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A forage brassica simulation model using APSIM: Model calibration and validation across multiple environments

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ABSTRACT

Forage brassicas have historically been used in high rainfall/irrigated temperate livestock systems, but there is increasing interest in diverse forage brassicas in drier mixed crop-livestock farming systems. Computer-based modelling is an important decision support tool used in agriculture to explore the adaptability of crops to different climates and agronomic management practices, but existing modelling tools for forage brassicas are limited to temperate environments. We parameterised the APSIM (Agricultural Production Systems Simulator) model for four forage brassica genotypes, including three diverse forage rape cultivars and a raphanobrassica. The model was calibrated using two experiments with repeated measures of biomass components, nutritive value, and leaf and canopy development. We then tested the model extensively using data from a diverse set of environments within Australian and New Zealand (23 sites across four agro-climatic zones). Model predictions of biomass were good for all the genotypes (NSE > 0.60, Nash-Sutcliffe efficiency; RMSE ~1.5 t DM/ha, root mean square error). Predictions of metabolisable energy yield were satisfactory for all genotypes (NSE 0.43–0.73; RMSE ~17.8 GJ ME/ha) but forage dry matter digestibility (DMD) were poorly predicted due to the small variation in observed data. Our robust and widely tested model can be confidently used to predict forage productivity of common and new forage brassicas across a wide range of production environments and agronomic management practices. This model will enable future work to develop a better understanding of the potential value of these important forage crops for livestock production systems.

1. Introduction

Forage brassicas (members of the *Brassicaceae* family) are common forage crops that have historically been used in intensive livestock and dairy systems throughout temperate climatic regions of the world including Europe, New Zealand and Australia (Wheeler et al., 1974). They are valued for their ability to produce high biomass yields with high metabolisable energy (ME) content (12.1–14.1 MJ ME/kg DM) and are often superior to grass-based pastures or other forage crops such as annual cereals (e.g., oats, wheat, barley, triticale) (Barry, 2013). Forage brassicas are integrated strategically to help fill gaps in forage supply and nutritive value at times of the year when other on-farm forages are unable to sustain growth of young animals or maintain adequate productivity in intensive livestock systems (e.g., dairy cows). Because they maintain nutritive value for longer than other forages, forage brassicas are widely used as a fodder bank that can be grazed during periods of poor growth of other forage sources (e.g., cold winter, or dry summer periods).

In Australia and New Zealand, a wide range of forage brassicas with varying functional traits suited to diverse applications are available to farmers. These include leafy-type forage brassicas like forage rapes (*Brassica napus* var. *biennis* L.), leafy turnip (*B. rapa* var. *rapifera* L. and *B. campestris* × *napus*), and raphanobrassica (*B. oleracea* var. *acephala* L. × *Raphanus sativus* L.), which can all be used as a multi-graze crop and exhibit genotypic variation in time to maturity and zones of adaptation. Kale (*B. oleracea* var. *acephala* L.), bulb turnips (*B. campestris* var. *rapa* L.) and swedes (*B. napus* var. *napobrassica* L.), are considered a single-graze crop, and are most often strip grazed as a high nutritive value 'fodder bank' (Ayres and Clements, 2002; de Ruiter et al., 2009).

While a range of forage brassicas are widely used in humid, higher-rainfall livestock and dairy systems in Australia and New Zealand, there is increasing interest in their application in drier mixed crop-livestock farming systems, where they can be used as both a feed for livestock and a break-crop in cereal cropping systems where there are limited

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well-suited alternatives. In recent years, dual-purpose canola (*B. napus* var. *annua* L.) has expanded in the higher rainfall mixed farming region (> 450 mm annual rainfall) of southern Australia (Kirkegaard et al., 2016), creating opportunities for complimentary forage brassicas that can further widen brassica grazing options throughout the year. Recent multi-environment studies have shown that autumn-sown forage brassicas can produce comparable biomass and often produce higher yields of ME and crude protein (CP) than forage oats and offer an extended grazing window compared to dual-purpose canola (Watt et al., 2021). Of the genotypes tested, forage rapes and raphanobrassica genotypes were found to be the most suitable for the drier environments found in the mixed farming zone of Australia and were able to sustain growth late in the season when other forage brassicas (e.g., leafy turnip and bulb turnip genotypes) had senesced due to water limitations (Watt et al., 2021).

There is increasing need to diversify forage systems to reduce periods of feed shortages and improve the quality of feed for livestock and this is becoming more urgent with a changing climate. Forage brassicas have the potential to mitigate these challenges across a broad range of environments and farming systems. However, to optimise the management of forage brassicas in Australian livestock farming systems, better understanding of their potential productivity across environments, matching agronomic management to resource availability (e.g., water and nutrient availability) and their timing of forage production and nutritive value is needed. Simulation models have been used to explore the value other crops to fill feed gaps when grown in a range of environments (Bell, 2008; Bell et al., 2018; Martin and Magne, 2015). While several simulation models are available to predict growth and nutritive value of a range of forages and pastures grown in dairy (e.g., DairyMod; Johnson et al., 2008), temperate pasture-livestock (e.g., GrassGro; Moore, Donnelly and Freer, 1997) and rangeland grazing systems (e.g., GRASP; McKeon et al., 2000; Rickert, Stuth and McKeon, 2000), only DairyMod has the capacity to simulate forage brassica crops, and this is limited to spring-summer sown crops grown in temperate environments. The Agricultural Production Systems Simulator (APSIM; Holzworth et al., 2014) is a well-known cropping systems model that is widely used for simulating broadacre crops across a range of environments and has become an important decision-support tool in cropping systems, and crop-livestock systems where it can be linked with other forage and livestock simulation models via a shared binary protocol (Moore et al., 2007). These capabilities of APSIM provide the ideal framework for the development of forage crop models, but despite the diversity of broadacre crop models available in APSIM, there is a limited array of widely tested forage crop models. This paper outlines the development and testing of a simulation model in APSIM to predict growth and nutritive value of several forage brassica genotypes that show promise for wider application across Australia and New Zealand.

Because of the commonality of forage brassicas with canola, we used the APSIM-canola model as a foundation, which has been extensively tested across a range of environments within Australia and internationally (Robertson and Lilley, 2016). A number of winter-type, dual--purpose canola varieties are available in the model and have been simulated across a range of locations (Lilley et al., 2015). Winter canola cultivars have similar phenological traits to forage rapes, with high vernalisation requirements causing a longer vegetative period than spring canola cultivars (Whish et al., 2020), which enables them to be used as a dual-purpose crop (i.e., grazing and grain). Other basic plant physiology is also quite similar between these brassica genotypes. These similarities make the APSIM-canola model a suitable template for the development of a forage brassica model. Forage rapes have been previously modelled using the APSIM-canola model by increasing the leaf size parameters and thermal time coefficients of a generic winter canola cultivar (Pembleton et al., 2013). However, this model was limited and did not account for the potential differences in plant attributes between forage rape 'types', and testing and subsequent application were limited to cool, temperate environments (Pembleton et al., 2021, 2016). Consequently, DM yield was often underpredicted in regions where late maturity cultivars were grown. We aimed to develop and test model parameters that distinguish between different forage brassica 'types' for dry matter (DM) production and nutritive value characteristics for a broad range of environments and management practices. We demonstrate that the forage brassica model outlined in this study can satisfactorily predict the productivity of forage brassicas across a very diverse range of environments.

2. Materials and methods

A two-stage process was used to calibrate and test a range of forage brassicas genotypes using the APSIM-canola model as a template (Robertson and Lilley, 2016) in APSIM-version 7.10. The first calibration stage used a dataset that was collected over two site-years and included a combination of multiple measures of biomass and its components, forage nutritive value of plant components, leaf and canopy development, and observations of crop phenological development (i.e., vegetative, buds visible, flowering). Soil water, nitrate-nitrogen (NO_3-N) and ammonium-nitrogen (NH_4-N) concentration were measured at the start and end of each experimental site-year (Table 1). This data was available for the several forage brassica genotypes as well as the reference canola crop. This enabled the simulations to be characterised using canola and then model parameters to be modified to accurately predict the growth of each forage brassica genotype.

The second evaluation stage involved testing the newly derived set of parameters for each genotype across a wider range of production environments, climatic conditions, and agronomic management practices. Using data from previous studies from Australia and New Zealand, simulations were developed for 23 experimental site-years where data on plant biomass (220 individual observations) and nutritive value (i.e., dry matter digestibility (DMD) and crude protein content (CP)) (102 individual observations) were available for these genotypes (or similar varieties) (see Table 2).

2.1. Stage 1: Calibration of biomass accumulation and partitioning, and nutritive value

Two experiments carried out at Tummaville, Queensland (QLD) (27.85 S, 151.45 E) in 2018 and 2019 were used to calibrate forage rape cultivars Goliath (late maturity giant-type rape), Winfred (early

Table 1
Summary of the observations of different plant growth attributes from two experimental years used for the calibration of each forage rape cultivar (*cv.* Goliath, HT-R24 and Winfred), raphanobrassica *cv.* Pallaton and the reference crop canola.

	No. of observations for:		
Plant growth attributes measured	Forage rapes	Raphanobrassica	Canola
Biomass			
Total biomass	10	10	10
Green biomass	10	10	10
Senesced biomass	5	5	4
Leaf/petiole biomass	8	8	7
Stem biomass	8	7	7
Nutritive value[1]			
Whole plant	8	8	7
Leaf/petiole	7	7	6
Stem	7	5	6
Leaf and canopy development			
Leaf number (mainstem)	15	15	15
Leaf area index	11	12	11
Radiation interception	11	12	11
Distribution of individual leaf size	2	2	2
Specific leaf area	2	2	2
Water and nitrogen uptake			
Start/End soil water	2	2	2
Start/End soil mineral N	2	2	2

[1] Dry matter digestibility (DMD) and crude protein (CP) content

Table 2
Summary of data sets used for the model testing of forage brassica genotypes parameterisations using APSIM.

	Site Characteristics					Reference crops			Forage brassica genotypes								No. observations/ genotype		
Site No.	Location (lat, long)	Agro-climatic zone	Soil type	APSoil No.	Sowing date	Canola	Cereal[1]	Field pea	Goliath rape	HT-R24 rape	Winfred rape	Interval rape	Leafmore rape	Titan rape	Bonar rape	Pallaton raphanobrassica	Biomass	DMD/ CP	Reference
1, 2	Tummaville, QLD[2] (−27.85, 151.45)	Sub-tropical, sub-humid	Black Vertosol	7	13-Jun-2018 12-Ap-2019	✓			✓	✓	✓					✓	10	8	Watt et al. (2021)
3	Pilton, QLD (−27.52, 151.59)	Sub-tropical, sub-humid	Brown Vertosol	33	21-May-2011		✓				✓			✓			1		Bell et al. (2020)
4	Formartin, QLD (−27.27, 151.25)	Sub-tropical, sub-humid	Black Vertosol	622-YP	21-Jun-2012		✓				✓	✓	✓				1		Bell et al. (2020)
5	Tulloona, QLD (−29.00, 150.02)	Sub-tropical, sub-humid	Grey Vertosol	238	05-Jun-2013			✓			✓	✓	✓				1		Bell et al. (2020)
6, 7	Iandra, NSW (−34.08, 148.37)	Temperate, sub-humid	Red Kandosol	*	21-Jun-2018 28-Mar-2019	✓			✓	✓	✓					✓	2	2	Watt et al. (2021)
8	Wagga Wagga, NSW (−35.06, 147.21)	Temperate, sub-humid	Red kandosol	*	18-Apr-2007	✓					✓						2		Kirkegaard et al. (2008)
9, 10	York, WA (−32.91, 118.23)	Dry Mediterranean	Grey sandy loam	1202	26-Jun-2018 28-Jun-2019	✓			✓	✓	✓					✓	6	4	Watt et al. (2021)
11	Lameroo, SA (−35.20, 140.30)	Dry Mediterranean	Sand over loam (midslope)	*	15-May-2019		✓		✓							✓	3	3	Flohr (unpubl. data)
12	Delegate, NSW (−37.03, 148.56)	Temperate, cool season wet	Podosol	1037-Generic	11-Mar-2010 14-Dec-2010	✓[3]					✓						6		Kirkegaard (unpubl. data)
13, 14	Elliott, TAS[4] (−41.06, 145.46)	Temperate, cool season wet	Clay loam	653	13-Nov-1999 13-Oct-2000										✓		58	22	Neilsen (2005)
15	Stonehouse, TAS (−42.18, 147.40)	Temperate, cool season wet	Medium clay	661	13-Nov-2009							✓					1	1	J. Lynch (unpubl. data)
16	Cambridge, TAS (−42.51, 147.26)	Temperate, cool season wet	Medium clay	661	22-Dec-2009							✓					1	1	J. Lynch (unpubl. data)
17	Mawbanna, TAS (−41.00, 145.22)	Temperate, cool season wet	Clay loam	656	26-Feb-2010							✓					4	1	K. Pembleton (unpubl. data)
18	Stanley, TAS (−40.45, 145.16)	Temperate, cool season wet	Clay loam	656	12-Apr-2010							✓					5	1	K. Pembleton

(*continued on next page*)

Table 2 (*continued*)

	Site Characteristics					Reference crops	Forage brassica genotypes			No. observations/ genotype		
												(unpubl. data)
19, 20	Terang, VIC[5] (−38.15, 142.54)	Temperate, cool season wet	Sandy clay loam	739	13-Dec-2004 20-Oct-2007			✓		12	12	Jacobs and Ward (2011)
21	Mt Gambier, SA[6] (−37.52, 140.45)	Temperate, cool season wet	Sandy loam	SE069	26-Mar-2007		✓	✓		1	1	K. Boston (unpubl. data); DairySA (2009)
22	Hastings, NZ[7] (−39.38, 176.50)	Temperate, cool season wet	Silt clay loam	1338	02-Nov-2011				✓	25		Chakwizira et al. (2014)
23	Lincoln, NZ[8] (−43.38, 172.29)	Temperate, cool season wet	Silt loam	1317	19-Nov-2008				✓	18		Fletcher and Chakwizira (2012)

Presence of that genotype in the experiment is indicated by a ✓; APSoil derived soil number from the database are provided except where a locally developed soil was used (*); DMD, dry matter digestibility; CP, crude protein.

[1] Cereal crops of wheat, barley or oats

[2] Two experimental sites used in the model calibration stage

[3] Two canola cultivars (Taurus and CBI406) as reference crop

[4] Elliott 1999 included four irrigation treatments (0%, 20%, 50% and 100%) and Elliott 2000 included six irrigation treatments (0%, 20%, 40%, 60%, 80% and 100%)

[5] Terang 2004 and 2007 both included six nitrogen treatments (0, 40, 80, 120, 160, 200 kg N/ha)

[6] Crop consisted of a Goliath/Winfred mixture

[7] Hastings 2011 included five nitrogen treatments (0, 25, 50, 100 and 200 kg N/ha)

[8] Lincoln 2009 included three nitrogen treatments (one application of 200 kg N/ha 16 days after sowing (DAS), one application of 200 kg N/ha applied 40 DAS or two applications of 200 kg N applied 16 DAS and 40 DAS)

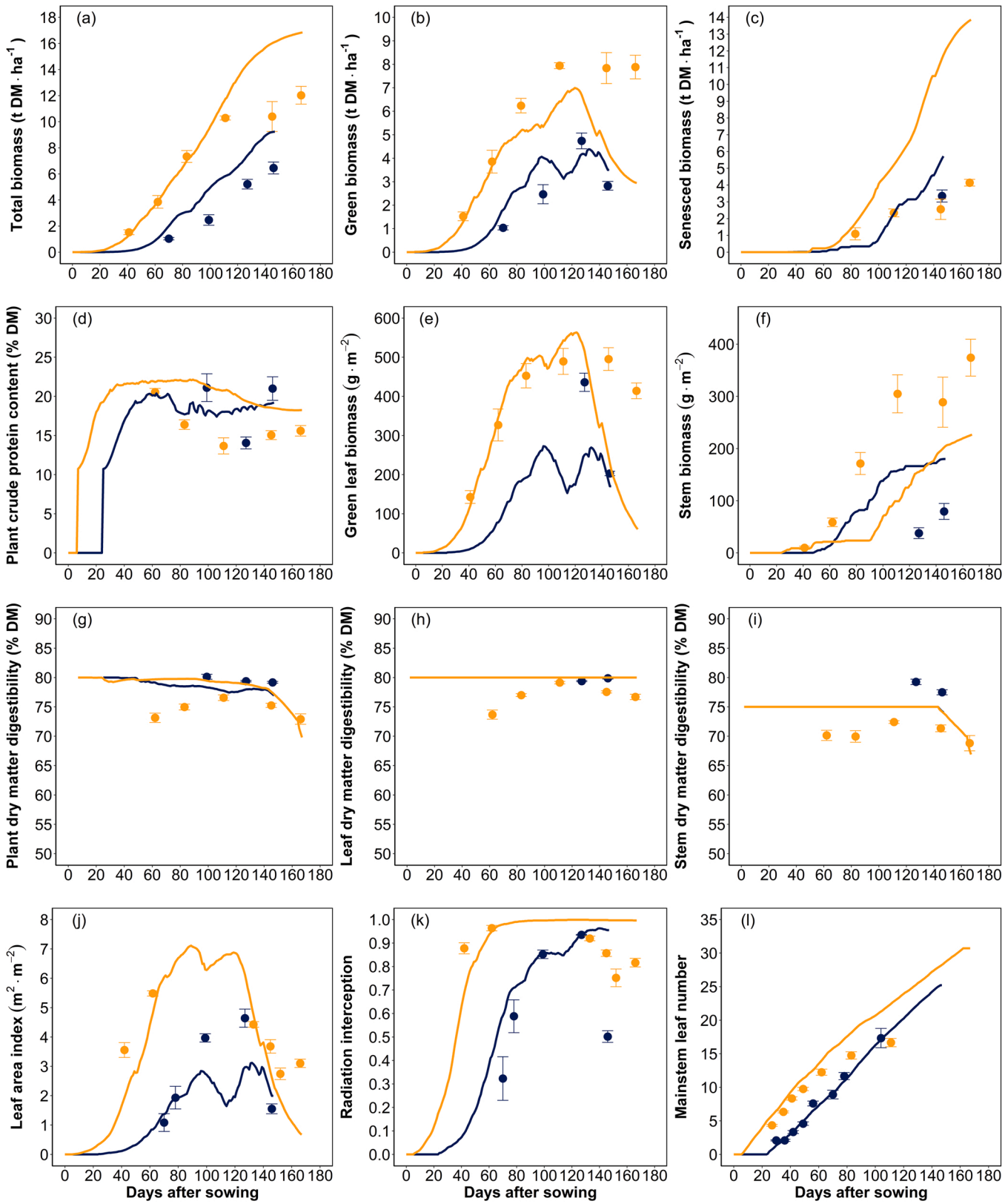

Fig. 1. Model simulations of forage rape *cv.* Winfred in APSIM (lines) compared with observations (dots) from calibration experiments in 2018 (blue) and 2019 (orange) for biomass and its components (a-c, and e-f), forage nutritive value (d and g-i), and leaf canopy and development (j-l) attributes for the parameterisations.

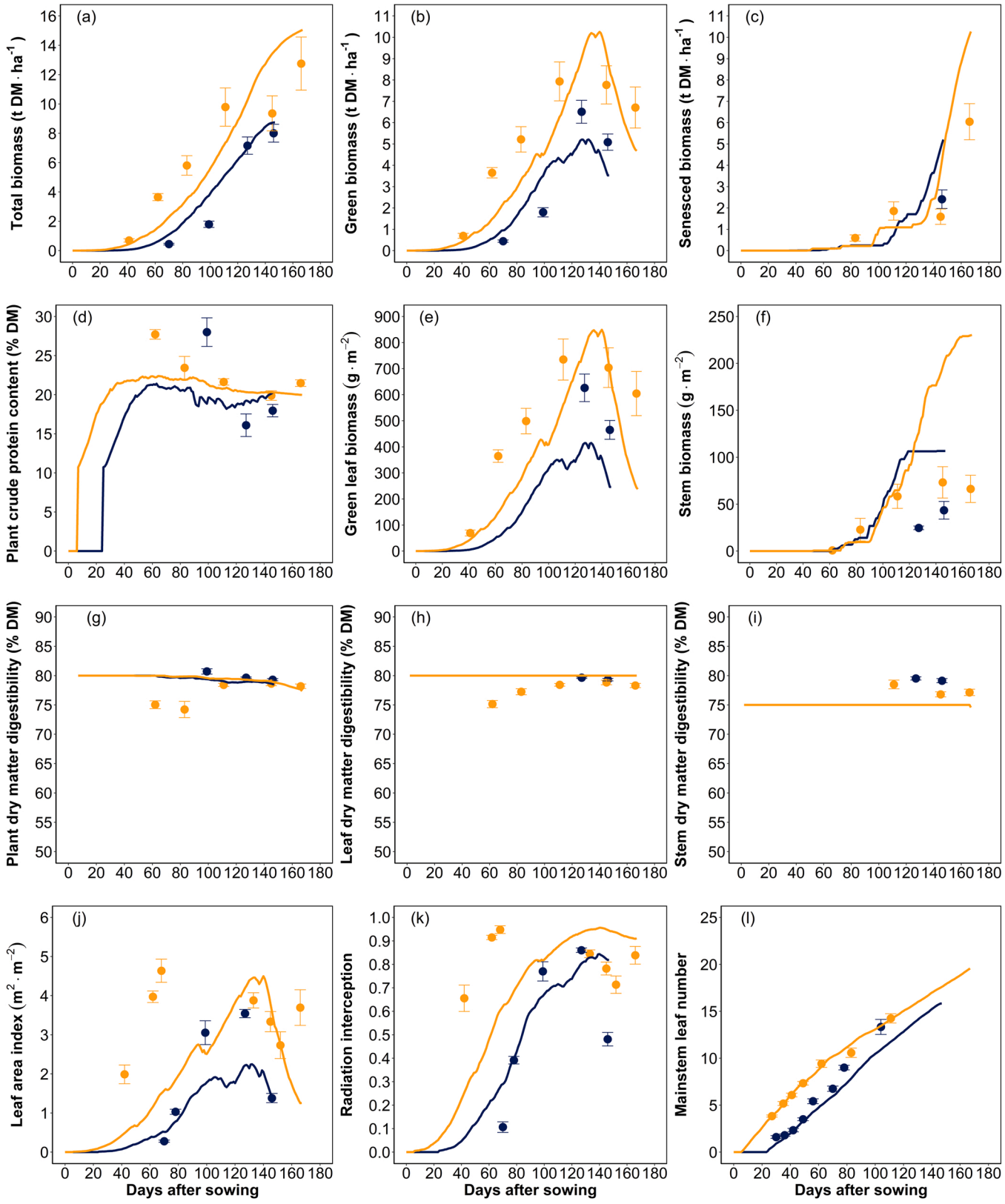

Fig. 2. Model simulations of raphanobrassica *cv.* Pallaton in APSIM (lines) compared with observations (dots) from calibration experiments in 2018 (blue) and 2019 (orange) for biomass and its components (a-c, and e-f), forage nutritive value (d and g-i), and leaf canopy and development (j-l) attributes for the parameterisations.

maturity leaf-type rape) and HT-R24 (late maturity herbicide tolerant rape), and raphanobrassica *cv*. Pallaton. These experiments are fully described in Watt et al. (2021). Briefly, these experiments included a broad range of forage brassica genotypes and reference crops of canola and forage oats that were sown in four replicated plots per genotype in a replicated block design. Experiment 1 was sown on the 20 June 2018 and received 193 mm rainfall and 135 mm supplemental irrigation. Experiment 2 was sown on the 12 April 2019 and received 30 mm of rainfall and 128 mm supplemental irrigation. Biomass, nutritive value, leaf and canopy development and soil water and nitrogen (N) uptake observations from both experiments were used to calibrate model parameters for the forage brassica genotypes (Table 1).

2.1.1. Collection of experimental observations

In both experiments, leaf number on the mainstem was recorded every 7–14 days from ~30 days after sowing (DAS) to ~75 DAS and then every 21 days until ~110 DAS. Recording of leaf number ceased once branching commenced as it was difficult to accurately count leaves thereafter. Total biomass was collected from 1 m^2 quadrats (taking care to avoid previously sampled areas) in the central rows of each replicated plot at 70, 99, 127 and 146 DAS in Experiment 1, and 41, 62, 83, 111, 145 and 166 DAS in Experiment 2. Samples were partitioned into leaf (leaf/petiole) and stem, except during the early stages of growth when little stem was present and instead only whole plant biomass was recorded. Samples were also separated into green and senesced leaf biomass. All samples were dried in a forced-draught oven at 60 °C until at constant dry weight and then weighed. Samples were ground through a 1 mm screen and analysed for DMD to determine metabolisable energy (ME; 0.172 × DMD% − 1.707; Freer, Dove and Nolan, 2007), and total N to determine crude protein (CP; Total N concentration × 6.25; AFIA, 2014) content, as described in detail by Watt et al. (2021). Leaf area of individual leaves was measured at 103 DAS in Experiment 1 and 40 DAS in Experiment 2 using three randomly sub-sampled plants taken from central rows in each replicate plot. Plants were partitioned into leaf and stem and leaf area was recorded using a leaf area meter (LI-3100 C Area Meter, Li-Cor Biosciences Inc., Lincoln Nebraska USA). Leaves from individual plants were dried in a forced-draught oven at 60 °C until at constant dry weight and specific leaf area of each genotype was calculated by dividing leaf area by leaf biomass. Leaf area index (LAI) and radiation interception (Ri) were recorded at 30, 70, 78, 99, 127 and 146 DAS in Experiment 1, and at 42, 62, 133, 145, 152 and 166 DAS in Experiment 2, using a AccuPAR PAR/LAI Ceptometer, Model LP-80 (Decagon Devices Inc., Pullman Western Australia). An additional measure for LAI and Ri was taken for Pallaton in 2019 at 68 DAS, as the crop had not yet reached full canopy closure at the previous sampling point. Recording for leaf canopy development were targeted at early vegetative and late vegetative/senescing stages of growth. Leaf distribution parameters (χ) for all genotypes was set at 2.0, within the typical range for a rape crop as specified by the operator's manual (Decagon devices Inc, 2013).

Soil cores were taken before sowing and at the end of each experiment to characterise the soil at the site for APSIM. Six soil cores 50 mm in diameter and 1800 mm depth were taken across each replicate block ($n = 4$ blocks) prior to sowing. Soil samples were partitioned into soil layers 0–150, 150–300, 300–600, 600–900, 900–1200, 1200–1500, 1500–1800 mm, split in half lengthwise and bulked within each block into separate bags for analysis of soil water and nutrients including organic carbon content, and NO_3-N and NH_4-N concentrations. Soil water samples were weighed immediately in the field and then dried at 105 °C until at constant dry weight and reweighed for gravimetric soil water content. Soil nutrients samples were dried at 40 °C for 3–5 days and finely ground for analysis at CSBP Soil and Plant Analysis Laboratory Bibra Lake, WA. At the end of each experiment two soil cores were taken in individual plots and were partitioned, dried, and analysed as above to determine final soil water and N status for each genotype.

2.1.2. Simulation set-up for calibration experiments in APSIM

Meteorological data for the simulations for these two sites were sourced via the Scientific Information for Land Owners (SILO) Long Paddock database (Jeffrey et al., 2001; https://www.longpaddock.qld.gov.au/silo/) with a suitable weather station located ~2 km from the sites (station no. 041306). A previously classified soil (APSoil No. 007) located ~2.5 km was selected from the APSoil database (https://www.apsim.info/apsim-model/apsoil/) and used for the simulations of both sites based on confirmation it matched the soil type, depth, organic carbon content, and soil texture for both experimental sites.

Starting volumetric soil water and soil N concentration in the simulations were set with volumetric soil water calculated by multiplying gravimetric soil water by the bulk density values measured for the selected soil. The reference crop, canola *cvv*. Wahoo in 2018 and Hyola970 CL in 2019 was used to further calibrate the simulation of each of the experiments based on starting soil water and N conditions. Some very minor adjustments were made to the canola lower limits in each of the APSoil soil layers to match the final soil water measured in each soil layer which resulted in an improved prediction of crop biomass for the reference crop. Canola lower limits were used for all forage brassica genotypes.

2.1.3. Modifications to forage brassica genotype-specific parameters

The calibration stage aimed to produce a functional forage brassica model by making only minor modifications to the generic crop parameters in the APSIM-canola model to improve the fit between predicted and observed data for each genotype. Initial parameters for the forage brassicas genotypes were based on the winter canola *cv*. Taurus because of its high vernalisation requirement. Modifications to parameters were made using observed data where possible, followed by exploring the sensitivity of the model to changes in parameter values. Refinements were made iteratively until a point was reached that optimised model agreement with observed values. The process targeted crop parameters for which experimental data were clearly different between canola and forage brassica genotypes (i.e., phenological development, leaf appearance rate, leaf size, specific leaf area). Model parameterisation was conducted stepwise, firstly focussed on crop phenology, then on canopy development and biomass partitioning, and finally on parameters driving nutritive value predictions.

Thermal time requirements for emergence, end juvenile and floral initiation stages were modified to account for the higher vernalisation requirements for each of the forage genotypes and the extended vegetative growing window (Supplementary Table 1). Changes were not made to thermal time between floral initiation, flowering, start or end grain filling or maturity as no data was available to support alternative parameters. Based on the observed data, leaf appearance rate of the forage rape cultivars were modified to increase initial leaf appearance rate (i.e., lower thermal time per leaf) during early vegetative growth stages (to leaf 10) and reduced rate thereafter compared to canola. For raphanobrassica, initial leaf appearance rate was modified to reflect the overall slower leaf appearance rate of this genotype than the forage rape cultivars and canola. Using observed data, leaf size (area per leaf) was also modified to reflect the larger size observed for the forage rape genotypes compared to canola. Changes to these leaf parameters were also supported by other data of forage rape leaf size and appearance rate (Neilsen, 2005). Leaf size parameters of the forage rapes *cvv*. Goliath and Winfred were best matched to those used for hybrid canola cultivars in the APSIM-canola model (e.g., CBI406, H46Y78). Larger leaf size was observed in raphanobrassica *cv*. Pallaton and forage rape *cv*. HT-R24 compared to the other forage rape cultivars, as documented also by others (Dumbleton et al., 2012; Westwood and Mulcock, 2012). Maximum and minimum range for specific leaf area were decreased for Pallaton based on observed specific leaf area (Supplementary Table 1). Further improvements to the biomass partitioning of leaf and stem for the forage brassica genotypes were made via modifications to the biomass partitioning parameters in the model to better reflect the higher

Table 3
Summary statistics of model performance of APSIM in predicting biomass production, and nutritive value of the different forage brassica genotypes across multi-environments spanning agro-climatic zones.

	Genotype				Agro-climatic zone			
	Early rape	Late rape	HT rape	Raphanobrassica	Sub-tropic, semi-humid	Temperate, sub-humid	Dry Mediterranean	Temperate, cool season wet
Biomass (t DM·ha^{-1})								
n	101	80	18	21	48	10	30	132
R^2	0.74	0.78	0.79	0.73	0.56	0.43	0.41	0.81
NSE	0.64	0.70	0.72	0.61	0.46	0.14	-0.11	0.73
RMSE	1.72	1.42	1.52	1.42	2.02	0.56	1.02	1.54
PBIAS (%)	-3.1	16.6	-9.3	-21.4	-17.2	-8.8	-0.4	8.0
Metabolisable energy yield (GJ ME·ha^{-1})								
n	31	40	14	17	32	8	22	40
R^2	0.51	0.75	0.68	0.70	0.36	0.18	0.29	0.72
NSE	0.43	0.73	0.60	0.57	0.19	-0.31	-1.04	0.64
RMSE	17.8	16.8	19.7	16.9	24.6	7.96	13.1	13.9
PBIAS (%)	-11.1	-0.5	-11.2	-17.7	-17.1	-9.7	4.4	-2.8
Dry matter digestibility (% DM)								
n	31	40	14	17	32	8	22	40
R^2	0.07	0.05	0.00	0.00	0.03	0.31	0.05	0.14
NSE	-0.70	-0.63	-0.68	-0.54	-0.39	0.24	-0.90	-5.72
RMSE	8.33	10.48	2.77	3.10	3.74	2.09	2.50	12.45
PBIAS (%)	-5.3	-7.9	0.4	2.1	1.7	-0.1	2.1	-12.6
Crude protein content (% DM)								
n	31	40	14	17	32	8	22	40
R^2	0.00	0.15	0.26	0.03	0.09	0.89	0.46	0.01
NSE	-0.24	0.03	-0.60	-0.17	-0.02	0.79	-7.07	-0.48
RMSE	5.53	4.36	4.46	6.13	4.04	1.82	7.32	4.74
PBIAS (%)	-4.7	8.5	20.6	13.5	7.0	-0.8	57.3	-9.2

n, number of observations; R^2, R-squared coefficient of determination; NSE, Nash-Sutcliffe efficiency score; RMSE , root mean square error; PBIAS, percent-bias.

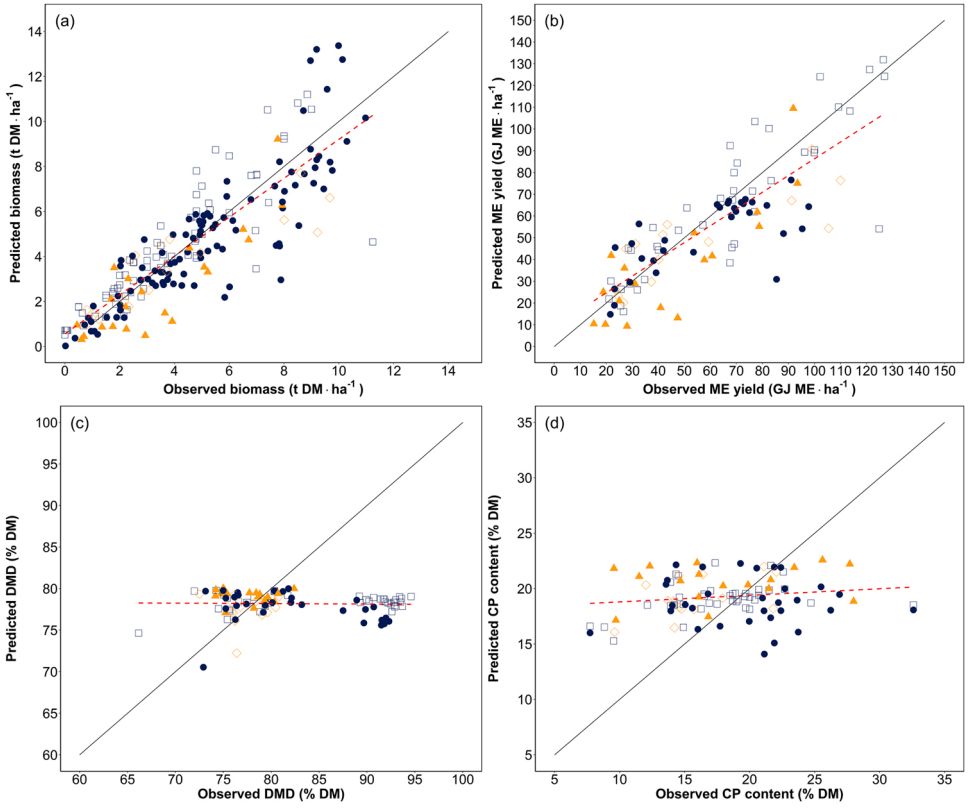

Fig. 3. Observed *v.* predicted (a) biomass, (b) metabolisable energy (ME) yield, (c) dry matter digestibility (DMD), and (d) crude protein (CP) content of forage brassica types: early rapes (blue solid circles), late rapes (blue open squares), raphanobrassica (orange solid triangles) and HT rape (orange open diamonds). Solid line represents 1:1 line and red dotted line represents linear regression. Statistical values for goodness of fit are shown in Table 3.

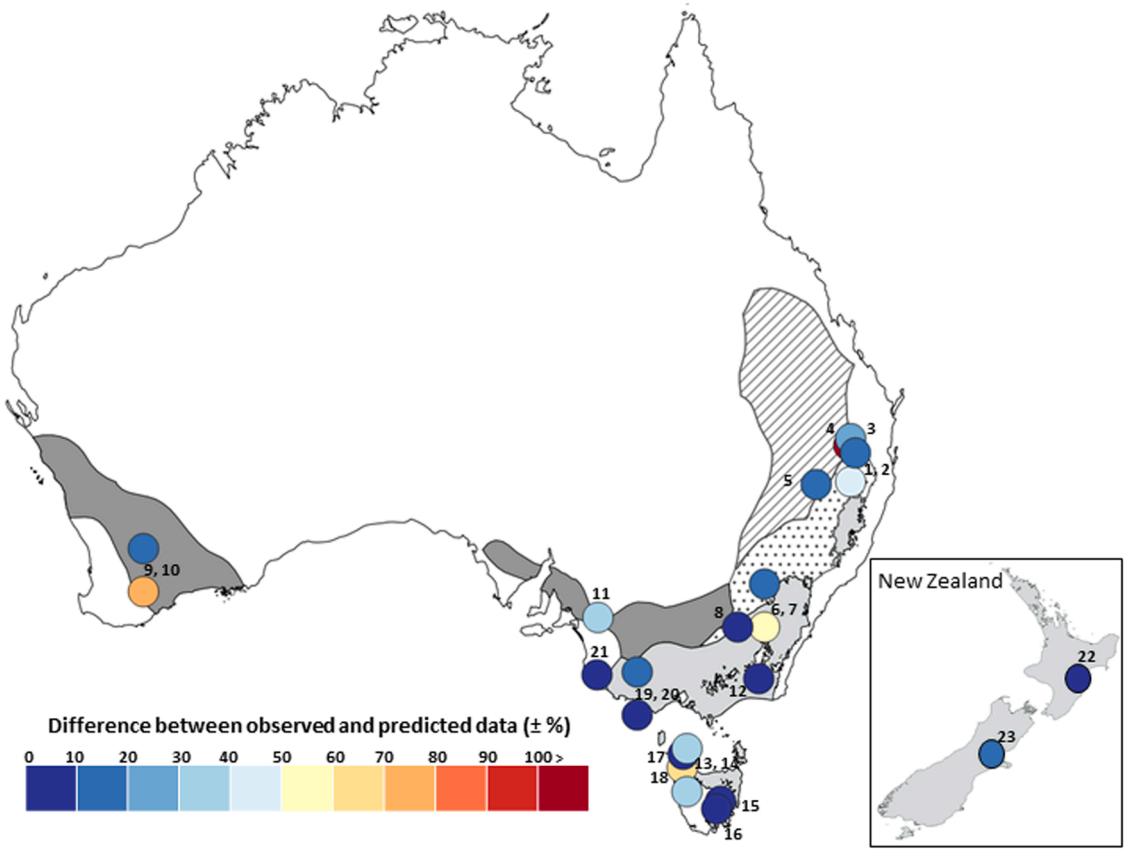

Fig. 4. The relative performance of the forage brassica model to predict biomass at 23 locations located in sub-tropic, semi-humid (grey lines), temperate, sub-humid (grey dots), dry Mediterranean (dark grey) and temperate, cool season wet environments (light grey) within Australia and New Zealand. Coloured dots for each site represent the average difference between observed and predicted biomass data for each site.

allocation to leaf in the forage brassica genotypes from emergence to floral initiation compared to canola. Compared to the parameters set for canola, the allocation to leaf was increased by 10%, 30% and 50% during the emergence, juvenile, and floral initiation stages, respectively. The DMD of green leaf and stem were also increased to better reflect the higher DMD value of the forage brassicas during the vegetative period compared to those set in the released canola crop model. Initially DMD values were set to those reported for similar forage brassica genotypes from *in vivo* studies (Sun et al., 2015a, 2012) and further modifications were made using the iterative process combined with visual inspection of the predicted and observed data for nutritive value (both total and plant components). To improve biomass partitioning between green and senesced biomass, changes to parameters driving leaf senescence in response to water stress were explored; however, these changes did not improve the model beyond the standard canola parameters. A summary of all key parameters for each genotype are detailed in Supplementary Table 1.

2.2. Stage 2: Testing of crop biomass production and nutritive value across environments

To test the new model parameterisations for the forage brassica genotypes across a wider range of environments and agronomic management practices (e.g., sowing times, fertiliser inputs, irrigation schedules), data were gathered from several sources where forage biomass and nutritive value were measured for the characterised genotypes (or equivalent varieties) and sufficient agronomic information was available to build simulations of these experiments (Table 2). The model test set included data on diverse forage brassicas from: (1) multi-environment experiments in a range of agro-climatic zones of Australia's mixed farming zone, including: sub-tropic semi-humid, temperate sub-humid, and dry Mediterranean environments (Watt et al., 2021; Flohr unpubl. data); (2) forage rapes grown for comparison with dual-purpose canola in temperate sub-humid (Kirkegaard et al., 2008), and temperate cool-season wet environments (Kirkegaard unpubl. data); (3) forage rape evaluations in temperate cool-season wet environments of southern Australia and previously used for modelling in APSIM (Pembleton et al., 2013); and (4) forage rape experiments in temperate cool-season wet environments of New Zealand (Chakwizira et al., 2014; Fletcher and Chakwizira, 2012) (Table 2). Many experiments involved other forage rape cultivars which were aligned to either Winfred (*cvv.* Leafmore, Interval and Titan) or Goliath (*cv.* Bonar) based on their relative maturity. Data was more limited to Australia's mixed farming zone for the recently released genotypes Pallaton raphanobrassica, and the hybrid type HT-R24 forage rape (Table 2). Data from sites at Elliot in Tasmania, Terang in Victoria, and Hastings and Lincoln in New Zealand (all temperate, cool season wet environments) included a range of irrigation and nitrogen treatments that enabled us to explore the capability of the model to predict forage brassica production under different agronomic management regimes (see Table 2).

2.2.1. Model testing using APSIM and test datasets

Simulations for each of the 23 experiments were built in APSIM using management and soil information documented for each of these studies. Soils used in the simulations were sourced from the APSoil database. Representative soils for each region were selected via consultation with scientists working in each region or via the Soils and Landscapes Grid of Australia (Grundy et al., 2015) and the SoilMapp iPad app (CSIRO, 2020) based on soil type, depth, and plant available water capacity (PAWC) (Table 2). Meteorological data for all Australian locations was

sourced via SILO Long Paddock database (Jeffrey et al., 2001) and data for New Zealand locations were sourced via the NIWA Virtual Climate Station Network (Cichota et al., 2008; Tait and Turner, 2005).

Soil N and/or water content were available for the majority of the sites, to initialise the simulated soil conditions. However, at the Pilton, Tulloona and Formartin sites starting soil conditions were not measured, so simulations were initialised by setting the starting soil N and water conditions to the crop lower limits and zero mineral N at the harvest date of a wheat crop sown in the previous year. Crop management, reflected seed bed preparation, sowing, N fertiliser and irrigation application at each experimental site. Where plant establishment numbers were not reported, plant establishment was estimated based on sowing rate and a 75% emergence rate.

Simulation outputs were tested against observed data for biomass, ME yield, and total plant DMD and CP, although many data sets were limited to biomass data only. Temperature, soil water and N stress response on plant photosynthesis was also output as an additional check of model performance. Where possible, reference crops were used to check that simulation of water and N resources were reasonable. In some cases, the soil N available at sowing was adjusted in order to adequately simulate growth of the reference crop.

Plant CP content, ME content and ME yield were calculated from APSIM crop output variables using the following equations:

(1) Plant CP content (% DM) = Total plant N concentration × 6.25
(2) ME (MJ/kg DM) = 0.172 × dry matter digestibility (% DM) – 1.707
(3) ME yield (GJ·ha^{-1}) = crop biomass (t DM·ha^{-1}) × ME (MJ·kg^{-1} DM)

2.3. Statistical analyses of model performance

Statistical analyses were used to evaluate the performance of the model simulations of biomass, ME yield, and total plant DMD and CP content. Analyses were carried out for each forage brassica genotype and partitioned to test the performance in each agro-climatic zone. This enabled sources of variability within the broader model testing data set to be identified. All statistical analyses were carried out using 'stats'(R Core Team, 2017), 'Metrics' (Harmer et al., 2018), and 'hydroGOF' (Zambrano-Bigiarini, 2020) packages in the statistical software program R (R Foundation, Vienna). The statistical analyses included: (1) coefficient of determination (R^2) that describes the variance between predicted and observed data when a linear regression is fitted (1 is optimal); (2) Nash-Sutcliffe efficiency score (NSE) that describes the relative magnitude between the residual variance and observed data variance (0.75–1 is very good, and ≤ 0.50 is unsatisfactory) (Moriasi et al., 2007; Nash and Sutcliffe, 1970); (3) root mean square error (RMSE) that indicates the error in the units being measured (0 is optimal); and (4) percent-bias (PBIAS) that measures the tendency of the predicted values to differ to the observed values (+ values indicates model under-estimation, and − value indicates model over-estimation; 0 optimal) (Moriasi et al., 2007; Yapo et al., 1996).

3. Results

3.1. Stage 1: Calibration of forage brassica genotypes

3.1.1. Biomass partitioning

The thermal time parameters derived for each forage brassica genotype achieved reasonable agreement with field phenological observations of floral initiation in both experiments (data not shown). Many of APSIM's processes are driven by crop phenology so modifications to the parameters in APSIM-canola also achieved improvements in predictions of other crop parameters such as biomass partitioning for the forage brassica genotypes. Changes to the phenology parameters greatly improved total biomass and green biomass of all the forage brassica genotypes, particularly green biomass later in the season (Figs. 1b and 2b). These changes had little influence on senesced biomass predictions for the forage rape cultivars, which were often overpredicted (Fig. 1c; Supplementary Figs. 2c and 3c). Senesced biomass of Pallaton raphanobrassica was reasonably well predicted in comparison to the forage rape cultivars (Fig. 2c). A larger discrepancy between observed and predicted total and senesced biomass occurred in 2019, compared to the 2018 experiment in the forage rapes, but this was also present in the reference canola crops (Fig. 1a and c; Supplementary Figs. 1–3a and c).

Modifications to the biomass partitioning in APSIM-canola were made to better reflect the higher leaf to stem ratio of the forage brassica genotypes and these significantly improved predictions of the allocation to leaf and stem. Large discrepancies between the plant allocations to leaf and stem between the two calibration years (Figs. 1e-f and 2e-f; Supplementary Figs. 2e-f and 3e-f) meant that further calibration to better predict biomass allocation were not possible within the current model framework. This seasonal divergence was also found in the canola reference crop where leaf was underpredicted, and stem overpredicted in 2019, but plant allocation predictions were much better in 2018 (Supplementary Fig. 1). Green leaf biomass of the forage rapes was relatively well predicted up to 120 DAS, but the model tended to underpredict at later times, mainly due to the model predicting greater leaf senescence than recorded in the experimental data. Leaf biomass predictions for Pallaton (Fig. 2e-f) were much better over the full growing season compared to the forage rape cultivars (Fig. 1e-f; Supplementary Figs. 2e-f and 3e-f).

3.1.2. Forage nutritive value

Forage nutritive value is linked to phenological stages in APSIM, so improvements in phenological parameters improved predicted forage nutritive value. However, further modifications were made to green leaf and green stem DMD parameters in APSIM-canola to more accurately predicted the higher DMD of green leaf and slower decline in DMD over time of the forage brassica genotypes compared to canola. As a result of these changes, the model closely predicted the DMD of the plant and its components (Figs. 1g-i and 2g-i; Supplementary Figs. 2g-i and 3g-i). Predictions of CP content were much more variable than DMD, but generally fell within the boundaries of the observed values (Figs. 1d and 2d; Supplementary Figs. 2d and 3d) and this was also the case for the canola reference crop (Supplementary Fig. 1d).

3.1.3. Leaf canopy and development

Modifications to the APSIM-canola model were required to reflect a more rapid leaf appearance rate in the forage rape cultivars during early growth (~1.4 times faster than canola), which was maintained thereafter compared to canola that increased dramatically as the crop approached floral initiation. Leaf appearance rate of raphanobrassica was much slower (i.e., more thermal time required per leaf) than both canola and forage rapes, especially after node number 10 (Supplementary Table 1). As a result of these changes, the model closely predicted leaf development for all forage brassica genotypes (Figs. 1l and 2l; Supplementary Figs. 2l and 3l). Predicted LAI and Ri for forage rapes *cv.* Goliath and Winfred were greatly improved by adjusting leaf size using the existing parameterisations for hybrid canola cultivars in the APSIM-canola model (Fig. 1j-k; Supplementary Fig. 2j-k). Further adjustments were needed for HT-R24 rape and raphanobrassica to better reflect the more rapid expansion of leaves (and increase in leaf biomass production) (Fig. 2j-k; Supplementary Fig. 3j-k). Specific leaf area parameters were also modified for raphanobrassica to match the observed leaf area, but forage rapes remained the same as canola (Supplementary Table 1). Observed leaf canopy data was collected using the same leaf distribution parameter for all genotypes, despite obvious differences in plant structure, particularly between the forage rapes and raphanobrassica. Although modifications to leaf size and specific leaf area improved the LAI and Ri for Pallaton, they were still often underpredicted, particularly during earlier growth periods (up to 80 DAS) (Fig. 2j-k). Further refinements of canopy development parameters in Pallaton were explored

but resulted in reduced model performance in other attributes, so further changes were not incorporated in the absence of additional supporting data. This was not the case for the forage rapes where LAI and Ri were relatively well predicted (Fig. 1j-k; Supplementary Figs. 2j-k and 3j-k).

3.2. Stage 2: Model testing

3.2.1. Biomass

When model performance was tested against an independent multi-environment data set the biomass for all genotypes was reasonably well predicted as indicated by the high NSE score (0.61–0.72), $R^2 > 0.73$, and RMSE values ranging from 1.4 to 1.7 t DM·ha^{-1}. The PBIAS values for all genotypes were < 25% and early rape genotype was close to optimal, indicating low model bias, but predicted biomass for late rape genotype (e.g., Goliath) and raphanobrassica were often underestimated and overestimated, respectively (Table 3; Fig. 3a).

Although there were differences in model performance between the agro-climatic zones, all sites had relatively low RMSE values ranging from 0.6 to 2 t DM·ha^{-1} (Table 3). Overall, the model predicted biomass with only a 0–39% difference to the observed data at 18 out of the 23 sites and this was distributed broadly across the agro-climatic zones (Fig. 4). Biomass was poorly predicted at two of the testing sites, but this was not consistent with other data collected at those sites or other corresponding agro-climatic zones (Fig. 4). The agreement of the model was particularly good in temperate, cool season wet environments (that made up 60% of our model testing data). The agreement of the model in sub-tropical, semi-humid environments (that made up 22% of our model testing data) was just below the satisfactory rating for model performance with an NSE of 0.46. However, the R^2 for this agro-climatic zone was 0.56 and the PBIAS was $< \pm$ 20% indicating that the observed data were evenly distributed within the predicted values (Table 3). The temperate, sub-humid, and dry Mediterranean environments had NSE values $< \pm$ 0.15 indicating poor model agreement, but the RMSE ranged between 0.5 and 1.0 t DM/ha, the R^2 values were > 0.4 and the PBIAS were close to 0, which indicated that the observed data were evenly distributed within the predicted data (Table 3).

3.2.2. Forage nutritive value

Predictions of plant DMD and CP content were poor for all genotypes, often achieving negative NSE scores and R^2 values well below 0.50 ($R^2 <$ 0.10 in most instances). This finding was also consistent across agro-climatic zones, with the only exception the temperate, sub-humid environments where CP content was predicted very well (NSE >0.75; R^2 >0.85). The RMSE for CP content of all genotypes and across all agro-climatic zones was approximately 5%, which represented around a 25% difference from the measured values. The PBIAS for CP content was $< \pm$ 20% for all genotypes and across all agro-climatic zones, except for the dry Mediterranean environment where CP content was largely underestimated (Table 3). While model predictions for CP content were very poor this was less the case for DMD with a low PBIAS and RMSE (~3%) for all genotypes, and agro-climatic zones (Table 3). However, the very low R^2 values and near-constant predicted DMD values indicated that the variability in DMD between genotypes (Fig. 3c) and agro-climatic zones (Supplementary Figure 4c) were not adequately captured by the model. For the temperate, cool season wet environment, the observed DMD values were high (82–95%) compared to other sites (66–87%) (see cluster in Fig. 3c; Supplementary Figure 4c), and this resulted in a larger negative PBIAS value for that agro-climatic zone data (Table 3).

Metabolisable energy yield (a function of both DMD content and biomass yield) was satisfactorily predicted for all forage brassica genotypes based on the high R^2 values > 0.5 and NSE scores (average 0.58). The only exception was for early rapes that had an NSE below the satisfactory threshold (0.43) but the R^2 was within the acceptable range (Table 3). The PBIAS for all genotypes were $< \pm$ 20% or close to optimal indicating that the observed data were evenly distributed within the predicted data; although the PBIAS value for raphanobrassica was more negative than the forage rapes (Table 3), indicating that the model tended to overestimate ME yield more for this genotype.

Similar to biomass, the model agreement for ME yield was strongest in temperate, cool season wet environments (Table 3) but the model prediction was less accurate across the other agro-climatic zones (Table 3). Despite this, the PBIAS for all agro-climatic zones was $< \pm$ 10%, with the exception of the sub-tropic, semi-humid environment that was slightly higher ($< \pm$ 20%). Further, the RMSE values in each agro-climatic zone were generally acceptable given the range of observed biomass values within each zone (Table 3). The greatest source of error for ME yield predictions came from inaccurate predictions of forage DMD rather than error in biomass.

4. Discussion

Development of this forage brassica model provides an opportunity to understand and refine agronomic management practices and identify the potential role of forage brassicas to complement the existing livestock feedbase. We have parameterised a model for three forage rape genotypes and a raphanobrassica that can predict their vegetative biomass and nutritive value characteristics across a broad range of agro-climatic zones (e.g., sub-tropic, semi-humid cf. temperate, cool season wet environments), and agronomic management practices. This model is significantly more robust and broadly applicable than other forage brassica models, such as DairyMod (Johnson, 2016). This new capacity adds considerably to the complement of forage and crop models available in the APSIM framework. Having this capability in APSIM allows broader exploration of forage brassicas in the farming system, including their interactions with available soil water and nutrients, production risk in the face of climate variability, and interactions with other crops and forages in rotation.

Forage rapes are the same species as grain and dual-purpose canola. The APSIM-canola model includes a broad suite of canola cultivars, including winter and hybrid canola types that have been added more recently. However, these winter and hybrid canola varieties have received limited testing compared to more broadly used conventional and triazine tolerant varieties (APSIM Initative, 2021; McCormick et al., 2015). In the calibration stage of our study, we found that the biomass components and leaf number of the canola reference crop was better predicted for the open pollinated triazine tolerant variety (e.g., Wahoo) compared to hybrid winter type canola (e.g., Hyola 970 CL). Despite these minor limitations, winter and hybrid canola are most similar to forage brassicas because they have higher vernalisation, larger leaf size, and differ in transpiration efficiency compared to traditional spring-type canola varieties (McCormick et al., 2015; Whish et al., 2020). This justified the use of winter canola *cv*. Taurus as a template for our forage brassica model.

Previous modelling of non-genotype specific forage rapes in temperate, cool season wet environments has been carried out in APSIM-canola using the French winter cultivar with modifications made to maximum leaf size and thermal time parameters (Pembleton et al., 2013). Unlike our model, the Pembleton et al. (2013) model did not differentiate between forage rape types and their unique plant attributes (e.g., maturity, giant vs. leaf-types, leaf size and appearance rate); and DM yield was often underpredicted. However, the R^2 value for both studies were similar (R^2 ~0.76). Modifications to the biomass partitioning was also made in our forage brassica model to account for the higher leaf to stem ratio of forage brassica crops compared to canola, which was not accounted for in the other study that only reported total biomass and not plant components. Furthermore, the Pembleton et al. (2013) model focussed on forage brassicas grown in temperate, cool season wet environments within south-eastern Australian dairy systems and the ability of the model to simulate forage brassica production across different agro-climatic zones (and production environments) was not tested. This demonstrates the broader application and robustness of

our forage brassica model in comparison.

One of the more difficult aspects of predicting plant biomass across both the forage brassicas and the canola reference crops was the prediction of green and senesced biomass. This was less well predicted for the forage brassica genotypes in the late-vegetative/early reproductive stages of growth. Better parameterisation of green biomass later in the season is especially important for future livestock systems modelling, as green biomass has higher nutritional value to grazing livestock. Furthermore, forage crops that can maintain vegetative production late in the season are highly advantageous for livestock systems since dry pastures and/or crop residues of lower nutritive value are usually the alternative forage sources and growing animals often require costly supplementation. There are several model parameters that control plant senescence including plant age, and those that alter the response of plants to environmental factors, such as N supply, temperature, and particularly water stress, which can be difficult to parameterise. Although modifications were made to leaf senescence rate from water stress using the iterative process in the calibration stage, model performance was not enhanced for any of the genotypes tested, and so these were kept the same as for the APSIM-canola model. Attributes to predict root depth, and water extraction in our forage brassica model were also kept the same as for the APSIM-canola model as we did not have data to support more crop specific parameterisation. Data from the two experiments used in the calibration stage represented crops grown under dry conditions, and the timing and intensity of water deficit stress varied between experiments, which also made parameterisations challenging. Water deficit stress is known to impact biomass production in forage brassicas (Chakwizira and Fletcher, 2012) and other crops (maize and sweet corn; Song et al., 2010; Stone et al., 2001) and is also known to impact leaf to stem ratio (Buxton and Casler, 1993), which may explain the seasonal divergence between stem biomass in 2018 and 2019 data used in the calibration stage.

Forage brassicas are known to respond differently to water deficit stress. Canola is considered more sensitive to water deficit stress than other brassica crops (Kirkegaard et al., 2021), but forage brassica genotypes also vary in their tolerance to water deficit stress. For example, forage rapes have a deep root systems and can extract moisture from deeper water layers than bulb turnips (Fletcher et al., 2010) and this makes them more suitable to drier environments. Forage rapes and raphanobrassica genotypes have been shown to outperform other forage brassica genotypes for both biomass production and nutritive value under dry seasonal conditions (Watt et al., 2021). In general, there is very limited data on the rooting depth or water extraction capabilities of different forage brassica genotypes, which are typically grown in environments that are rarely water limited. The difficulty to accurately measure plant senescence in the field, and insufficient quality field data on root depth, water extraction, and water deficit stress response on a genotype level, made appropriate model parameterisation for green and senesced biomass, and leaf and stem biomass more challenging and more work is needed to further enhance model performance. However, the model parameterisations could adequately predict total crop biomass production across a wide range of environments varying in water availability, so the fundamental relationships between water stress and growth are likely to be robust.

A key requirement in forage models is the ability to predict forage nutritive value for livestock, which is largely unnecessary in grain crop models. Although there has been more recent interest in the nutritive value of forage and dual-purpose crops in APSIM (Bell et al., 2009) many parameters such as DMD, which are important to quantify for livestock production systems, are not available in all crop models. The wheat and forage sorghum models are the only crop models where available DMD parameters have been tested, although testing for these are limited (Bell et al., 2009; Pembleton et al., 2013). Many of the APSIM crop models have been developed using historical data sets that have extensive information on crop phenology, biomass, and yield, but minimal data on crop nutritive value at the various stages of growth or for the different plant components (i.e., leaf and stem). In this study, we made significant changes to the DMD parameters in APSIM-canola in order to predict the high nutritive value for forage brassicas during their vegetative growth stage (stage of highest nutritive value). Although DMD predictions for the forage brassicas were improved by the iterative modifications made to the green leaf and stem DMD parameters during the calibration stage, many of the statistical analyses indicated potential to further improve model performance, especially the need to better capture the variability in DMD over time and across environments. The DMD parameters in APSIM use stage of plant growth and biomass partitioning (i.e., leaf, stem, pod etc.) for DMD predictions. However, environmental stresses, such extreme temperatures, water deficit stress, and shading are also known to impact plant digestibility as they influence the lignification of plant tissues, as well as leaf to stem ratio (Buxton and Casler, 1993). The current processes of APSIM for DMD may explain why the predictions failed to capture the variability of observed DMD data across the different environments. Despite our efforts to modify the DMD parameters in our model, improvements in the way that APSIM predicts DMD currently (i.e., based on growth stage and biomass partitioning) will need to be refined before further improvements can be made. Since water deficit stress also impacts the leaf to stem ratio, more genotype-specific modifications for water deficit stress using quality field data, may also enhance the ability of the model to predict DMD. While model performance statistics here were generally poor for DMD, observed data captured a relatively small range, mainly during the vegetative growth stage, when grazing is most likely. Further, in reality DMD values above 70% are likely to have minimal impact on animal dry matter intake and thus, animal production outcomes (Blaxter et al., 1961) and observed DMD values in our model testing set were above this value. A further challenge in simulating the observed DMD values is the different laboratory methods used by the various data sources. All observed DMD data in our model test set were obtained using near infrared reflectance spectrophotometry (NIRS) from different feed testing laboratories and few of those data sources mentioned any use of wet chemistry methods to validate NIRS predictions. Nearly 50% of observed DMD values were within the range of 87–95% DMD, which were much higher than those reported in studies that validated NIRS predictions with wet chemistry (Watt et al., 2021) or used *in vivo* digestibility measures (Sun et al., 2015b, 2012). These much higher DMD values were especially poorly predicted by the model. Collection of good crop nutritive value data, that is validated by wet chemistry, is needed for future forage model developments. Further, nutritive value data over the entire growing period is needed as our calibration data set was limited to the vegetative stage of growth and provided little variability in observed data.

The model was unable to capture the large variability of observed CP content and since CP is an important nutrient for livestock, this will limit its application in combination with livestock grazing systems models. The issues with CP content are fundamental as N content (used to calculated CP content) is calculated from plant N uptake and biomass, which is one of the main components in all APSIM crop models and is driven by other main crop components: crop biomass and root system (Wang et al., 2002). Furthermore, N demand, uptake and accumulation has been well-tested for a number of cereal and legume crops with close agreement between predicted and observed data (Chen et al., 2016; Probert et al., 1998; Robertson et al., 2002). Poor predictions of forage crop CP content has been previously reported (Pembleton et al., 2013) and our study further affirms the need to better adapt the N content component of the APSIM model to more accurately predict N accumulation and partitioning, especially for forage crops. The N cycle of forage crops are considerably complex as N is removed at various times via biomass removal during grazing and then partially returned via animal excreta (Jarvis, 1993; Pakrou and Dillon, 2000), compared to grain only crops where N accumulates in the seed during grain fill and is removed at harvest (Asseng et al., 2002). APSIM is also predominantly used for broadacre crops in rainfed systems where N may also be limited. Some of

our model testing data sets from the temperate, cool season wet environments, may represent environments with excess N supply that may be problematic for many brassicas which are known to take up luxury amounts of N when it is available. These processes may not be handled appropriately by the current model.

A further limitation of the current parameterisations for forage brassicas outlined here is the phenology parameters were developed from phenology data from a narrow range of environments with limited vernalisation, photo-period and thermal time drivers of plant development. The data collected in field experiments are from a single location and over a limited growing window mainly targeting the vegetative stage, hence predictions of reproductive development is likely to need further attention if this is desired in future model capabilities. Despite this, the phenology parameters derived for each of the genotypes generated plant growth and biomass allocations that closely agree with observations of biomass, nutritive value, and floral initiation date (where this occurred in experiments). Further, in most cases, management of forage brassicas will target keeping them in a vegetative growth stage, and hence applying the model outside this period (e.g., to predict seed yield) is unlikely to be of wide interest and would require further work before the model would be suitable outside its application as a forage crop as intended here. Since forage brassicas are used for grazing by livestock, regrowth, and defoliation parameters in the APSIM crop models will need to be addressed for future modelling work. We did not test these in our current model, largely due to the lack of quality data for testing and limitation of the APSIM-Classic model in resetting crop stage, and the mobilisation of nutrients during regrowth (McCormick et al., 2012). The increasing use of APSIM for crop/forage-livestock modelling (Holzworth et al., 2018) and the current developments of APSIM Next Generation (Holzworth et al., 2018) are likely to improve capture of regrowth processes and may improve integrated forage-livestock systems simulations in the future.

5. Conclusion

This study has demonstrated that APSIM can now be used to satisfactorily predict forage productivity for several forage brassica genotypes during the vegetative stages of growth across multiple production environments and agronomic management practices. These forage brassica models have furthered our capacity to explore the potential production of different forage brassica genotypes and their contribution to the feedbase in livestock systems in a range of environments. However, further model developments may be required for more sophisticated integrated forage-livestock simulations where aspects such as biomass partitioning, regrowth after grazing, and nutritive value parameters in later stages of plant growth will be more critical.

CRediT authorship contribution statement

Lucinda J. Watt: Conceptualization, Methodology, Investigation, Validation, Formal analysis, Resources, Writing – original draft, Visualisation. **Lindsay W. Bell:** Writing – review & editing, Supervision, Project administration, Funding acquisition. **Keith G. Pembleton:** Writing – review & editing, Resources.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.eja.2022.126517.

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