 308-24	Amilcar 58 (HND)	Feed the Future Legume Innovation Lab and USDA (2018)
MHC 2-13-49	<i>Experimental line</i>	J. C. Rosas, personal communication, 11 May 2020
MIB 397-72	Honduras Nutritivo (HND)	Rosas et al. (2016)
MPN 103-137	INTA Precoz (NIC)	J. C. Rosas, personal communication, 11 May 2020
SJC 730-79	Rojo Chorti (HND); CENTA EAC (SLV)	Feed the Future Legume Innovation Lab and USDA (2018); J. C. Rosas, personal communication, 11 May 2020
SRC 2-18-1	DEORHO (HND); CENTA Nahuat (SLV); INTA Matagalpa (NIC)	Feed the Future Legume Innovation Lab and USDA (2018); J. C. Rosas, personal communication, 11 May 2020
SX 14825-7-1	INTA Fuerte Sequia (NIC); Campechano JR (HND)	Ferrufino (2014); Feed the Future Legume Innovation Lab and USDA (2018)

Note. CRI, Costa Rica; HND, Honduras; NIC, Nicaragua; PAN, Panama; SLV, El Salvador.

(Beebe, 2012). In Central America, heat stress particularly limits production in the lowlands (Beebe, 2012; Beebe et al., 2011). We accessed publicly available data repositories to obtain rainfall, temperature, and soil data. An initial set of climatic data were obtained from the Agrometeorological indicators from 1979 to present derived from reanalysis dataset, also known as AgERA5 (Boogaard & van der Grijn, 2020; Copernicus Climate Change Service, 2020). Climatic variables and indices were computed following Kehel et al. (2016), Aguilar et al. (2005) and Challinor et al. (2016) using the R package *climatrends* (de Sousa et al., 2020). Table 3 describes variables and indices from Aguilar et al. (2005) and Kehel et al. (2016), which were used without major modifications. The climatic indices listed in Table 4 are based on Challinor et al. (2016), with thresholds adapted to common bean. Both temperature-based and rainfall-based climatic variables and indices were computed for the whole span of the growing season (i.e., from planting to harvest) of each trial plot. Additionally, temperature-based variables and indices were computed for the three phenological stages: vegetative, flowering, and grain development. Summarized variables and indices by trial location for the three phenological stages

are provided in Supplemental Table S1 to describe the climate variability among locations. The phenological stage definitions were according to de Medeiros et al. (2016) and Fernández de Córdova et al. (1986).

For soil variables (Table 5) we used data from Soil-Grids250m v2.0 from four depth layers, 0–5, 5–15, 15–30, and 30–60 cm (Poggio et al., 2021). We selected the soil horizons following Ho et al. (2005). Soil water content was extracted from the Global High-Resolution Soil-Water Balance (Trabucco & Zomer, 2019) and averaged across the growing season of each trial plot.

2.3 | Plackett–Luce Model

The statistical model applied to analyze the rankings of genotypes is an extension of the Plackett–Luce model (Luce, 1959; Plackett, 1975) implemented in the R package *PlackettLuce* (Turner et al., 2020). The Plackett–Luce model is a classic approach to analyze ranking data based on Luce's axiom of choice (Luce, 1959; Turner et al., 2020). The version implemented in the *PlackettLuce* package is a generalization of

TABLE 3 Climatic indices that have a possible influence on bean variety performance. Adapted from Aguilar et al. (2005) and Kehel et al. (2016)

Covariate	Description	Unit
minDT	Minimum daytime temperature	°C
maxDT	Maximum daytime temperature	°C
minNT	Minimum nighttime temperature	°C
maxNT	Maximum nighttime temperature	°C
DTR	Diurnal temperature range: mean difference between daily maximum temperature and daily minimum temperature	°C
SU	Summer days: number of days with maximum temperature >30 °C	°C
TR	Tropical nights: number of nights with maximum temperature >25 °C	°C
WSDI	Maximum warm spell duration, consecutive days with temperature >90 th percentile	Days
CSDI	Maximum cold spell duration, consecutive nights with temperature <10 th percentile	Days
T10p	10 th percentile of night temperature	°C
T90p	90 th percentile of day temperature	°C
MLDS	Maximum length of consecutive days with precipitation <1 mm	Days
MLWS	Maximum length of consecutive days with precipitation ≥1 mm	Days
R10mm	Number of heavy precipitation days 10 ≥ rain <20 mm	Days
R20mm	Number of very heavy precipitation days rain ≥ 20 mm	Days
Rx1day	Maximum 1-d precipitation	mm
Rx5day	Maximum 5-d precipitation	mm
R95p	Total precipitation when rain >95 th percentile	mm
R99p	Total precipitation when rain >99 th percentile	mm
Rtotal	Total precipitation (mm) in wet days, rain ≥ 1	mm
SDII	Simple daily intensity index, total precipitation divided by the number of wet days	mm d ⁻¹
SRF	Daily solar radiation flux	J

TABLE 4 Climatic sensitivity indices, thresholds, and references used to adjust the thresholds to common bean requirements. Adapted from Challinor et al. (2016)

Index	Description	Threshold °C	Reference ^a
hts_mean	High-temperature stress using daily mean temperature, expressed as the percentage number of days a certain threshold is exceeded.	Min = 19, Max = 25	Agtunong et al. (1992)
hts_max	High-temperature stress using daily maximum temperature.	Min = 26, Max = 32	Gross and Kigel (1994)
hse	Heat-stress event, expressed as the percentage of the number of days in which a certain threshold is exceeded for at least two consecutive days.	>35	Gross and Kigel (1994)

^aFor threshold adjustment.

the Plackett–Luce model to allow handling of ties and partial rankings (Turner et al., 2020). For a given set S of J genotypes, $S = \{i_1, i_2, \dots, i_j\}$, the probability that an element i_j is selected from S is denoted by the following:

$$P(i_j|S) = \frac{\alpha_{i_j}}{\sum_{i \in S} \alpha_i}$$

where $\alpha_i \geq 0$ represents the worth of the genotype i . A genotype with higher worth value is more likely to be preferred over other items with lower worth. The worth parameter values are estimated by maximum likelihood (Turner et al., 2020). Considering genotypes A, B, and C, $A > C > B$ denotes that A is ranked higher than C, and C is ranked higher than B. To have finite maximum likelihood estimates, the network of wins and losses produced by the rankings needs

TABLE 5 Description of soil variables retrieved from SoilGrids250m v2.0 (Poggio et al., 2021)

Variable	Description	Units
cec	Cation exchange capacity of the soil	cmol ⁺ kg ⁻¹
cfvo	Volumetric fraction of coarse fragments (>2 mm)	cm ³ 100 cm ⁻³ (vol%)
clay	Proportion of clay particles (< 0.002 mm) in the fine earth fraction	g 100 g ⁻¹ (%)
nitrogen	Total nitrogen (N)	g kg ⁻¹
phh2o	Soil pH in water	pH
sand	Proportion of sand particles (>0.05 mm) in the fine earth fraction	g 100 g ⁻¹ (%)
silt	Proportion of silt particles (≥0.002 mm and ≤0.05 mm) in the fine earth fraction	g 100 g ⁻¹ (%)
soc	Soil organic carbon content in the fine earth fraction	g kg ⁻¹
ocd	Organic carbon density	kg m ⁻³

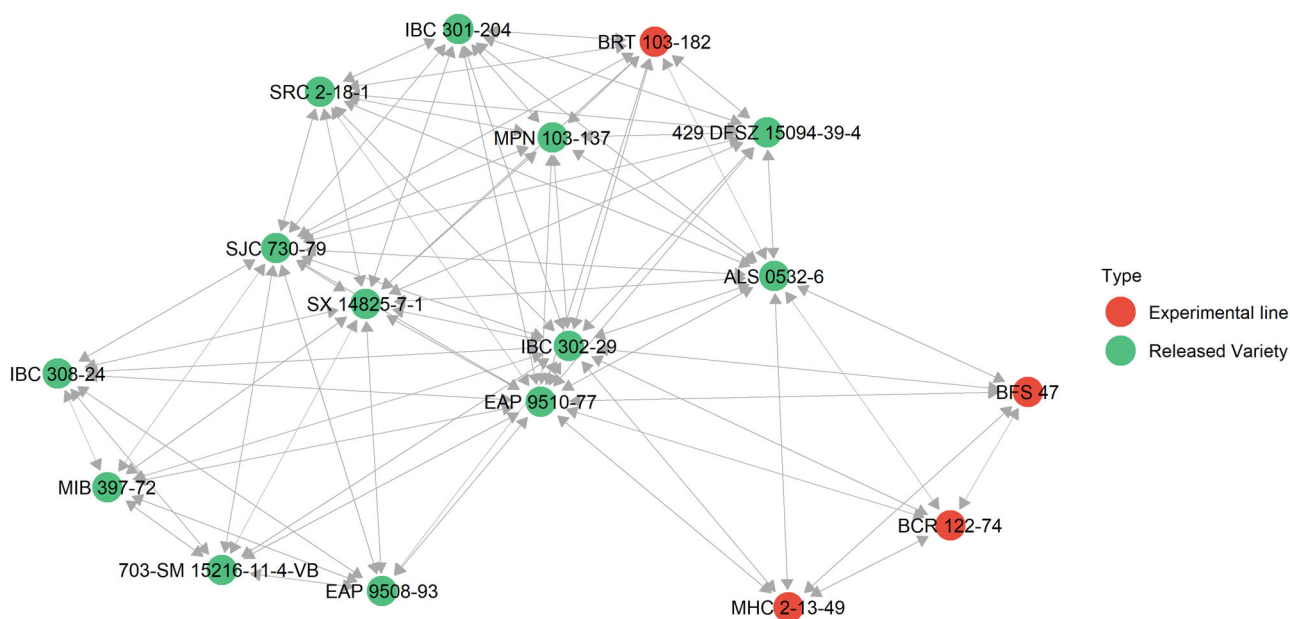


FIGURE 2 Connectivity network of genotypes evaluated in the tricot trials. The arrows indicate wins (outgoing) and losses (incoming) among genotype pairs. The graph drawing algorithm places directly compared genotypes close to each other (Fruchterman & Reingold, 1991)

to be strongly connected (Turner et al., 2020). A strongly connected network is when a path of wins and losses exists—either directly or indirectly—between every pair of items (Turner et al., 2020). Figure 2 shows the strongly connected network of genotypes evaluated in the tricot trials. The location of the nodes in Figure 2 is automatically determined by the Fruchterman–Reingold algorithm (Fruchterman & Reingold, 1991). The Fruchterman–Reingold is a force-directed placement algorithm, which tries to optimize the location of the nodes for visualization purposes following two principles: (a) connected nodes should be drawn next to each other and (b) nodes should not be drawn too close to each other (Fruchterman & Reingold, 1991). Therefore, genotypes that were compared directly in the tricot trials will likely be nearer than those which were not. Figure 2 was made with the R package *GGally*, which uses the Fruchterman–Reingold

algorithm implemented in the R package *sna* (Butts, 2020; Schloerke et al., 2021).

2.4 | Model-based recursive partitioning with Plackett–Luce trees

The original Plackett–Luce model does not account for external factors that may influence the probability of an item to be preferred (Turner et al., 2020). To consider environmental factors in the model, we used an extension in which the Plackett–Luce model is combined with model-based recursive partitioning (Zeileis et al., 2008). It is implemented as Plackett–Luce trees in the R package *PlackettLuce* (Turner et al., 2020). The method involves the following four steps from Turner et al. (2020) and Zeileis et al. (2008):

TABLE 6 Planting seasons for common bean in Central America from different studies

Geographic area	Planting season name	Planting time frame	Study
Central America	Primera	April	(García-Solera & Ramírez, 2012)
	Postrera	August–September	
	Apante or Winter	December–March	
Nicaragua	Primera	May	(Gourdji et al., 2015)
	Postrera	September	
	Apante	November	
Honduras	Primavera or Primera	15 May–20 June	(Escoto, 2013)
	Postrera or Segunda	End of August–October	
	Postrera tardía or Apante	November–January	
Costa Rica ^a	Huetar Norte	End of November to beginning of January	(Hernández Fonseca, 2009)
	Brunca 1	May	
	Brunca 2	End of September to end of October	
	Chorotega 1	November–December	
	Chorotega 2	September–October	
	Valle Central and Puriscal	15 September–First week of October	
	Turrialba	December	
Costa Rica	Brunca 1	May	(Vargas et al., 2018)
	Brunca 2	October	
	Huetar Norte	November–December	

^aIn Costa Rica, seasons are usually named as Primera and Segunda, with changes in the time frame of Segunda depending on the region (J. C. Hernández, personal communication, 4 May 2021).

1. A Plackett–Luce model is fitted to the complete dataset.
2. The stability of worth parameter values, as influenced by the covariates, is assessed for each covariate.
3. If a significant instability is detected, the data is partitioned by the covariate with the strongest instability based on a cut-point providing the highest improvement of the model fit.
4. Steps 1–3 are repeated for each branch of the tree until no more instabilities are detected or if the resultant partitions are smaller than a given size threshold.

2.5 | Model selection and validation

We first applied a forward variable selection with blocked cross-validation to select variables that are generalizable across the study region (Roberts et al., 2017). We used blocked cross-validation using trials as blocks, further referred to as leave-one-trial-out cross-validation. This partitioning structure aims to account for the geographical and temporal heterogeneity posed by the aggregation of several tricot trial datasets. We assume that each trial represents a particular combination of location and time in some way equivalent to an environment. This is also motivated by the complex arrangement of planting seasons (Primera, Postrera, & Apante) across Central America (Table 6). Similar blocking strategies

have been recently applied to validate predictive models of genotype performance (Neyhart et al., 2021).

Models implemented with the recursive partitioning framework can be tuned by adjusting the alpha hyperparameter that conditions the tree size (Hothorn et al., 2006). Low alpha values may result in low power for detecting dependencies between the covariates and the response variable (Hothorn et al., 2006). To overcome this, Hothorn et al. (2006) suggest setting a very large value for the alpha hyperparameter to assure that any dependence is detected. Therefore, we used a large alpha value ($\alpha = .9$) in the forward variable selection to ensure that most dependence is detected. Overfitting is prevented by subsequent pruning the final tree using the Akaike information criteria (AIC) (Akaike, 1974). We used the resulting Plackett–Luce tree to predict variety performance in the subsequent analysis steps (Section 2.7). A potential limitation of a single tree is its instability, which can be overcome using ensembles of trees (Strobl et al., 2009). On the other hand, a single tree is more interpretable than ensembles (Strobl et al., 2009). Here, we present our approach using a single tree to facilitate interpretation and conceptual clarity. In future work, potential instability can be addressed by using ensembles.

Since Plackett–Luce trees are fitted by maximum likelihood, we used the model deviance as the goodness of fit metric computed on the hold-out data within the cross-validation procedure. To provide a more interpretable metric,

we also computed McFadden's pseudo- R^2 (McFadden, 1973). As an accuracy metric, we calculated Kendall's W (Kendall & Smith, 1939) with the R package *DescTools* (Signorell et al., 2021). Kendall's W measures the concordance between the observed and the predicted rankings. As each trial has a different sample size, we calculated weighted averages of Kendall's W and McFadden's pseudo- R^2 using the test fold size as weights. To evaluate for remaining spatial structure not accounted for in the model, we subjected models with two other sets of covariates to cross-validation for comparison: (a) a model with selected covariates by the forward selection plus geolocation covariates and (b) a model with only geolocation covariates. We followed van Etten, de Sousa, et al. (2019) for the selection of geolocation covariates: latitude, longitude, longitude + latitude, and longitude – latitude (rotated axes).

2.6 | Modeling and predicting planting dates

We extracted climatic indices to predict genotype performance for the growing period observed in each trial plot. To make predictions of variety performance for unobserved locations, the growing period for these locations needs to be predicted. Predefined planting calendars are often used in agricultural modeling, but this can lead to unrealistic results, as planting dates change across seasons. Farmers usually decide when to plant based on their experience and seasonal weather patterns. Here, we used survival analysis (Kleinbaum & Klein, 2012b) to estimate unobserved planting dates for each planting season in the study region. We fitted a Cox proportional hazard regression model with time-dependent covariates, an extension of the original Cox model (Cox, 1972; Therneau & Grambsch, 2000). Given a subject i , the hazard function assumed in the Cox proportional hazard regression model is as follows:

$$\lambda_i(t) = \lambda_0(t) e^{X_i(t)\beta}$$

where λ_0 is the hazard baseline function, $X_i(t)$ is the vector of time-varying covariates for subject i , and β is the vector of coefficients (Therneau & Grambsch, 2000).

To fit the Cox regression model, we used the R package *survival* (Therneau, 2021). Survival analysis needs to define the observation period for modeling. For each season, we defined the start of the observation period as 1 April for the Primera season, 1 August for the Postrera season, and 1 October for the Apante season. These dates correspond to roughly 1 mo before each season is expected to begin. The end of each observation period is defined by the latest observed planting date of each season in the aggregated dataset. Previous studies have found that growing seasons follow rainfall patterns in Central America (Alfaro et al., 2018; García-Solera & Ramírez, 2012; Gourdjji et al., 2015). In the case of the

Primera season, farmers wait for the onset of the rainy season after the dry season. On the other hand, during the Segunda rainy season, farmers look for short dry periods that facilitate planting. Therefore, we selected the following variables that putatively influence bean planting dates: daily precipitation (DP), daily accumulated precipitation (DAP), and daily solar radiation flux (DSRF).

For each Cox regression model, one for each planting season, we first applied a stepwise model selection by AIC using the function *step* available in base R (R Core Team, 2022). To assess the model's goodness of fit, we used the proportional hazard assumption test implemented in the function *cox.zph* of the *survival* package (Therneau, 2021), which is the approach proposed by Grambsch and Therneau (1994). The proportional hazard assumption test is passed when the p value of the chi-square statistic for each variable in the model is nonsignificant (Kleinbaum & Klein, 2012a). The prediction ability of the model is assessed by the c index, which is the probability of concordance of the observed survival against the predicted survival (Harrell, 2015; Harrell et al., 1982). We predicted survival curves with covariate data for the target locations and for each of the past 20 yr that were subsequently used in the prediction of genotype performance. From each predicted survival curve, we extract the number of days that intersect the survival curve at 0.25 survival probability, hence 0.75 probability to plant the day after that number of days. We choose this late cutoff to avoid undefined values in the predicted survival curve, which can be potentially caused by unfavorable weather conditions. This number of days is subsequently added to the start date of the corresponding observing period to obtain the planting date. The end date of the growing period is calculated by adding the average number of days of the growing season observed in the sampled trial data.

2.7 | Predictions of genotype performance

Several studies have proposed using environmental covariates to account for genotype \times environment interaction in the analysis of multi-environment trials (Piepho et al., 1998; van Eeuwijk et al., 1996). Predictions of genotype performance at new locations are less common, but recent studies have demonstrated its feasibility (Buntaran et al., 2021; van Etten, de Sousa, et al., 2019). To provide a visual representation of the spatiotemporal information generated by the model predictions, we applied a spatial mapping approach.

We defined the target region to predict the genotype performance as the whole area covered by Costa Rica, El Salvador, Honduras, and Nicaragua. We made a base raster layer as a template for the predictions using the same spatial resolution of AgERA5 (approximately 11 by 11 km). Cell-wise predictions were produced for each planting season for the whole study region covering the four countries included in

the modeling stage. To obtain a temporal representation of current climatic conditions, we predicted genotype performance for each of the past 20 yr (2000–2019 inclusive) and then averaged the predicted performance to have a representative prediction for each planting season. For each of the 20 yr, we predicted the growing seasons using the Cox proportional hazard regression model described in Section 2.6. The climatic data were extracted for the periods corresponding to each of the predicted growing seasons (i.e., from planting to harvest) to compute the climatic variables and indices selected in the forward selection process described in the Section 2.5. We created a raster map with each cell containing the experimental line names of the top three performing genotypes according to the averaged predictions.

We provided the ranking probabilities of a genotype to be in its current position and not in any other position in the event that the trial is repeated. To this end, we calculated the probability of each genotype to be in the top three or not. The procedure is summarized as follows:

1. We fitted a Plackett–Luce tree with the entire aggregated observed dataset.
2. For each of the resulting nodes in the tree obtained under Step 1, we extracted the worth estimates and the quasi-standard errors (Firth & De Menezes, 2004) using the *qvcalc* function available from the *PlackettLuce* package.
3. For each node, we determined the probability for each rank position for each genotype. This can be done analytically; however, we used a Monte Carlo strategy for convenience. We drew one million samples for each genotype from a normal distribution centered on their worth, with the quasi-standard error as its standard deviation, using base R function *rnorm*. Then we converted the sampled worth values to ranks.
4. We calculated relative frequencies of rank from the sampled ranks.
5. For each of the cells in the target raster, we predicted in which node each cell falls for each season using the model fitted in Step 1.
6. Using the outputs from Steps 4 and 5, we computed the probabilities for each genotype to be either in the top three or not.

Therefore, the top three best-performing genotypes referred to previously are the three genotypes with highest ranking probabilities of being in the top three.

The R package *terra* was used for handling raster format data (Hijmans, 2021). The maps were plotted using the R packages *ggplot2* (Wickham, 2016) and *sf* (Pebesma, 2018). Data for mapping the administrative boundaries were obtained from the GADM database (Hijmans, 2010).

2.8 | Uncertainty assessment of model predictions

To estimate the uncertainty of predicted rank probabilities, we calculated the normalized entropy of the rank probabilities for the genotypes with higher probability of being in the top three. We followed Wu et al. (2021), who characterize uncertainty in ranking probabilities using Shannon's entropy defined as follows:

$$H(x) = - \sum_{i=1}^n P(x=i) \log_b P(x=i)$$

For the case of genotype rankings, $P(x=i)$ is the probability of genotype x to be ranked in position i in a given trial. In our case, we focused on the probability of genotypes being in the top three, so we used the following equation:

$$H(x) = - (P(x \leq 3) \log_b P(x \leq 3) + P(x \geq 4) \log_b P(x \geq 4))$$

The unit of entropy depends on b , which is the base of the logarithm (Wu et al., 2021). We used the common base-2 logarithm, where the unit of entropy is the bit. The entropy is normalized to range between 0 and 1 by dividing the range of maximum and minimum entropy for the number of n elements in the ranking (Wu et al., 2021). An entropy value of 1 represents high uncertainty.

2.9 | Applicability assessment of model predictions

To assess the applicability of model predictions from an environmental perspective, we calculated the area of applicability (AOA) as described by Meyer and Pebesma (2021). This provides geographic boundaries to separate areas where the relationship learned by the model with the training data can be extrapolated from those that cannot (Meyer & Pebesma, 2021). Furthermore, the AOA identifies the areas where the model performance estimated with cross-validation applies (Meyer & Pebesma, 2021). The AOA is derived from the dissimilarity index (DI), which is the distance in the multi-dimensional space of the predictor variables between training data and new data from locations used for predictions (Meyer & Pebesma, 2021). The AOA is a binary outcome calculated after applying a threshold on the DI. Cell points that surpass the threshold are labeled as 0 and otherwise as 1. The threshold on the DI is defined by the maximum DI of the training data in the cross-validation considering only the data points that do not occur on the same fold. Hence the same blocking structure of the cross-validation folds is used in the calculation

TABLE 7 Deviance, pseudo- R^2 , and Kendall's W comparing four models, no covariates, environmental covariates, covariates and geolocation, and geolocation only

Model	Deviance	Pseudo- R^2	Kendall's W
No covariates	6,183	.6679	0.5203
Environmental covariates	6,033	.6831	0.5215
Environmental covariates + geolocation	6,393	.6590	0.5146
Only geolocation	6,350	.6596	0.5122

of the DI and subsequently in the derived AOA. We calculated the AOA with the function *aoa* implemented in R package *CAST* (Meyer, 2018).

3 | RESULTS AND DISCUSSION

3.1 | Model selection and validation

The forward variable selection procedure selected the following variables: warm spell duration index (WSDI), R20mm, T10p, *hts_mean_19_flo*. The model with environmental covariates produced better cross-validated values of deviance, pseudo- R^2 and Kendall's W values compared with the baseline model without covariates (Table 7). The models that include geolocation covariates produced a worse fit than the model with environmental covariates. Therefore, the model with environmental covariates effectively accounts for the spatial structure of the aggregated dataset.

The AIC-pruned tree using all the data (Figure 3) makes a split based on the WSDI, which is the number of days with temperature above the 90th percentile (de Sousa et al., 2020). Terminal nodes 2 and 3 in Figure 3 present the estimated worth values for the different resulting subsets of data after the split with variable WSDI. Node 3 presents the genotypic worth values for all plots with conditions of more than 4 d with temperature higher than the 90th percentile. In these warm conditions, the top three genotypes are: IBC 308-24, MHC 2-13-49, and SX 14825-7-1. The genotype IBC 308-24 was released in Honduras as 'Amilcar 58' (Feed the Future Legume Innovation Lab & USDA, 2018). In the case of genotype MHC 2-13-49, it is an experimental line developed mainly for resistance against web blight [*Thanatephorus cucumeris* (Frank) Donk] (Rosas, unpublished data, 2022). The genotype SX 14825-7-1 was released in Honduras in 2011 as 'Campechano JR' and in Nicaragua as 'INTA Fuerte Sequía'. It was selected within a community-based participatory plant breeding program in Honduras, and it is well adapted to high temperature conditions (Vargas et al., 2011).

While some genotypes were not grown and evaluated together in the field, as shown in Figure 2, the Plackett–Luce tree model with environmental covariates allows to make those comparisons considering the different environmental conditions among trial locations.

Figure 3 shows the presence of genotype \times environment interaction between the two sets of environments differentiated by the Plackett–Luce tree model. For example, the experimental line BRT 103–182 performed well in the less warm conditions (Node 2) but poorly in the warmer conditions (Node 3).

In general terms, the split made by WSDI is consistent with existing knowledge about the effect of high temperature on the performance of common bean genotypes (Beebe, 2012; Beebe et al., 2011). van Etten, de Sousa, et al. (2019) did a preliminary study of a subset of the data (the trials in Nicaragua only) and identified maximum night temperature as the major factor influencing differences in common bean genotype performance. The interpretation of van Etten, de Sousa, et al. (2019) was that the main difference between varieties was their level of heat stress tolerance. We identified a similar effect of heat stress in our study. There is a weak, positive correlation between WSDI and maximum night temperature ($r = 0.09$, $p = 1 \times 10^{-4}$). The current analysis has not identified additional environmental factors. The current dataset is larger than that of the Nicaragua study but also holds more varieties. Also, WSDI may be more generalizable across geographical space than maximum night temperature or may capture other environmental influences beyond heat stress. In future applications, more covariates and interactions between them could be identified using machine-learning methods (for example, using ensembles of Plackett–Luce trees).

3.2 | Survival analysis to predict planting dates

The coefficients estimated by the Cox regression model for the three seasons are presented in Table 8. For instance, in the case of the Primera season model, a millimeter change in the daily accumulated precipitation is associated with $\sim 0.5\%$ increase in the probability of planting. The variable importance is described by the magnitude of the Z value and the exponentiated coefficients provide the multiplicative effect of each covariate on the estimated risk (Therneau & Grambsch, 2000).

For the Primera season, the stepwise model selection removed DP, keeping only DAP as covariate in the model. In the case of the Postrera season, the stepwise model selection suggested all the three variables should be kept in the model. However, we detected a large violation of the proportional hazard assumption. We overcame this by removing DAP from the Postrera season model, keeping DSRF and DP.

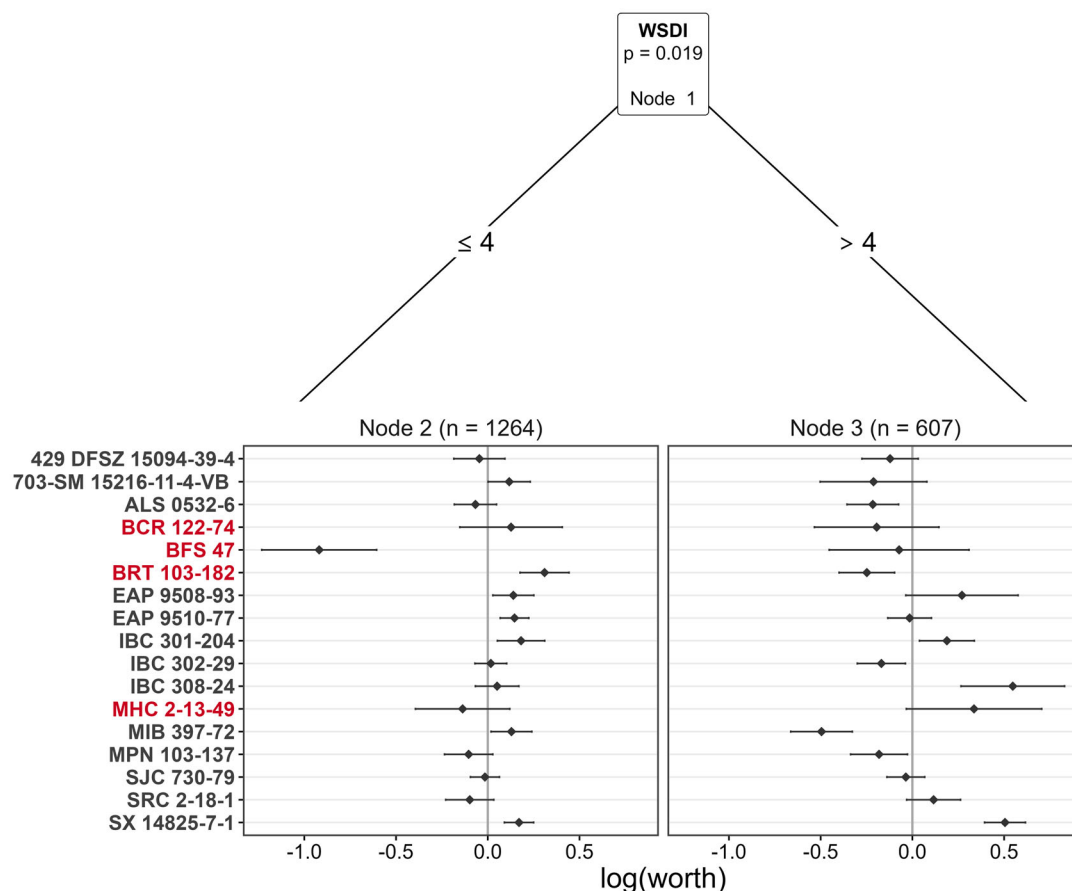


FIGURE 3 Plackett–Luce tree plot of the model fitted with aggregated data from all the trials. The x axis indicates the worth parameter estimates in logarithmic scale, which are the probabilities of each genotype to be ranked first. The bars represent quasi-standard error, and the central vertical gray bar is the zero intercept for each node. WSDI, warm spell duration index. Color codes for genotypes: red, experimental line; gray, released variety

TABLE 8 Estimated Cox regression model coefficients for the three planting seasons

Season model	Variable	coef	exp(coef)	se(coef)	Z	p
Primera	DAP	0.005	1.005	4.968×10^{-4}	10.83	$2 \times 10^{-16}***$
Postrera	DP	0.008	1.008	0.004	2.047	.0407*
	DSRF	8.930×10^{-8}	1.000	1.622×10^{-8}	5.505	$3.69 \times 10^{-8}***$
Apante	DP	-0.051	0.95	0.013	-3.854	$1.161 \times 10^{-4}***$

Note. DP, daily precipitation; DAP, daily accumulated precipitation; DSRF, daily solar radiation flux.

*Significant at the .05 probability level. **Significant at the .01 probability level. ***Significant at the .001 probability level.

This improved the model from the initial fit with a modest improvement in the ability of prediction and only a moderate violation of the proportional hazard assumption (Table 9). The final model for the Apante season only has DP as covariate after applying the stepwise model selection.

The Cox regression model of the Primera season has a *c* index of 0.808 (SE = 0.03)—considered a good prediction ability—while the Postrera and Apante models have *c* index values of 0.563 (SE = 0.012) and 0.625 (SE = 0.013) respec-

tively, which are relatively low, but still better than using a fixed planting date.

For the Primera season, it makes sense that accumulated precipitation influences farmers' decision to plant because, generally, farmers wait until the onset of the rainy season. The Postrera season starts before the second peak of the bimodal rainfall distribution (Alfaro et al., 2018; García-Solera & Ramírez, 2012). As this occurs during the rainy season, farmers need to identify a time window of sunny days to plant. For

TABLE 9 Results of the proportional hazard assumption tests for the three models (Primera, Postrera, Apante)

Season model	Covariates	χ^2	df	<i>p</i>
Primera	DAP	1.76	1	.18
	Global ^a	1.76	1	.18
Postrera	DP	0.583	1	.4450
	DSRF	10.223	1	.0014
	Global ^a	12.901	2	.0016
Apante	DP	6.12	1	.013
	Global ^a	6.12	1	0.013

Note. DP, daily precipitation; DAP, daily accumulated precipitation; DSRF, daily solar radiation flux. ^aGlobal, global test with all variables.

the Apante season model, the influence of daily precipitation might be linked to the drier conditions of this season; hence, farmers wait to notice some stability of precipitation to decide to plant.

We consider our results a good first approximation to model planting dates in function of observed data and climatic covariates. Previous studies have applied survival analysis to seasonal forecasting (Maia & Meinke, 2010). However, to the best of our knowledge, the approach presented here is the first application of a Cox model with time-dependent covariates to predict crop planting dates. Further refinement is required in this research field such as adjustment in terms of optimal starting point of observation, required sample size, and selection of additional covariates. This was not the main objective of the present work, and the approach might be considered as an ad hoc solution to the problem of obtaining planting dates to be used as inputs in the genotype performance model. We believe that our findings can support further exploration and development of the application of survival analysis to model planting dates especially when the alternative is the use of unrealistic fixed planting dates.

3.3 | Maps of predicted genotype performance

The average estimated performance of common bean genotypes across the four countries in the study region for the Primera, Postrera, and Apante seasons is presented in Figures 4a, 5a, and 6a, respectively. Figures 4b, 5b, and 6b present the normalized entropy for the ranking probabilities. Low entropy values represent areas where the predictions of ranking probability have low uncertainty. For instance, genotypes predicted to be in the top three for a given area with low entropy have a high probability to be in the top three in a long series of repetitions of the same experiment. Figures 4c, 5c, and 6c present the AOA, which differentiates areas where

model predictions are supported by the sample data from those from where they are not. For the three seasons, a group of seven genotypes is in the top three (Table 10); within that group, ranking positions swap depending on the season and the location. A consistent pattern across the seasons is that areas in which the top three is either SRC 2-18-1 > SX 14825-7-1 > ALS 0532-6 or SRC 2-18-1 > ALS 0532-6 > SX 14825-7-1 have the lowest entropy and good AOA. Therefore, these two predicted rankings are the most reliable across seasons. The predictions are also consistent with the known traits of the genotypes. For instance, genotypes ALS 0532-6 and SX 14825-7-1 are tolerant to drought and heat, while genotype SRC 2-18-1 is tolerant to heat (Table 10). These three genotypes seem to perform well across the Central America dry corridor.

Differences in entropy values seem to be driven by the representativeness of genotypes in each of the trials. For instance, Costa Rica presented the highest levels of entropy compared with the rest of Central America. Genotypes SX 14825-7-1 and SRC 2-18-1 were not evaluated in Costa Rica. On the other hand, areas with relatively high entropy in El Salvador, Honduras, and Nicaragua are those in which BCR 122-74 is present in the top three, which was only evaluated in Costa Rica. Genotype ALS 0532-6 is in the top three in areas with lowest entropy and was evaluated in 10 of the 14 trials (Figure 7).

The AOA values that indicate the areas in which the model predictions cannot be applied correspond to locations well known to be unsuitable for common bean production because of the unfavorable climatic conditions. Many of these locations are within conservation areas. For instance, Costa Rica's Talamanca Mountain range was identified as having no applicability of the models in the three seasons. In this case, the environmental constraints are the high altitude, cold temperatures, and humid conditions (Oostra et al., 2008). Another example is the Indio Maíz Biological Reserve in Nicaragua. This area is very humid with annual precipitation of >4,000 mm consisting of tropical forest and swampland (Jordan et al., 2019). We mapped all modeling results for demonstration reasons also covering the area of no applicability; however, in future applications, these areas can be masked. Overall, the AOA maps show that the trials jointly cover most environmental conditions under which bean growing occurs in Central America. This is an indication of the potential of aggregating trial results across space and time to make predictions across the whole region.

In the case of the Primera season, in a large portion of the predicted area the top three genotypes are SX 14825-7-1 > SRC 2-18-1 > BCR 122-74. The exception is Costa Rica, where genotype SRC 2-18-1 is not in the top three in a large part of the country. From an environmental perspective, the largest unrepresented area delimited by the AOA (Figure 4c) is Costa Rica's Talamanca Mountain range (described above).

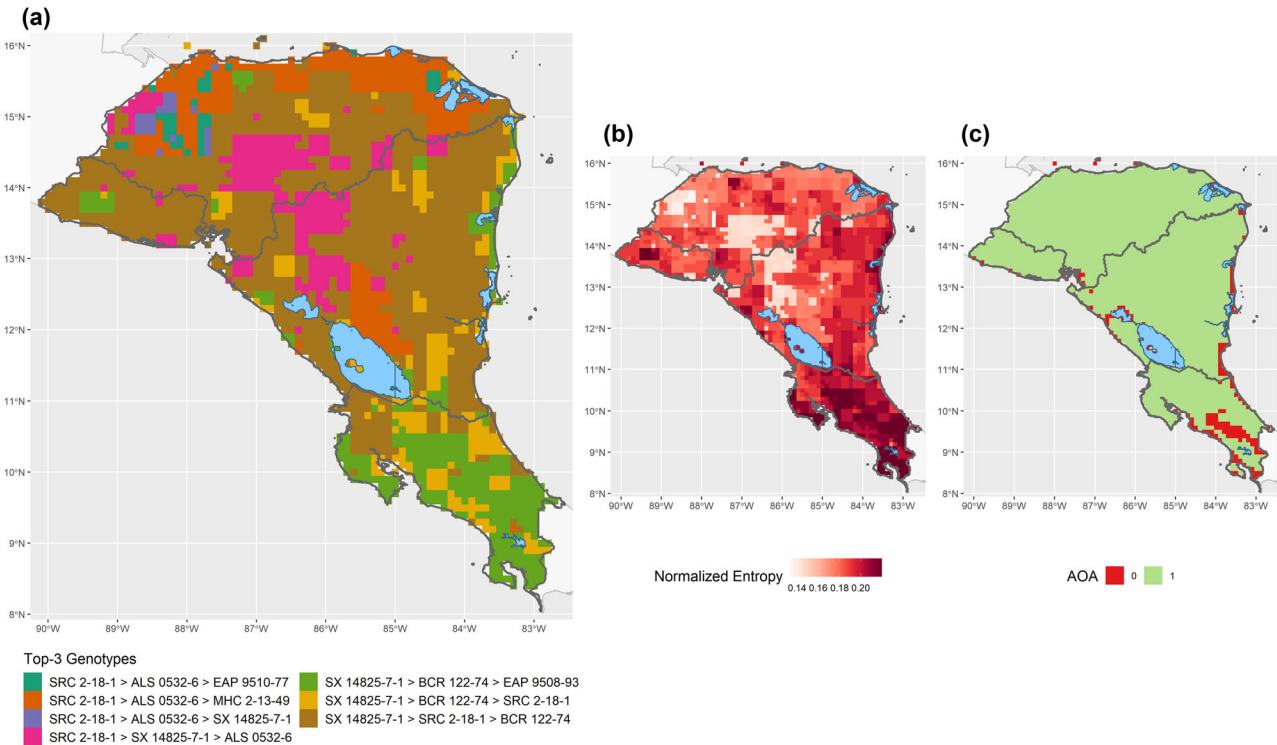


FIGURE 4 (a) Map of genotypes with the higher probability of being in the top three across the study region for the Primera season. (b) Normalized entropy (0–1) of the genotypes with higher probability of being in the top three; the legend scale is constrained to easily visualize the differences. (c) Area of applicability (AOA) for the Primera season; areas in red denote no applicability of the model

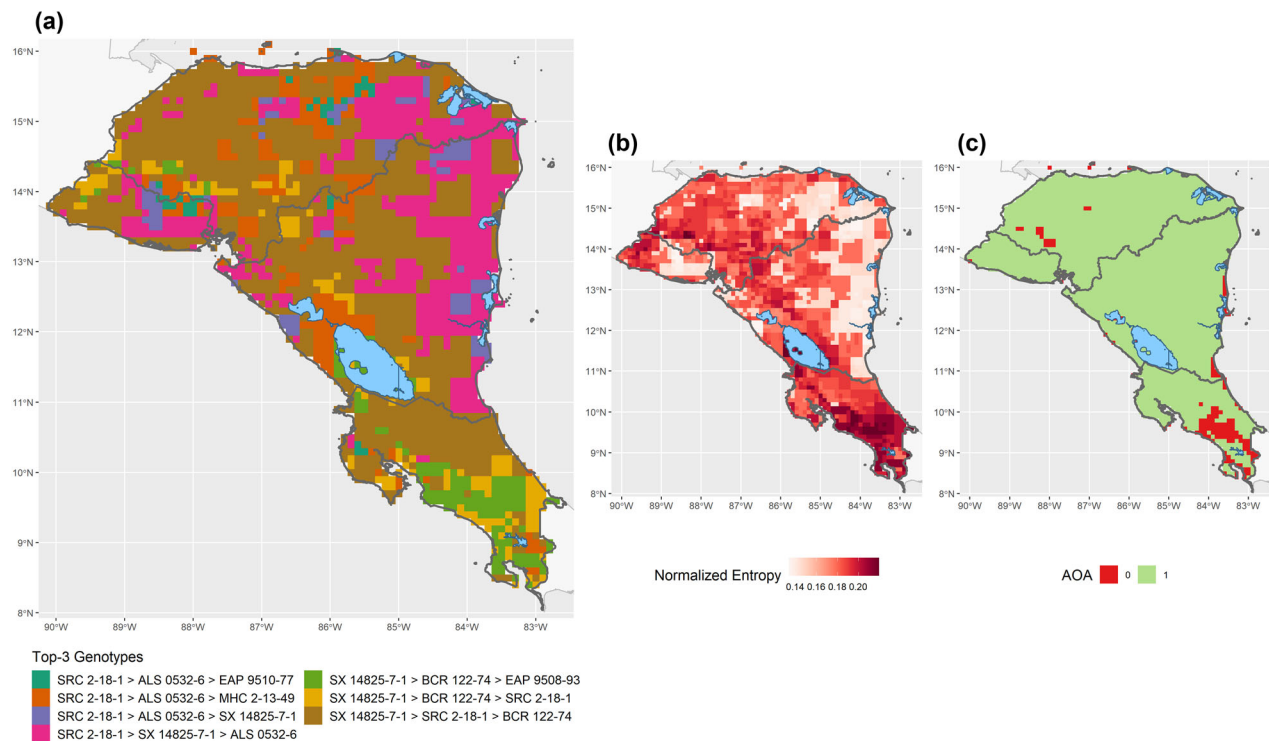


FIGURE 5 (a) Map of genotypes with the higher probability of being in the top three across the study region for the Postrera season. (b) Normalized entropy (0–1) of the genotypes with higher probability of being in the top three; the legend scale is constrained to easily visualize the differences. (c) Area of applicability (AOA) for the Postrera season; areas in red denote no applicability of the model

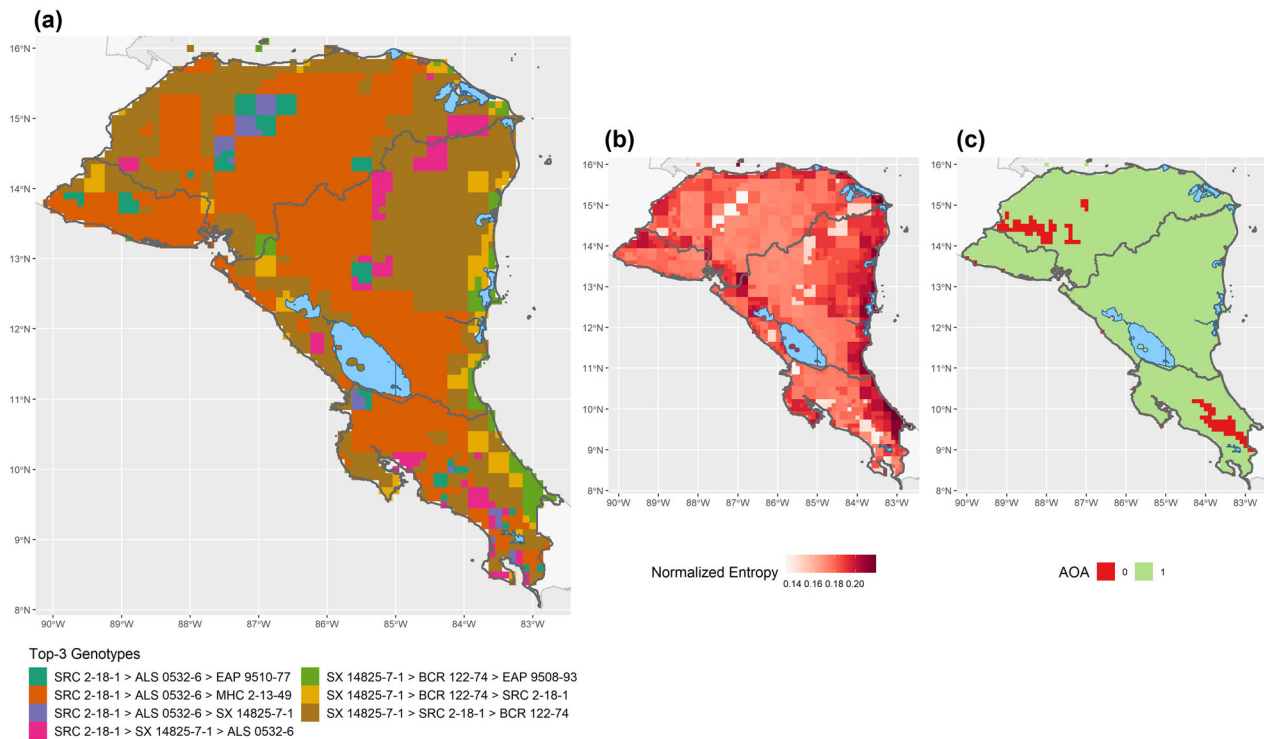


FIGURE 6 (a) Map of genotypes with the higher probability of being in the top three across the study region for the Apante season. (b) Normalized entropy (0–1) of the genotypes with higher probability of being in the top three; the legend scale is constrained to easily visualize the differences. (c) Area of applicability (AOA) for the Apante season; areas in red denote no applicability of the model

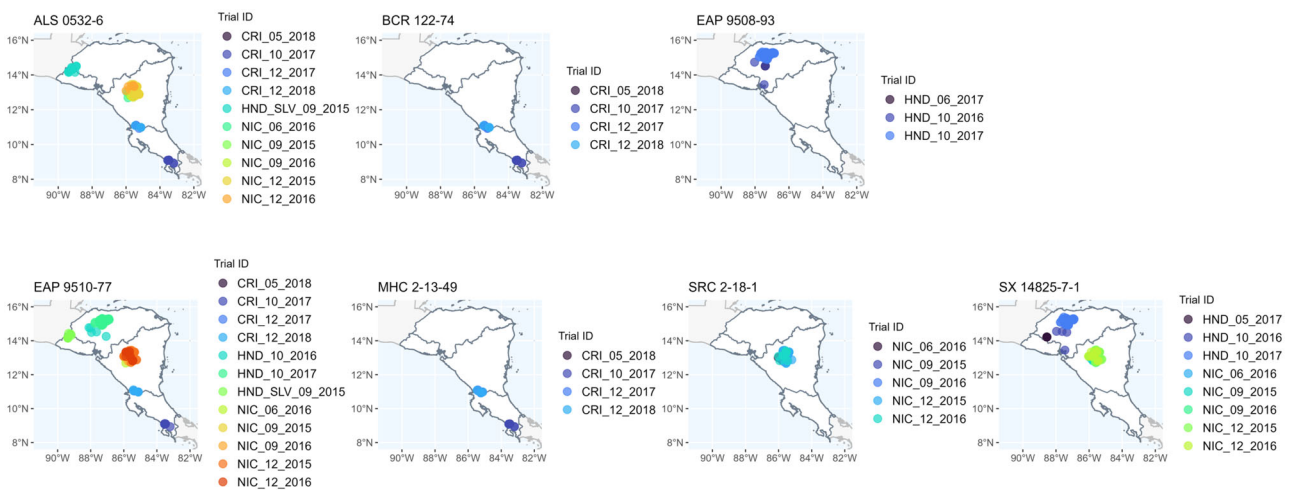


FIGURE 7 Presence of genotypes included in the top three in at least one of the trials

For the Postrera season, Figure 5a shows that areas in which the top three are SX 14825-7-1 > SRC 2-18-1 > BCR 122-74 are similarly large to those predicted for the Primera season, but the areas where the top three are SRC 2-18-1 > SX 14825-7-1 > ALS 0532-6 are larger in El Salvador, Honduras, and Nicaragua. This area has the lowest values of entropy, indicating that these genotypes have a high probability of not being

outperformed by other genotypes (Figure 5b). The AOA for the Postrera season has a similar pattern as the Primera season with an additional small area in Honduras with environmental conditions not covered by the trials (Figure 5c).

The map of predictions of the top three genotypes for the Apante season shows a major difference with the Primera and Postrera seasons. In this case, in most of the area the

TABLE 10 Experimental and variety names, year of release, and main traits of best-performing small red bean genotypes predicted by the model

Experimental name	Variety name (Country)	Released year	Traits	Reference
ALS 0532-6	Tolupan Rojo (HND)	2019	Resistant to Angular Leaf Spot [<i>Pseudocercospora griseola</i> (Sacc.) Crous & Braun], <i>Bean Common Mosaic Virus</i> (BCMV), <i>Bean Golden Yellow Mosaic Virus</i> (BGYMV), and bean rust [<i>Uromyces appendiculatus</i> (Pers.:Pers.) Unger]; Tolerant to anthracnose [<i>Colletotrichum lindemuthianum</i> (Sacc. & Magnus) Lams.-Scrib.] and common bacteria blight [<i>Xanthomonas campestris</i> pv. <i>Phaseoli</i> Smith (Dye)]; Good adaptability to drought, heat, and soils with low fertility.	Feed the Future Legume Innovation Lab and USDA (2018); Rosas et al. (2019)
BCR 122-74	Experimental line	–	Resistant to <i>Bean Golden Yellow Mosaic Virus</i> (BGYMV) and <i>Bean Common Mosaic Virus</i> (BCMV).	J. C. Rosas, personal communication, 4 Feb 2022
EAP 9508-93	Cedron (HND)	2007	Resistant to common bean rust [<i>Uromyces appendiculatus</i> (Pers.:Pers.) Unger] and anthracnose [<i>Colletotrichum lindemuthianum</i> (Sacc. & Magnus) Lams.-Scrib.], but susceptible to angular leaf spot [<i>Pseudocercospora griseola</i> (Sacc.) Crous & Braun]; It is recommended for regions with altitude within 800–1200 m asl, 800–1200 mm annual precipitation, and 18–24 °C average temperature.	Rosas et al. (2009)
EAP 9510-77	Amadeus 77 (HND); INTA Rojo (NIC); Cabécar (CRD); CENTA San Andrés (SLV); IDIAP R3 (PAN)	2003	Resistant to <i>Bean Golden Mosaic Virus</i> (BGMV) and <i>Bean Common Mosaic Virus</i> (BCMV). Wide adaptation; It was developed as heat tolerant with coastal regions of Central America as target locations.	Rosas, Beaver, Escoto, et al. (2004)
MHC 2-13-49	Experimental line		Resistant to web blight [<i>Thanatephorus cucumeris</i> (Frank) Donk], <i>Bean Golden Yellow Mosaic Virus</i> (BGYMV), and <i>Bean Common Mosaic Virus</i> (BCMV).	J. C. Rosas, personal communication, 4 Feb 2022
SRC 2-18-1	DEORHO (HND); INTA Matagalpa (NIC); CENTA Nahuat (SLV)	2007	Resistant to <i>Bean Common Mosaic Virus</i> (BCMV) and <i>Bean Golden Yellow Mosaic Virus</i> (BGYMV); Tolerant to high temperatures.	J. C. Rosas, personal communication, 4 Feb 2022
SX 14825-7-1	INTA Fuerte Sequía (NIC); Campechano JR (HND)	2009; 2011, respectively	Dark-red grain; Resistant to <i>Bean Golden Yellow Mosaic Virus</i> (BGMV) and <i>Bean Common Mosaic Virus</i> (BCMV); Good adaptation to drought, heat, and low fertility soils.	Reyes et al., 2016; Vargas et al. (2011)

Note. CRI, Costa Rica; HND, Honduras; NIC, Nicaragua; PAN, Panama; SLV, El Salvador.

top three are SRC 2-18-1 > ALS 0532-6 > MHC 2-13-49 (Figure 6a). Relative to Primera and Postrera, a much larger area has genotype MHC 2-13-49 ranking third in the top three. Still, the areas with the lowest entropy (Figure 6b) are those in which the top three are SRC 2-18-1 > SX 14825-7-1 > ALS 0532-6 (Figure 6a). Therefore, the main difference in terms of entropy for the Apante season seems to be presence of either MHC 2-13-49 or ALS 0532-6 in the top three. The genotype MHC 2-13-49 was only evaluated in Costa Rica (Figure 7). In areas where this variety is among the top three, entropy values are higher than in areas in which ALS 0532-6 is among the top three. The latter variety has less uncertainty associated with it, as it was evaluated in 10 out of 14 trials across the four countries. The AOA for the Apante season is similar to the one for the Postrera season with an increase in Honduras for areas in which the environmental conditions were not represented in the trials. These areas mainly correspond to the locations of the Pacayita Volcano Biological Reserve, the Opalaca Biological Reserve, and the Cacique Lempira Señor de las Montañas Biosphere Reserve. Another important change is that most of the coastal areas delineated as with no applicability in the cases of Primera and Postrera are classified as having good applicability in the Apante season. However, in the case of Apante, the coastal areas present high levels of entropy. This highlights the importance of considering both uncertainty assessments—the entropy and the AOA—as they are complementary.

One use of the predictions from the data synthesis is to identify promising locations for new genotype evaluations. For instance, EAP 9508-93 has been released only in Honduras as ‘Cedrón’ and the present study only included tricot trials in Honduras (Figure 7). Yet, EAP 9508-93 was found to belong to the top three genotypes in most parts of Costa Rica (Figure 4a). Relatively high entropy in those areas indicates that a direct recommendation to introduce this genotype in Costa Rica is not warranted, but our findings suggest it is a relevant candidate for future evaluations, which are required to release this variety also in Costa Rica. Another example is ALS 0532-6, a relatively new genotype again released only in Honduras but tested across the four countries. The low entropy in areas where this genotype belongs to the top three (in Costa Rica, El Salvador, Nicaragua) indicates relatively large certainty about its superior performance. Therefore, this genotype is considered a good candidate for introduction in these areas. The results of this study feed directly into decision making on common bean breeding, which is well coordinated in Central America (Reyes et al., 2016). Another enabling factor is that market preferences are relatively homogeneous in Central America, and food quality traits are considered by farmers in tricot trials (Supplemental Figure S1). Within countries, our findings can be used to recommend genotypes directly to farmers.

4 | CONCLUSIONS

We demonstrated the use of a data synthesis approach to aggregate data from on-farm trials to produce location-specific information about common bean genotype performance across four countries in Central America.

The use of environmental covariates in the Plackett–Luce tree model allowed us to identify WSDI, a proxy for elevated heat, as the main abiotic factor influencing the genotype performance across the study region. The approach also allowed taking advantage of the different locations and growing seasons represented in the aggregated dataset in contrast to what might be possible when single trials are analyzed in isolation.

The maps of predicted variety performance produced with our data synthesis approach can provide useful insights for (a) local plant breeding programs to target new locations for testing and (b) extension agents to generate recommendations for farmers. The combination of entropy and the AOA allowed us to quantify the uncertainty of two different dimensions: the rankings and the environmental conditions. We expect our data synthesis methodology to be applicable to other crops and regions.

While the analysis of ranking data is less common in the evaluation of crop varieties, significative efforts have been made recently to facilitate both the collection and analysis of tricot trial data. For data collection, the digital platform ClimMob provides the required functionality to collect and store the data in a standardized format (van Etten et al., 2017). A challenge for the aggregation of trials from different countries is the different naming used for released varieties. For future cases, we concur with Rosas, Beaver, Beebe, et al. (2004) that coordinated regional releases—in contrast to individual releases—help to avoid this problem. For the large number of already released materials under different names, an open-access database with harmonized variety names might facilitate variety identification across countries. For instance, a solution has been proposed within the breeding management system Breedbase (Morales et al., 2022). Still, further developments are required to also provide a solution to a wider audience including farmers. With regards to the modeling and analytical stage, most of the developments made within our work are being fed into the R package *gosset*, which complements the functionality of the package *PlackettLuce*. This will help researchers to apply the methods presented in this study to other datasets.

Our work also enables further synthesis of a larger dataset. As more tricot trial data becomes available, it could be aggregated and iteratively reanalyzed using the data synthesis approach. Two promising next steps are the use of ensembles of Plackett–Luce trees (Plackett–Luce Forests) and the integration of tricot and nontricot on-farm trial data.

DATA AVAILABILITY STATEMENT

All the R code and the data required to replicate the results are available in GitHub (https://github.com/AgrDataSci/Data_synthesis_bean_tricot_CA). We used R for all the statistical analysis (R Core Team, 2022). In addition to R packages cited in the main text, we also used: *ag5Tools* (Brown & de Sousa, 2022), *caret* (Kuhn, 2022), *colorspace* (Zeileis et al., 2009), *dplyr* (Wickham, François, et al., 2022), *ggparty* (Borkovec & Madin, 2019), *janitor* (Firke, 2021), *network* (Butts, 2008), *RColorBrewer* (Neuwirth, 2022), *readr* (Wickham, Hester, et al., 2022), *stringr* (Wickham, 2019), *survminer* (Kassambara et al., 2021), *partykit* (Hothorn & Zeileis, 2015), *qvcalc* (Firth, 2020), *patchwork* (Pedersen, 2020), and *viridisLite* (Garnier et al., 2021).

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AUTHOR CONTRIBUTIONS

David Brown: Conceptualization; Data curation; Formal analysis; Methodology; Software; Validation; Visualization; Writing-original draft; Writing-review & editing. Sytze de Bruin: Conceptualization; Formal analysis; Methodology; Supervision; Writing-review & editing. Kauê de Sousa: Data curation; Formal analysis; Methodology; Resources; Software; Validation; Visualization. Amílcar Aguilar: Investigation; Project administration; Resources. Mirna Barrios: Investigation; Project administration; Resources. Néstor Chaves: Investigation; Project administration; Resources. Marvin Gómez: Investigation; Project administration; Resources. Juan Carlos Hernández: Investigation; Project administration; Resources. Lewis Machida: Writing-review & editing. Brandon Madriz: Resources; Software. Pablo Mejía: Investigation; Project administration; Resources. Leida Mercado: Investigation; Resources. Mainor Pavón: Investigation; Project administration; Resources. Juan Carlos Rosas: Conceptualization; Investigation; Resources; Writing-

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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