Assessment of Genetic Gain Trends for Yield in IRRI Rice Varieties in the Philippines Using “era” Trial Studies and Implications for Future Rice Breeding

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Abstract

Rice is a staple crop for 3.5 billion people in the world. To meet the challenges of the rice production for food security and demand due to population increase, yield improvement due to a rice variety's genetic characteristics is imperative. Two studies presented in this paper were undertaken at the International Rice Research Institute (IRRI) in the Philippines, to assess genetic gains for yield in rice varieties bred over the past 50 years. These studies are called as "Era" studies as the varieties used for trials were released during long and distinct periods. Due to the differences in time periods of studies, varieties and locations, the studies were treated separately so as to not to compromise the data analyses. The studies demonstrated that IRRI developed varieties have achieved genetic gains and levels of genetic gains were

dependent on correction or otherwise for maturities. In Study 1, the highest level of genetic gain was 0.70% at about a 23 kg ha^{-1} annual yield increase when not corrected for maturity followed by a genetic gain of 0.62% when corrected for maturity. In Study 2, the highest level of genetic gain was 0.74% at about a 19 kg ha^{-1} annual yield increase when corrected for maturity followed by 0.66% genetic gain when not corrected for maturity. Implications for breeding programs are discussed, however, the studies were not intended to compare genetic gains achieved through different breeding methods nor to compare genetic gains achieved using plot trials versus realized genetic gains for crops grown under farmers' management.

Key words: Rice varieties, genetic gain, Era trials

1. BACKGROUND

Rice is the staple food for 3.5 billion people. Within this decade, an estimated 40 million tons of additional rice will be needed to feed the increasing global population (OECD/FAO, 2019). Climate change is projected to decrease yield in major rice-exporting countries, such as Thailand and Vietnam in Southeast Asia (Teng et al., 2016), impacting on the regional importing countries and rice reserves needed for food security. In the 1960s, the International Rice Research Institute (IRRI) led the "Green Revolution" in rice with the release of variety IR8, especially in South Asia (Khush, 1999). New rice varieties have since been released over the past 55 years in many countries of Asia and other parts of the world to increase rice production through improved yield combined with resistance to and/or tolerance of pests and diseases.

It is projected that, due to climate change—especially temperature increases—there will be a direct impact due to reduction in the yields of four major crops including in rice (Zhao et al., 2017). Rice will be globally impacted indirectly due to increased water demand (Zhao et al., 2017). Due to population growth, consumption of rice is set to increase to over 578 million tons with the average consumption of rice globally projected to increase by 1 kg to reach 55 kg annually during 2019–28, while the area utilized for

48 rice production within this decade is expected to increase by only 1% (OECD/FAO 2019) Therefore,
49 increase in rice production on the farm needs to be achieved by yield improvement of new varieties
50 coupled with optimum agronomic practices. It is imperative that plant breeding programs release new
51 climate-resilient varieties that have higher yields under variable climatic conditions to overcome the
52 challenges to food security.

53 Genetic gains for key traits, including yield, are imperative for successful adoption of varieties at the farm
54 gate level for sustainability and farmer profitability. Genetic gain can be simply defined as the amount of
55 increase in performance that is achieved annually through artificial selection (Xu et al., 2017). To
56 understand the progress made in plant breeding of the crops through artificial selection and breeding,
57 assessment of genetic gain for yield has been conducted in different major crops. Assessment of genetic
58 trends in varieties can provide an estimate of the rate of genetic gain for yield achieved in the breeding
59 program where the varieties originated.

60 Various researchers have used different methods to analyze and estimate genetic gain using a large
61 number of historical datasets generated and collated from different breeding programs that have
62 conducted trials using different varieties. In the United States, it was estimated that maize breeding
63 resulted in genetic gains of 63 kg ha^{-1} $year^{-1}$ for the first 30 years between 1930 and 1960 and of 110 kg
64 ha^{-1} $year^{-1}$ over the next 40 years (Duvick, 2005a). In the wheat breeding program at the International
65 Maize and Wheat Improvement Center (CIMMYT) in Mexico, Crespo-Herrera et al. (2018) assessed genetic
66 gain and showed that, for grain yield, it was 38 kg ha^{-1} $year^{-1}$ (1.8%) in low-yield environments and 57 kg
67 ha^{-1} $year^{-1}$ (1.4%) in medium-yielding environments; across the environments, yield gain was 48 kg ha^{-1}
68 $year^{-1}$ (1.6%). In Germany, Laidig et al. (2014), who analyzed genetic trends for yield improvement across
69 environments for 12 different crop type varieties released over 30 years from different breeding
70 programs, concluded that all the improved crops species tested showed improvements in yield; the lowest

71 genetic trend for dry matter yield was in Italian ryegrass (0.16% annually) and the highest was for winter
72 canola or winter oil seed rape (1.86% annually).
73 In rice, there have been very limited genetic gain studies conducted, especially in Asia where rice is the
74 main staple grain. The only study prior to this one in Southeast Asia was done by Peng et al. (2000) at the
75 International Rice Research Institute, Los Banos, Philippines in 1996 with an estimated 1% yield (75-81
76 kg/ha) improvement per year. In Brazil, Breseghello et al. (2011) conducted genetic gain analyses for 25
77 years of upland rice breeding and concluded that annual gain for grain yield was not significant between
78 1984 and 1992. However, it was 15.7 kg ha^{-1} $year^{-1}$ (0.53%) between 1992 and 2002; and nearly tripled
79 between 2002 and 2009 with a gain of 45.0 kg ha^{-1} $year^{-1}$ (1.44%). More recently in India, Kumar et al.
80 (2020) reported genetic gains of 0.68–1.9% for grain yield in rice varieties grown between 2005 and 2014
81 under different levels of moisture stress conditions.
82 The IRRI breeding program over the decades has had defined objectives in each decade of the program
83 (Peng and Khush 2003). In the first decade (1960-1969) due to lodging among tall rice varieties leading to
84 lower yield, focus was on incorporation of gene conferring lower height (dwarfism) commencing with IR8
85 which led to higher yield. During 1970–1979, emphasis was on multiple disease and insect resistances.
86 During 1980–1989, emphasis was on good grain quality that resulted in IR64. During 1990–1999, hybrids
87 and new plant-type breeding incorporated yield gain with biotic stress resistance and gain quality. By
88 2000–2009, more emphasis was given to molecular breeding approaches to enhance various desired traits
89 and yield improvement and, later, abiotic stress tolerances. IRRI breeders focused on developing high-
90 yielding varieties with multiple stresses, pests and disease tolerances in predominantly irrigated and
91 rainfed environments. Therefore, assessing genetic gain is necessary in such a mature breeding program
92 to understand the progress made during the life of the program and to ensure that higher-yielding
93 varieties continue to be released in the future.

Genetic gain for yield and other traits can be assessed by utilizing historical data from breeding programs although this can be labor- and resource-intensive and requires collation of large sets of consistent standardized historical data. In maize, long-term studies of sequential series of successful hybrids were assessed by adding data from additional new varieties (Duvick et al., 2005a). In their review, Smith et al. (2014) refer to the term "Era trials used by Duvick (2005b) for the method to assess yield improvements in maize crops by including varieties released over different years using data from evaluations conducted in single or across multiple environments (Multi-Environment Trials or MET). Although there are several methods with their own limitations to assess genetic gain for historically-released varieties, Rutkoski (2019) showed that "Era" trials can be used to estimate rates of genetic gain in a shorter timeframe and genetic performance of varieties can be assessed with this method in lieu of large sets of interconnected historical data.

In rice, it is critical that genetic gain for yield is achieved to meet increasing demands as mentioned in OECD/FAO (2019). It is important to understand if increased yields have been achieved through plant breeding and selections (Duvick, 2005a) and thereby drive the changes needed in breeding strategies and methods to achieve targeted yield gain outcomes. Therefore, to understand genetic gain achieved in IRRI's rice breeding program over the past 50 years, two "Era" studies were undertaken during different time periods using different number and combinations of varieties with the second study including later-released varieties. It was expected that these studies would contribute to learning more about the genetic gains achieved in rice thus far at IRRI. Additionally, it was expected that the new knowledge would lead to further exploration of breeding strategies at IRRI to improve genetic gain and provide a clear understanding of the gains yet to be achieved.

2. MATERIALS AND METHODS

This paper describes two "Era" studies conducted at IRRI in Los Baños, Philippines, utilizing its bred varieties in field trials. The varieties used were released from 1966 through to those released at the

respective times that the two studies were conducted. Plot trials conducted at the locations were used to collect the data. Study 1 used 44 varieties and lines available at the time (Table 1) and was undertaken during two dry seasons and two wet seasons during 2013 and 2015. Study 2 used 22 varieties (Table 2) was undertaken during one dry season and two wet seasons during 2016 and 2017. Different sets of varieties were used in Study 1 and Study 2. Only 12 entries were common between Study 1 and Study 2 and therefore data for Study 1 and 2 was not combined for analysis.as that would only lead to a lower number of common lines being taken into account for analyses.

For Study 2, IRRI Multi Environment Trials (MET, Supplementary Table 1) additional data was included in the analyses for some varieties common between "Era" and MET trials adding to the data robustness. These MET trials were conducted in wet season in 2016 and two dry seasons in 2016 and 2017, in one common location Los Banos between "Era" trial and in additional locations in the Philippines. These additional locations in the Philippines included Midsayap, Muñoz, Musuan, Agusan, Ubay, and San Mateo.

Variety selection for Study 1

Forty-four IRRI-developed entries, released between 1966 and 2013 commencing with IR8 in 1966 to IRRI 168 in 2013, were included in Study 1. These varieties were selected based on the area to which they were grown by farmers during their period of maximum use in Southeast Asia (Brennan & Malabayabas, 2011). Thirty-eight varieties had been released for irrigated environments. Two rainfed varieties (IRRI 119 and IRRI 164) and four hybrid varieties were included (Table 1).

TABLE 1 Study 1 variety list by type and in chronological order by year of release

Serial number	**Variety designation**	Pedigree of the line	Category of variety type	**Year of release**
1	IR8	PETA/DEEGEOWOOGEN	Irrigated	1966
2	IR20	IR262-24-3/TKM6	Irrigated	1969
3	IR24	IR8/IR127-2-2	Irrigated	1971

4	IR26	IR24/TKM6	Irrigated	1973
5	IR32	IR20*2/ONIVARA//CR94-13	Irrigated	1975
6	IR36	IR1561-228-1-2/IR1737//CR94-13	Irrigated	1976
7	IR42	IR1561-228-1-2/IR1737//CR94-13	Irrigated	1977
8	IR50	IR2153-14-1-6-2/IR28//IR36	Irrigated	1979
9	IR58	IR28/KWANGCHANGAI//IR36	Irrigated	1983
10	IR60	IR4432-53-33/PTB33//IR36	Irrigated	1983
11	IR62	ARIKARAI///IR24/TKM6//IR20*4/ONIVARA/4/IR 1561-228-1-2/IR1737//CR94-13	Irrigated	1984
12	IR64	IR5657-33-2-1/IR2061-465-1-5-5	Irrigated	1985
13	IR66	IR13240-108-2-2-3/IR9129-209-2-2-2-1	Irrigated	1987
14	IR70	IR19660-73-4/IR54//IR9828-36-3	Irrigated	1988
15	IR72	IR19661-9-2-3-3/IR15795-199-3-3//IR9129-209-2-2-2-1	Irrigated	1988
16	IR74	IR19661-131-1-2/IR15795-199-3-3	Irrigated	1988
17	IRRI 102	IR4215-301-2-2-6/BG90-2//IR19661-131-1-2	Irrigated	1991
18	IRRI 103	IR4547-4-1-2/IR1905-81-3-1//IR25621-94-3-2	Irrigated	1991
19	IRRI 104	IR33021-39-2-2/IR32429-47-3-2-2	Irrigated	1992
20	IRRI 105	IR24594-204-1-3-2-6-2/IR28222-9-2-2-2-2	Irrigated	1994
21	IRRI 106	IR35293-125-3-2-3/IR32429-47-3-2-2//IRRI 103	Irrigated	1994
22	IRRI 108	IR28239-94-2-3-6-2/IR64	Irrigated	1995
23	IRRI 109	IR72/IR24632-34-2	Irrigated	1995
24	IRRI 115	IR48613-54-3-3-1/IR28239-94-2-3-6-2	Irrigated	1997
25	IRRI 116	IR72/IR48525-100-1-2	Irrigated	1997
26	IRRI 118	IRRI102/IR39292-142-3-2-3	Irrigated	1997
27	IRRI 119	IR43581-57-3-3-6/IR26940-20-3-3-3-1//KHAODAWKMALI105	Rainfed	1997
28	IRRI 121	IR58025A/IR34686-179-1-2-1R	Hybrid	1997

29	IRRI 122	IR50401-77-2-1-3/IR42068-22-3-3-1-3	Irrigated	2000
30	IRRI 123	IR47761-27-1-3-6/IRRI108	Irrigated	2000
31	IRRI 135	IR1561*3/HABIGANJDW8//5*IR64	Irrigated	2002
32	IRRI 136	IR1561*2/OBARTHII//4*IR64	Irrigated	2002
33	IRRI 138	IR68897A/IR60819-34-2R	Hybrid	2002
34	IRRI 141	IR44625-139-2-2-3/IR32822-94-3-3-2-2	Irrigated	2003
35	IRRI 144	IR68897A/IR71604-4-1-4-4-4-2-2-2R	Hybrid	2006
36	IRRI 145	IR44699-21-1-3-4/IR66438-167-3-3-2-3	Irrigated	2007
37	IRRI 146	IRRI134/IR70479-45-2-3//IR64680-81-2-2-1-3	Irrigated	2007
38	IRRI 150	IR68077-82-2-2-2-3/IR59548-122-1-4-1	Irrigated	2007
39	IRRI 151	IR00A112/IRRI106	Irrigated	2009
40	IRRI 154	IR73012-137-2-2-2/IRRI104	Irrigated	2009
41	IRRI 156	IR72870-102-2-2-1-3/IR72870-19-2-2-3	Irrigated	2011
42	IRRI 158	IR80559A/IR60819-34-2R	Hybrid	2011
43	IRRI 164	IR43/IR65564-22-2-3//IR68	Rainfed	2011
44	IRRI 168	IR72904-65-1-3-3/IR73012-137-2-2-2	Irrigated	2013

Variety selection for Study 2

The entries for Study 2 were selected based on their year of release starting from the release of IR8 in 1966. Entries included IRRI varieties (Table 2) developed for irrigated rice in Southeast Asia. Therefore, 22 varieties released up to 2016 for irrigated environments were selected. However, unlike in the Study 1, rainfed entries were used in separate trials (data not presented here) as rainfed varieties performance under irrigated conditions may be very different under non-water limited conditions. Hybrid entries were not used along with inbred entries as they are generally considered to yield higher than inbred varieties. Additionally, data from varieties common to all “Era” trials and the MET (Supplementary Table 1) trials conducted in seven locations including Los Baños, in the Philippines (2016–2017) were included in the

147 analysis. This was done to increase data robustness as it would involve several environments other than

148 the one environment used in the “Era” trial.

149 **TABLE 2** Study 2 variety list by type and in chronological order by year of release

Serial number	Variety designation	Pedigree of the line	Category of variety type	Year of release
1	IR8	PETA/DEEGEOWOOGEN	Irrigated	1966
2	IR24	IR8/IR127-2-2	Irrigated	1971
3	IR34	BPI 76/CHIANUNG YU 280	Irrigated	1975
4	IR36	IR1561-228-1-2/IR1737//CR94-13	Irrigated	1976
5	IR52	BPI 76*2/KAOHSIUNG 68	Irrigated	1980
6	IR64	IR5657-33-2-1/IR2061-465-1-5-5	Irrigated	1985
7	IR 72	IR19661-9-2-3-3/IR15795-199-3-3//IR9129-209-2-2-2-1	Irrigated	1988
8	IRRI 104	IR33021-39-2-2/IR50404	Irrigated	1992
9	IRRI 105	IR 24594-204-1-3-2-6-2/IR 28222-9-2-2-2-2	Irrigated	1994
10	IRRI 108	IR 28239-94-2-3-6-2/IR64	Irrigated	1995
11	IRRI 115	IR48613-54-3-3-1/IR28239-94-2-3-6-2	Irrigated	1997
12	IRRI 123	IR47761-27-1-3-6/IRRI108	Irrigated	2000
13	IRRI 141	IR44625-139-2-2-3/IR32822-94-3-3-2-2	Irrigated	2003
14	IRRI 143	IR64 (WH)/ADAY SEL//3*IR 64	Irrigated	2006
15	IRRI 154	IR73012-137-2-2-2/PSB RC10 (IR50404-57-2-2-3)	Irrigated	2009
16	IRRI 174	IR00A117/IR 64	Irrigated	2013
17	IRRI 179	IR73008-138-2-2-2/IR68544-29-2-1-3-1-2//IR72870-19-2-2-3	Irrigated	2014
18	IRRI 180	ADDAY LOCAL SEL	Irrigated	2014
19	IRRI 181	IR80894-18-2-2-3	Irrigated	2014

20	IRRI 186	IR02A127/IR 64	Irrigated	2015
21	IRRI 192	Huang-Hua-Zhan*2/OM 1723	Rainfed	2016
22	IRRI 193	IR 68077-82-2-2-2-3/IR00A117	Irrigated	2016

150

151 **Field trials and environments for Study 1**

152 All trials were conducted on IRRI's experiment station at Los Baños. The field trials were replicated over 2
153 years during the 2013 and 2014 wet seasons (WS) and the 2014 and 2015 dry seasons (DS). Generally, in
154 the Philippines, the monsoon wet season has low solar radiation and high relative humidity and pest and
155 disease pressure. During the dry season, temperature, evaporative demand, and solar radiation are high
156 and relative humidity and pest disease pressures are low.

157 **Trial design and data collection for Study 1**

158 Field trials were a Randomized Complete Block Design (RCBD) with four replications. Each plot size was
159 10.8 m^2 (5.4m x 2.0 m) with 10 rows (20 cm x 20-cm spacing with two or three plants $hill^{-1}$). Plot sizes were
160 as recommended by IRRI statisticians and used in IRRI trials over the years.
161 Trial data were collected and collated for analysis at appropriate stages following IRRI's standard
162 evaluation system (SES; IRRI, 2014). Data collected included flowering time (FLW), plant height (PH), and
163 number of productive tillers (TN); maturity was calculated by adding 30 days to the 50% flowering date.
164 Grain yield was determined by harvesting 25 hills per row from the six inner rows (harvest area was 6.0
165 m^2), adjusting to 14% moisture content, and calculating yield in kg/ ha^{-1}. Yield day^{-1} was calculated by
166 dividing grain yield by the number of days to maturity.

167 **Field trials and environments for Study 2**

168 These "Era" trials represented 2 years 3 seasons during 2016 wet season and 2017 wet season and 2017
169 dry season at IRRI Los Baños, Philippines. Seeding and transplant were done in accordance with the

appropriate seeding and transplanting practices used for the IRRI MET trials. Manual harvesting was conducted; border rows were not harvested. Data were collected on any missing hills and were accounted for in the analysis.

Simultaneous with the "Era" trials conducted in a single location at Los Baños, Multi Environment Trials (MET) were also conducted in 2016 and 2017 wet and dry seasons in 7 locations across Philippines in Munoz, Midsayap, Musuan, Augusan, Isabella Ubay and Los Baños.

Trial design and data collection for Study 2

For both "Era" trials and Multi Environment Trials (MET) trials, the trial plot design was Alpha Lattice except for MET level 2 2017 wet season trials which was Partially Balanced Incomplete Block design. Individual plot size was uniformly 5.4 meters x 2 meters with 26 hills for length and 10 hills at width of each plot. Border rows were not harvested to minimize border effects. The data was collected from "Era" trials varieties from one wet season each in 2016 and 2017, and one dry season in 2017. Data was also collected for one dry season in 2017 and two wet seasons in 2016 and 2017 from MET1 and MET 2 level trials conducted in all the Philippines locations including in Los Baños location

Data analyses

Only yield and maturity data were considered for analyses in the two studies. Estimations of genetic gain and analyses are detailed below. Pest and disease and environmental data as co-variates were not considered in these analyses. LS Means for Study 1 are presented in Supplementary Table 2. Trial heritability estimates for Study 1 are in Supplementary Table 3. LS Means for Study 2 are in Supplementary Table 4. Trial heritability estimates for Study 2 are in Supplementary Table 5. Details of methods used for the data analyses are described below. Pedigrees of the varieties were not used for phenotypic data analyses.

Relationship among varieties

Kinship matrices account for relationships among individuals and the higher the value, the closer the relationship between the varieties or lines, in general. Kinship matrices for varieties in the two studies were done using the pedigrees recorded for the entries. Kinship among the rice varieties/lines was estimated in both studies to understand if the relationships among varieties could contribute either positively or negatively to the estimated genetic gain. Very close relationships among varieties could narrow the genetic pool and might adversely contribute to the estimated genetic gain.

Statistical analyses

Study 1

Phenotypic data for grain yield were analyzed separately by season (wet and dry) using the mixed model:

$$y_{ijklm} = \mu + g_i + s_j + gs_{ij} + b_k + \varepsilon_{ijk} \quad (1)$$

where $y_{ijk}$is the grain yield measurement for the *i*th genotype in the *j*th year and *k*th complete block; μ is the overall mean; $g_i$is the fixed effect of genotype; s_j is the random effect of the specific season; $gs_{ij}$is the random effect of the interaction between the genotype and the specific season; b_k is the random effect of complete block, also referred to as replicate; and $\varepsilon_{ijklm}$is the residual error.

All random effects were assumed independently and identically distributed (i.i.d). To correct for days to maturity, days to maturity collected on the same plot as the grain yield data was included in model 1.

From model 1, the least-square means and standard errors for grain yield and grain yield corrected for days to maturity were estimated per variety, per season. To obtain a combined mean across seasons, these least-square means were used as the response variable in the linear regression model:

$$y_{ij} = \mu + g_i + w_j + \varepsilon_{ij} \quad (2)$$

where $y_{ij}$is the mean yield for genotype *i* and season *j*, $g_i$is the effect of genotype, $w_j$is the effect of the weather season, and $\varepsilon_{ij}$is the residual error assumed i.i.d.

From model 2, the least-square mean for grain yield and grain yield corrected for days to maturity across all seasons were estimated.

To assess genetic trends in varieties, means data were used as the response variable in the linear regression model

$$y_i = \mu + \alpha d_i + \varepsilon_i \quad (3)$$

where $y_i$is the mean yield of variety *i*; d_i is the continuous year date when the variety was released minus 1966, which was the earliest variety release year in the dataset; α is the fixed regression coefficient for the genetic trend in yield; and ε_{ijk} is the residual error with $\varepsilon_i \sim N\left(0, R{\sigma_\varepsilon}^2\right)$ where *R* is a matrix with the diagonal equal to the squared standard error of the least-square means.

Model 3 was fitted using the combined means across seasonal data, using wet season data, and using dry season data separately. Model 3 was fitted for both grain yield and grain yield corrected for maturity.

Study 2

Phenotypic data used for this study originated from both the MET and "Era" trials. For each trial containing varieties sampled for this study that follows the alpha lattice design, phenotypic data for yield and days to maturity were analyzed using the mixed model:

$$y_{ijk} = \mu + g_i + r_j + b_{k(j)} + \varepsilon_{ijk} \quad (4)$$

where $y_{ijk}$is the phenotypic measurement for the *i*th genotype in the *j*th replicate and *k*th block; μ is the trial mean; g_i is the effect of genotype; $r_j$is the random effect of replicate; $b_{k(j)}$ is the random effect of block nested within *j*th replicate; and ε_{ijk} is the residual error. All random terms were assumed i.i.d. While for MET data that uses the partially balanced incomplete block design, phenotypic data for yield and days to maturity were analyzed using the mixed model:

$$y_{ij} = \mu + g_i + b_j + \varepsilon_{ij} \quad (5)$$

where y_{ij} is the phenotypic measurement for the *i*th genotype in the *j*th block; μ is the trial mean; g_i is the effect of genotype; b_j is the random effect of block; and ε_{ij} is the residual error. All random terms were assumed i.i.d. From models 4 and 5, least-square means and standard errors were computed for yield and days to maturity per trial.

The trial-specific least-square mean yields for each variety sampled for Study 2 were used as the response variable in the mixed model:

$$y_{ijk} = \mu + g_i + s_j + t_k + gs_{ij} + \varepsilon_{ijk} \quad (6)$$

where $y_{ijk}$is the least square mean for the *i*th genotype in the *j*th season and *k*th trial; μ is the mean; g_i is the effect of genotype; s_j is the effect of the specific growing season; t_k is the random effect of trial assumed i.i.d; $gs_{i,j}$ is random effect of the interaction between genotype *i* and season *j* assumed i.i.d.; and $\varepsilon_{ijk} \sim N\left(0, R{\sigma_\varepsilon}^2\right)$ where *R* is a matrix with the diagonal equal to the squared standard error of the least-square means. To correct for maturity, a co-variate for days to maturity was included in model 6. Model 6 was fitted using both wet and dry seasons data, using wet season data alone, and using dry season data alone. Least-square means and standard errors were then computed for grain yield and grain yield corrected for maturity for each variety across seasons and in dry and wet seasons separately.

Genetic trends in varieties were assessed using model 3 as in Study 1.

Software used

Analyses for the two studies were carried out in the R statistical programming language and environment (R Development Core Team, 2016), using the packages *lme4* and *lsmeans* (Lenth, 2016). Kinship between

varieties included in both studies were estimated based on pedigree using the R package *nadiv* (Wolak, 2012).

3. RESULTS

Results Summary

Genetic Trend Model Estimate of variety mean yields in Los Baños, Philippines has been presented in Table 3 There was considerable variation for *per se* yield among varieties in both Study 1 (Supplementary LS Means Tables 2 and Supplementary trial heritabilities Table 3 respectively) and Study 2 (Supplementary LS Means Tables 4 and Supplementary trial heritabilities Table 5 respectively).

In Study 1, the highest level of genetic gain was in the wet season when data were not corrected for maturity. It was 0.70% with a yield increase of about 23 kg $ha^{-1}year^{-1}$. In Study 2, the highest level of genetic gain was 0.74% with a yield increase of about 19 kg ha^{-1} $year^{-1}$ during the wet season when the data were corrected for maturity. There was a difference of about 4 kg ha^{-1} $year^{-1}$ for the highest values of genetic gain between the studies (Table 3). These were followed by genetic gain of 0.62% (20 kg ha^{-1} $year^{-1}$) when corrected for maturity during the wet season in Study 1 and a genetic gain of 0.66% (17 kg ha^{-1} $year^{-1}$) when not corrected for maturity in the wet season in Study 2.

TABLE 3 Genetic Trend Model Estimate of variety mean yields for IRRI varieties in Studies 1 and 2

Study	Season	Controlled for maturity	Baseline yield± standard error	Increase of yield in kg ha^{-1} $year^{-1}$	Yield gain per year	Model R Squared
1	Dry	No	6525.73 ± 214.82 (3.3e-30)	17.32 ± 7.13 (2.0e-02)	0.27%	0.12
1	Wet	No	3305.85 ± 166.73 (6.1e-23)	23.13 ± 5.54 (1.5e-04)	0.70%	0.29
1	Wet and dry	No	4915.87 ± 140.98 (1.2e-32)	20.23 ± 4.68 (9.4e-05)	0.41%	0.31
1	Dry	Yes	6541.79 ± 221.32 (9.8e-30)	16.49 ± 7.3 (2.9e-02)	0.25%	0.11

1	Wet	Yes	3376.64 ± 172.7 (1.0e-22)	20.81 ± 5.63 (6.3e-04)	0.62%	0.25
1	Wet and dry	Yes	4958.17 ± 147.32 (5.2e-32)	18.51 ± 4.89 (4.8e-04)	0.37%	0.25
2	Dry	No	3802.86 ± 327.72 (2.5e-10)	13.02 ± 8.98 (1.6e-01)	0.34%	0.10
2	Wet	No	2729.77 ± 158.09 (1.7e-13)	17.92 ± 4.28 (4.6e-04)	0.66%	0.47
2	Wet and dry	No	3171.47 ± 120.82 (5.7e-17)	17.35 ± 3.32 (4.2e-05)	0.55%	0.58
2	Dry	Yes	3866.37 ± 385.18 (3.0e-09)	14.79 ± 10.59 (1.8e-01)	0.38%	0.09
2	Wet	Yes	2624.13 ± 151.5 (1.7e-13)	19.4 ± 4.09 (1.2e-04)	0.74%	0.53
2	Wet and dry	Yes	3164.63 ± 153.99 (6.4e-15)	19.35 ± 4.26 (2.0e-04)	0.61%	0.51

Notes: 1. The values in the column containing baseline yield and standard error are followed by p values in parentheses.
Note 2. Results from two independently conducted studies are shown for wet and dry seasons combined, dry season alone, and wet season alone.

Table 3 shows an increase of yield in kg ha^{-1} $year^{-1}$ and yield gain in $year^{-1}$ ha^{-1} when controlled for maturity or not controlled for maturity under the dry and wet seasons. Genetic trends in IRRI variety yields in Los Baños, Philippines over a 50-year period, not controlled for maturity and controlled for maturity are shown in Figures 1 and 2, respectively.

There were some differences for *per se* yield between the two studies. Study 1, in general, seems to have a higher yield during 2013–2014 compared to Study 2 in 2016–2017 (Supplementary LS Means Tables 2 and 3, respectively). In practical terms, yield increases in kg ha^{-1} $year^{-1}$ were not very different between the two studies despite differences in the number of entries and locations.

During the when the data were not corrected for maturity in Study 1, yield increase was 17.32 kg ha^{-1} $year^{-1}$ with a standard deviation of 7.13 kg ha^{-1} and a genetic gain of 0.27% per year. Likewise, in Study 2, the yield increase was 13.02 kg ha^{-1} $year^{-1}$ with a standard deviation of 8.98 kg ha^{-1} and a genetic gain of 0.34% per year.

296 During the wet season when the data were not corrected for maturity in Study 1, the yield increase was
297 23.13 ha^{-1} $year^{-1}$± 5.54 kg ha^{-1} with a percent genetic gain of 0.70% per year. However, for the when data
298 were not corrected for maturity in Study 2, the yield increase was 17.92 ha^{-1} $year^{-1}$± 4.28 kg ha^{-1} with a
299 genetic gain of 0.66% per year. The yield increases in Studies 1 and 2 show very similar values and percent
300 genetic gain.
301 In Study 1 when data were not corrected for maturity and wet and dry season data were combined, the
302 yield increase was 20.23 ha^{-1} $year^{-1}$± 4.68 kg ha^{-1} with a genetic gain of 0.41% per year. However, in Study
303 2, the yield increase was 17.35 ha^{-1} $year^{-1}$± 3.32 kg ha^{-1} with a genetic gain of 0.55% per year. The yield
304 increases in both studies show very similar values and the percent genetic gains were also similar when
305 wet and dry seasons' data were combined.
306 In Study 1 during the when data were corrected for maturity, the yield increase was 16.49 ha^{-1} $year^{-1}$± 7.3
307 kg ha^{-1} with an annual genetic gain of 0.25%, which was slightly lower than when the data were not
308 corrected for maturity. In Study 2 during when data were corrected for maturity, the yield increase was
309 14.79 ha^{-1} $year^{-1}$± 10.59 kg ha^{-1} with a genetic gain of 0.38%. This was very similar to when the data were
310 not corrected for maturity. In both studies, correcting for maturity did not seem to make much difference
311 in the yield increases or percentage of genetic gain per year during the dry seasons.
312 In Study 1 during the wet season, when the data were corrected for maturity, the yield increases was
313 20.81 ha^{-1} $year^{-1}$± 5.63 kg ha^{-1} with a genetic gain of 0.62%. These values were slightly lower compared to
314 when the data were not corrected for maturity. In Study 2 during the wet season, when data were
315 corrected for maturity, the yield increase was 19.4 ha^{-1} $year^{-1}$± 4.09 kg ha^{-1} with a genetic gain of 0.74%.
316 These values were similar to when the data were not corrected for maturity. Correcting for maturity once
317 again did not seem to make much difference in either the yield increases or percentage of genetic gain.
318 In Study 1 when data were corrected for maturity and wet and dry season data were combined, the yield
319 increase per year per hectare was 18.51 ha^{-1} $year^{-1}$± 4.89 kg ha^{-1} with a genetic gain of 0.37% per year.

However, in Study 2 when wet and dry seasons data were combined and the data were corrected for maturity, the yield increase was 19.35 ha^{-1} $year^{-1}$± 4.26kg ha^{-1} with a genetic gain of 0.61%percent per year. Correcting for maturity did not make much difference for genetic gain.

Figure 1. Genetic trends in IRRI variety yields in the Philippines, when not controlled for maturity.

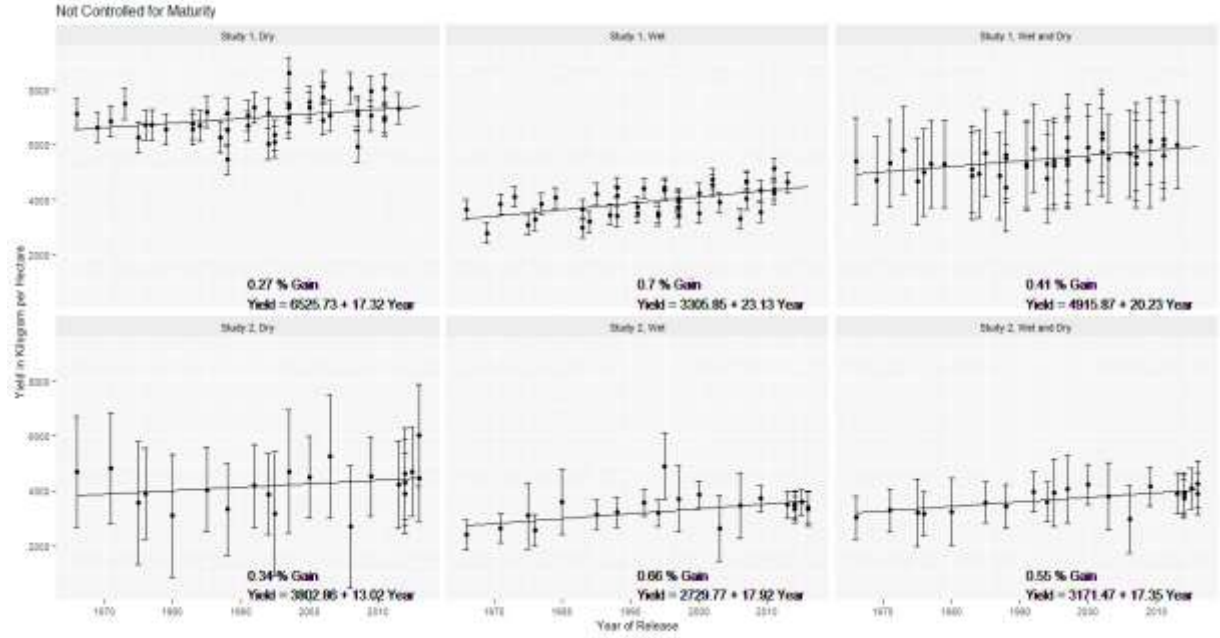
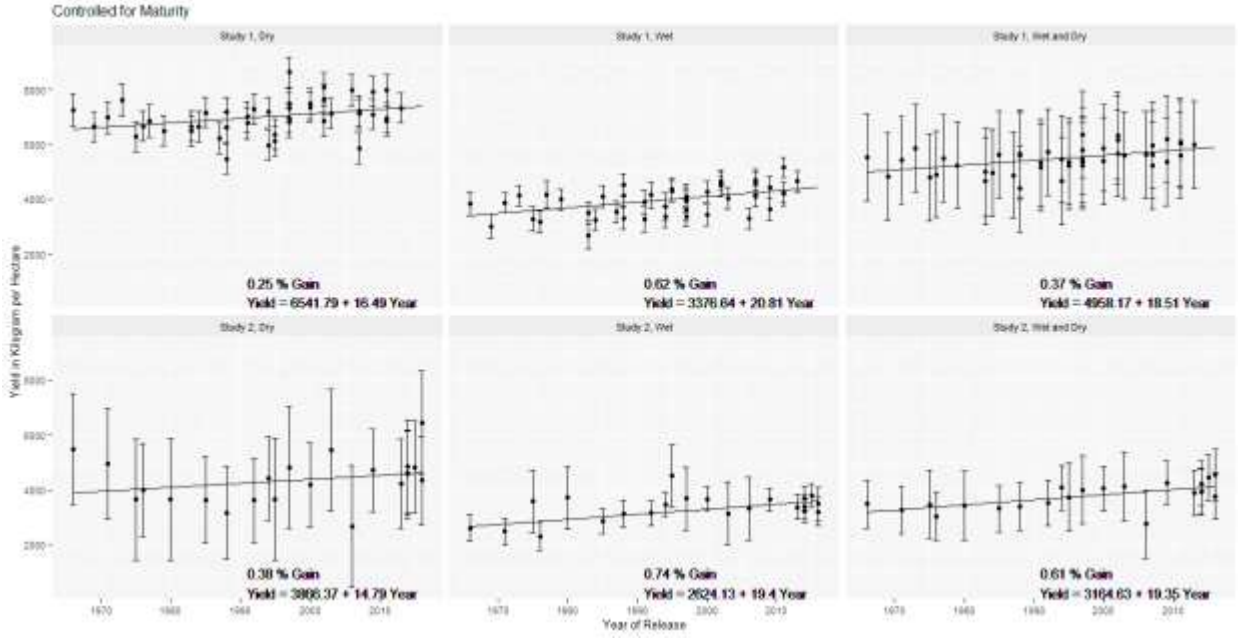


Figure 2. Genetic trends in IRRI variety yields in the Philippines when controlled for maturity



The Figures 1 and 2 show that there is an increasing genetic gain trend among IRRI varieties over a 50 year period. The base line grain yield, as indicated by the regression constant, is higher for Study 1 compared for Study 2, in dry, wet and combined season. In Study 1, only data from one location were used, while in Study 2, data from both the "Era" trials and the MET with seven locations were used.

For Study 1, increase in yield as indicated by the slope of the regression lines are higher when grain yield was not corrected for days to maturity while in Study 2 it was observed that the increase in yield was higher when yield was corrected for days to maturity.

Likewise, percentages of genetic gain per year in Study 1 are higher when grain yield was not corrected for days to maturity, while in Study 2, it was observed that percentage of genetic gain was higher when grain yield was corrected for days to maturity.

In both studies, it was observed that increase in yield and percentage of genetic gain per year is higher in wet season. This is true for grain yield both controlled and not controlled for days to maturity.

In Study 1, grain yield corrected and not corrected for days to maturity did not make a significant difference in the analyzed data for base line yield, yield increase, and percentage of genetic gain per year.

In Study 2, grain yield corrected and not corrected for days to maturity did make a significant difference in the analyzed data for yield increase and percentage of genetic gain, per year but not for base line yield.

Each point in Figures 1 and 2 corresponds to the mean yield of a variety measured in kg ha^{-1} at the Zeigler Experiment Station in IRRI during dry and wet seasons combined (right), during the dry season alone (left), and during the wet season alone (middle) in Study 1 (top) and Study 2 (bottom). The dotted lines show the linear regression between variety mean yield and year of variety release. At the lower right corner of each panel, the percent gain in annual yield and the linear regression equation are displayed.

Variety relationship

Kinship matrices, which explain the relationship between and among varieties, were calculated to understand if close relationship if any, between and among varieties could be a factor in contributing either positively or negatively to the estimated genetic gain. Kinship heat maps of varieties used in the studies were generated (Figures 3 and 4 for Studies 1 and 2, respectively) to display the relationships visually. Kinship matrices for varieties in the two studies were done using pedigrees recorded for the entries. The relationships among the varieties used were assessed and are shown in the kinship matrices tables for Study 1 (Supplementary Table 6) and Study 2 (Supplementary Table 7). Coefficients of parentage based on pedigrees for Studies 1 and 2 are in Supplementary Tables 8 and 9, respectively. Coefficient of parents is a measure of germplasm diversity used in these studies.

In Study 1, the kinship matrix for popular/mega varieties showed that only IR36 seemed to have higher levels of relationship values (>0.4) with 12 out of 44 varieties (27%). IR 64 had higher levels of relationship (>0.4) although there were only with three other varieties. IR72 had higher levels of relationship (>0.4) with 7 of 44 varieties used (Supplementary Table 6).

In Study 2, the kinship matrix showed that only IR64 seemed to have higher relationships (>0.4) with 6 of 22 varieties. IR36 and IR72 had only three and two varieties, respectively, with higher levels of relationship (>0.4) (Supplementary Table 7). To some extent, this explains that IRRI varieties released so far do not necessarily come from a very narrow genetic base pool of lines

377 **Figure 3. Kinship heat map of varieties used in Study 1**

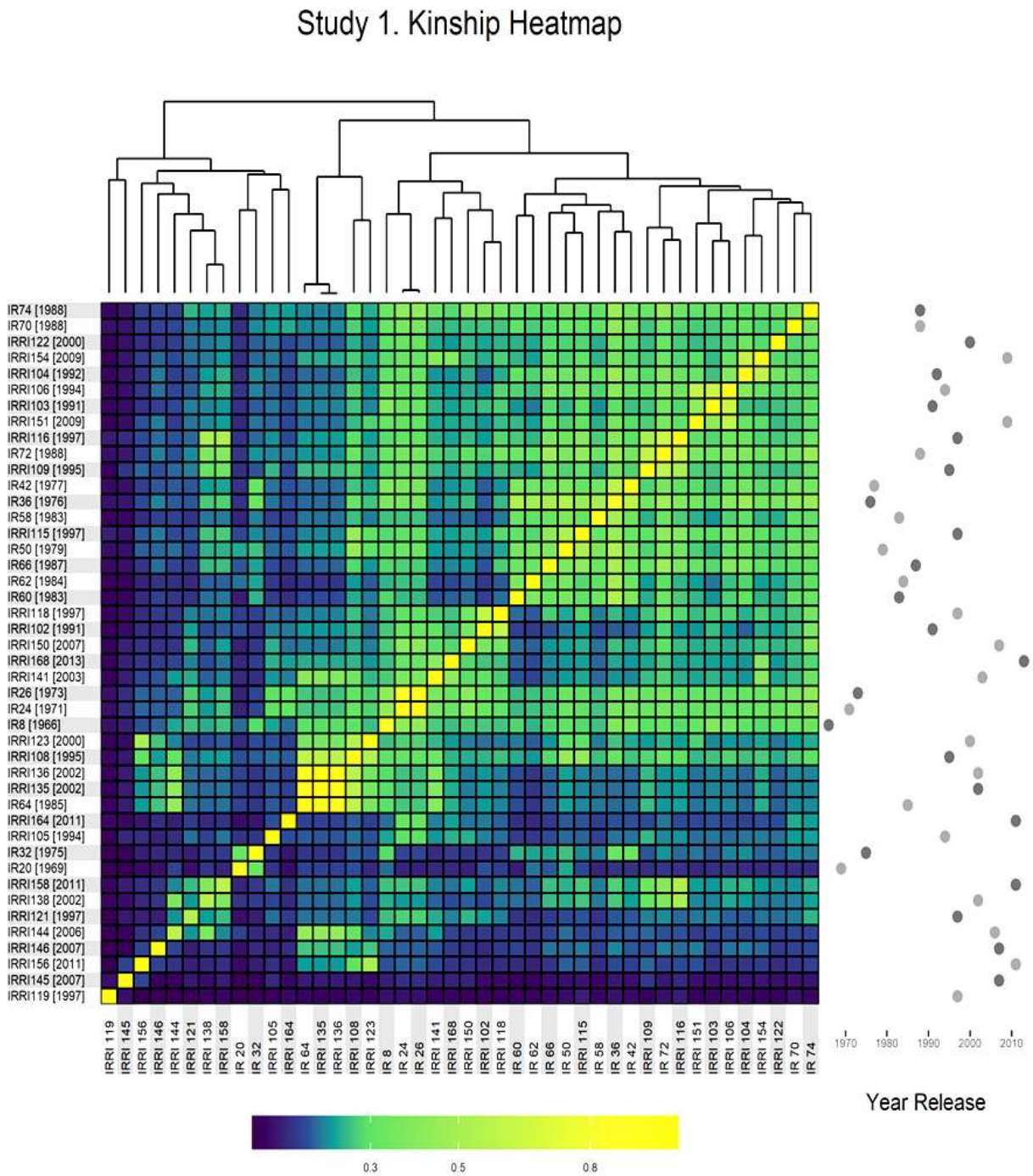


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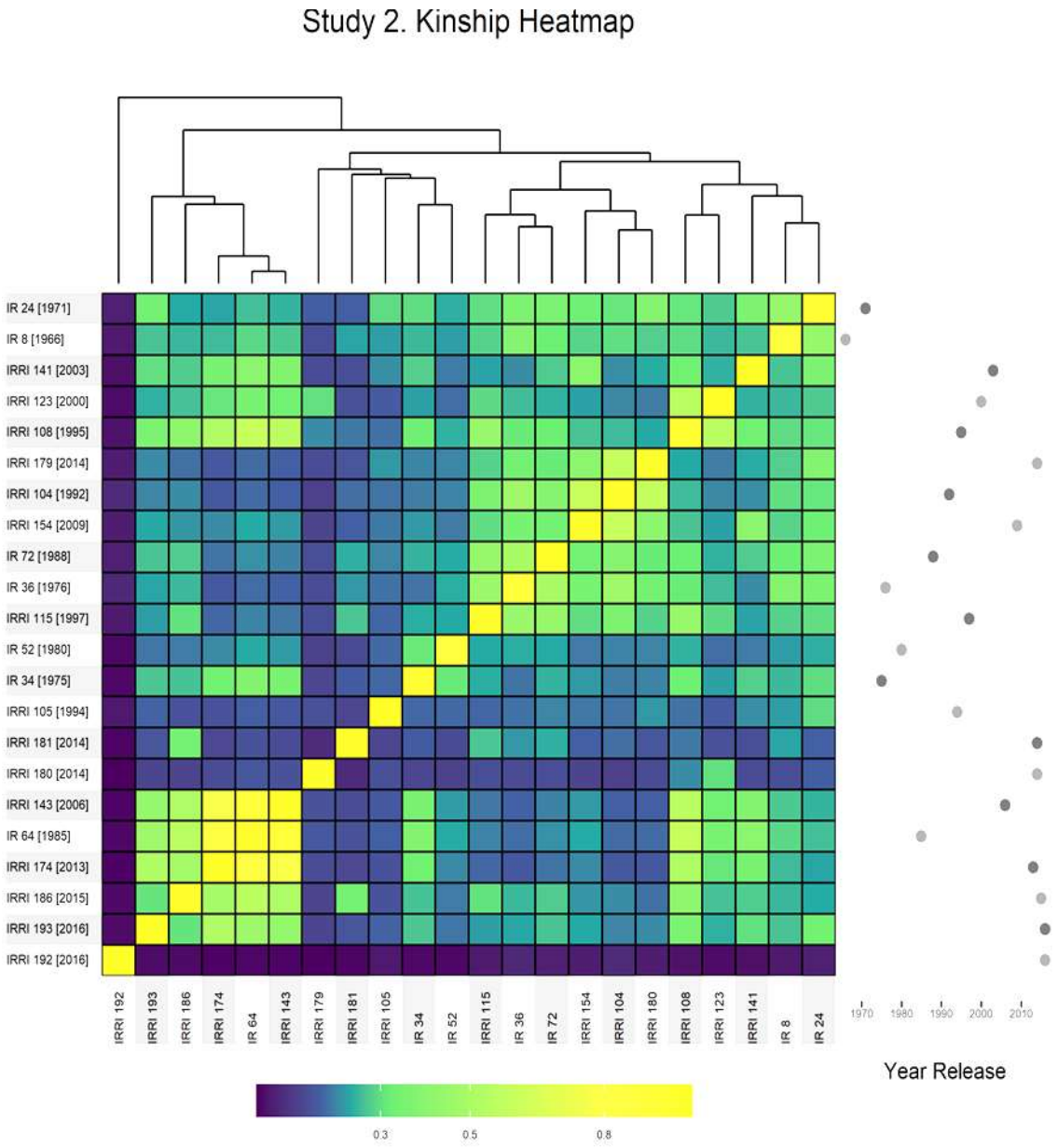
Figure 4. Kinship heat map of varieties used in Study 2



4. DISCUSSIONS and CONCLUSIONS

The data from the two studies (Table 3) clearly show similar levels of genetic trend among irrigated varieties released at IRRI from 1966 to 2016, suggesting that they achieved greater than a zero rate of genetic gain. In Study 1, the highest level of genetic gain per year was 0.70% in the wet season when not corrected for maturity. In Study 2, the highest level of genetic gain was 0.74% in the wet season when corrected for maturity. Yield increase was 23 kg ha^{-1} $year^{-1}$ in Study 1 and 19 kg ha^{-1} $year^{-1}$ in Study 2. The lowest level of genetic gain in Study 1 was 0.25% in the dry season when data were corrected for maturity. In Study 2, the lowest level of genetic gain was 0.34% in the dry season when data were not corrected for maturity.

Comparison of rice with other staple crops, such as wheat, is of interest. The genetic gain from both studies in the wet season was very similar to the 0.7% $year^{-1}$ gain in advanced spring bread wheat (*Triticum aestivum* L.) lines evaluated in Mexico by CIMMYT from 1977 to 2008 (Lopes et al., 2012) and from 1995 to 2009 with yield gains of 27 kg ha^{-1} $year^{-1}$ at 0.65% genetic gain (Sharma et al., 2012). This rate was also similar to yield increases in bread wheat (25 kg ha^{-1} $year^{-1}$) in Australia measured from 1958 to 2007 (Sadras & Lawson, 2011) and yield increases of 35.1 kg ha^{-1} $year^{-1}$ or 0.88% $year^{-1}$ in Spain from 1930 to 2000 (Sanchez-Garcia et al., 2013). This was also comparable to yield increases in barley grown in the U.K with a genetic gain of 0.39% between 1880 and 1980 (Riggs et al., 1981).

Graybosch & Peterson (2010) reported a genetic gain level of 1.1% in winter wheat on the Great Plains of North America from 1959 to 2008, which was similar to that reported by Peng et al. (2000). From 50 years of wheat breeding in Brazil, Rodrigues et al. (2007) assessed that the genetic gain for grain yield was 44.9 kg ha^{-1} $year^{-1}$. However, in studies conducted by Brennan et al. (2004) to assess annual rate of genetic gain

412 in the wheat breeding program in Wagga Wagga, Australia, they assessed that the annual rate of gain was
413 3.19% while the annual rates of gain in northeastern and southeastern Australia were 2.75 and 3.92%,
414 respectively. In their studies, Brennan & Bialowas (2001) determined that 54% of the gain was due to
415 varieties and 46% to other factors.
416 In both studies, correction for maturity did not appear to make much difference for the analyzed data for
417 yield increases and percentages of annual genetic gain. Additional data from METs (Supplementary Table
418 1), while they added to the data points for increased robustness, they did not make much difference in
419 the genetic trend of one study over the other. Higher *per se* yield in both studies during the dry seasons
420 did not make any difference in the genetic gains seen in these varieties under both trials and years.
421 However, the estimated genetic gains in both studies were lower than the genetic gain of 1% estimated
422 for irrigated rice with yield increases ranging from 75 to 81 kg ha^{-1} $year^{-1}$ in trials conducted by Peng et al.
423 (2000).

424 There are key differences in the genetic gain study conducted in 1996 by the Peng *et al* (2000) and the
425 two studies as described below.
426 Twice the number of varieties were used in Study 1 with 12 entries common in the two studies. Both
427 studies included all the major varieties released up to the years when they were conducted. However, the
428 later-released entries included in Study 2 did not seem to make any difference in genetic gains. Peng et
429 al. (2000) used nine IRRI-bred varieties and two breeding lines and one external breeding line spanning
430 29 years totaling up to 12 entries ((1966–1995). As previously mentioned, Study 1 included 37 IRRI-
431 developed varieties, two rainfed varieties, and five hybrid varieties spanning 47 years (1966–2013)
432 totaling up to 44 entries. There were eight varieties common to between Study 1 and Peng et al. (2000)
433 study. Study 2 had 21 irrigated varieties and one rainfed variety in the “Era” studies spanning 50 years
434 (1966–2016). There were four entries were common between the Study 2 and Peng et al. (2000) study.

435 Interestingly, the kinship matrices (Figures 3 and 4 and Supplementary Tables 6 and 7) displayed
436 relatedness among the varieties based on their pedigrees. It was important to understand if the lines
437 chosen were highly related to each other and/or to the mega-varieties, such as IR36, IR64, and IR72, based
438 on the pedigree, which may have contributed negatively or positively to the genetic gain observed or if
439 the genetic base was too narrow. Among the 44 varieties in Study 1, only IR36 showed similarity to 12
440 varieties with a kinship value greater than 0.4. In Study 2, among the 22 varieties, only IR36 was similar to
441 three varieties with a value greater than or equal to 0.4. In Study 1, IR64 was only similar to three varieties
442 with a kinship value of 0.4. In Study 2, IR64 was similar to six varieties with kinship values based on
443 pedigrees greater than 0.4. The Peng et al. (2000) study also used IR36 and, although the kinship matrix
444 values could not be developed directly as there are no data on the exact seedlot ID for that year in the
445 IRRI databases. However, based on Study 1 data, only three varieties (IR50, IR60, and IR 72) seem to have
446 a higher level of similarity to IR36 with values greater than 0.4 in the Peng et al. (2000) study. Coefficient
447 of parents based on the pedigrees of the germplasm used in the studies also showed diverse germplasm.
448 This analysis showed that the varieties used in the two studies did not come from a very narrow gene
449 pool. Perhaps for future genetic gain assessment studies, researchers should explore the critical minimum
450 number of varieties that should be included.
451 In general*, per se* yields were higher in both dry and wet seasons for Study 1, compared to Study 2 where
452 yields were lower in general. In Study 1 there was data only from one location. In Study 2, in which data
453 from both "Era" and MET trials in the Philippines were utilized, and due to environmental differences,
454 average yield would perhaps be lower than the single-site data in Study 1. In Peng et al. (2000) study,
455 yields presented in that paper were overall higher than both studies in this paper. These *per se* yield
456 differences perhaps could be attributed to year-to year variation in yield during conduct of the studies. In
457 the future, it would be worth recording weather data at all locations and use as a co-variate to assess
458 year-to-year variation impact on estimating genetic gain, which perhaps would also depend on stability of

yield across the years and across environments—especially under climate change scenarios. This will also help to assess the impact of climate change on varietal performance and to develop strategies in breeding programs to mitigate effects of climate change.

Interestingly, in both studies, the highest values for annual genetic gain were seen in the wet season rather than the dry season, although *per se* yield in the dry season, as expected, was higher than in the wet seasons. Annual genetic gains were similar in the dry seasons in both studies irrespective of maturity correction. Evaluation during the wet season was not performed in the "Era" experiment conducted in the Peng et al. (2000) although the objective stated in that paper was to determine the yield trend of rice cultivars/lines developed since 1966. In the two studies presented here, evaluations were conducted both in the dry and wet seasons to understand the genetic gain of varieties from a production standpoint as, in Southeast Asia, more rice is grown during the wet seasons.

Higher levels of genetic gain for yield seen in the wet season could also be due to enhanced differences among some varieties with improved pest and disease tolerances providing better yields compared to varieties that are not so tolerant of pests and diseases. Therefore, in newly developed and released varieties, genetic gain for yield must be measured in both seasons to demonstrate the yield potential of a variety predominantly during the dry season and to assess genetic gain for yield when varieties have to withstand higher pest and disease pressures during wet seasonal conditions. This will provide information on average performance of a variety under different seasonal conditions that are more relevant to practical variety release purposes. In the future, it would be worth utilizing pest and diseases data as a covariates to assess year-to-year variation impact on estimating genetic gain across the years and across environments, especially under climate change scenarios. Peng et al. (2010) also emphasized maintenance breeding.

It should be noted that "Era" trial method has its own limitations. While Study 1 included a larger set of varieties evaluated in one location only, due resource limitations, Study 2 included fewer varieties but

with data from more locations albeit in the Philippines only. Maturity was one covariate used in this study however, correcting for maturities did not seem to make significant differences either increase in yield per tons per hectare per year or percent genetic gain. Ideally, such studies need to be conducted across environments and across years with commonality of some varieties used between years to increase connectedness among varieties between the years. For all practical purposes, conducting such "Era" trials across key environments in numerous rice-producing countries would be resource-intensive. Rutkoski (2019), in her studies compared various methods for assessing genetic gain, stated that utilization of estimated breeding values (EBVs) by including long- term check varieties as the method which gave second high level of precision and lowest level of error among all the methods she compared. However, she noted that, for the EBV method to work well, EBV estimation required accurate records of pedigrees from the time that the breeding program began to estimate additive relationships among lines and having good connectivity between years. Rutkoski (2019) also concluded that, when a breeding program does not meet the requisites for EBV estimations, the "Era" method can be used instead because data are not needed from historical datasets. The EBV experiments can be designed to ensure achieving precision, efficiency, correlation and reducing error although they require the availability of varieties released over the years and resources to conduct new trials. She also recommended that, to improve efficiency, several varieties released annually could be used instead of just one variety. In Studies 1 and 2, an effort was made to source more than one variety per year, although for the older varieties, it was difficult to find authentic sources of seed for older varieties in addition to requiring larger and more resource-intensive trials.

One limitation in both the Peng et al. (2000) study and Studies 1 and 2 was their preliminary nature since they did not have large sets of historical data like those included in other crops that have utilized multiple locations spanning several decades. Ideally, yield trials should always be conducted in multiple environments and years and have genotype x location (GxL) interactions. Also, annual variations need to

be accounted for including the variety's stability of performance. The Peng et al. (2000) study conducted trials in two locations—IRRI, Los Baños and PhilRice, Muñoz). The data were pooled from the trials conducted in Los Baños and Munoz. In Study 1, the "Era" trials were only conducted at IRRI, Los Baños since trials could not be conducted at multiple locations due to insufficient resources. In Study 2, "Era" trials were conducted only in IRRI, Los Baños, but additional data from other MET locations (Supplementary Table 1) in the Philippines for varieties common to "Era" and MET trials were included in the analyses to increase the robustness of analyses. It should also be noted that the genotype x year (GxY) interaction is often as large or larger than the genotype x location (GxL) within a reasonably delineated target population of environments (TPEs) (Cooper et al., 1999; Atlin et al*.,* 2000).

Conducting trials across TPEs across years for assessment of genetic gain of varieties, although necessary, is both resource and labor intensive, especially where research funds are limited. To overcome such resource limitations for testing advanced lines under different environments in different rice producing countries and thereby develop data on agronomic adaptation, pest and disease tolerances and selections for locally desired traits, IRRI developed a network system named International Network for Genetic Evaluation of Rice (INGER) for sharing and evaluating advanced lines in among rice-producing countries. INGER has enabled national country breeders to further select the best performers for agronomic adaptation and yield performance over several years and under the national systems' varietal release protocols. This network also allows national country partners to utilize best performers and develop crosses for selections in the local environments. Data from INGER trials could be used for estimations of genetic gains going forward with larger historical datasets to overcome limitations of conducting new large trials spanning multi locations. It should be noted that INGER network system has led to over 1,200 varieties being released and that popular mega varieties, such as IR36, IR64, and IR72 (Mackill & Khush, 2018; Khush, 1981) have also been released to farmers in the partner countries and high performers among these would also provide connectedness for the data. Evenson and Gollin (1997) conducted

economic analyses and calculated that the average value of the varieties released through INGER to be 2.5 million USD variety^{-1} year^{-1} (in 1997 dollars). In their analysis, Brennan & Malabayabas (2011) reported that such network-based sharing contributed to yield improvement in Southeast Asian countries. This type of sharing and testing of advanced lines has significantly impacted on yield improvements in rice production environments as shown by these economic estimates. Improved yields would also accomplish genetic gain of varieties in the countries and for the CGIAR and IRRI, alignment to food security goals as part of the mission. Sharing germplasm to a wide array of countries with and without CGIAR/IRRI rice breeding activities, also increases diversity of the improved lines in national breeding programs thereby increasing the elite pools of germplasm in partner countries and ensures that no rice-producing country is left behind (Khush & Virk, 2005).

A key limitation of such a system of sharing advanced breeding lines or pre-variety lines is that the testing and selections of early-stage IRRI breeding lines would not be done in the countries, thereby missing out on selections for some key traits during early stages of breeding. Therefore, it is desirable that breeding programs develop early-stage breeding regional networks at least in some key countries and select for desired traits suited to rice production areas, achieve a high probability of achieving genetic gain on an annual basis. However, development of an early-stage breeding regional network would require cooperation from all partners in the National Agricultural Research and Extension System (NARES) countries and would be resource-intensive. Several NARES partner countries also have their own national rice breeding programs where IRRI-shared germplasm is utilized both for direct variety releases and crosses therefore, a system of co-operative-early-stage regional breeding by sharing early stage germplasm at least in some regional targeted countries would be desirable to support goals of higher productivity through genetic gain. These early-stage selections from the regional breeding networks could flow into advanced line/pre-variety networks such as INGER and expand the testing in a wider number of

554 countries and provide data for genetic gain assessments using historical sets of data from all INGER
555 partners and measure the effectiveness of breeding.
556 While different methods can be adopted to estimate genetic gain, some key factors that contribute to
557 genetic gain need to be noted. A key factor in yield improvement in crops such as maize has been the
558 coupling of improved management practices with variety improvement. Duvick (2005b), in an assessment
559 of genetic gain in hybrid maize, found that 50–60% of the on-farm yield gains were due to genetic
560 improvement of varieties while about 40–50% were due to changes in management responsible for the
561 improvements in agronomic practices. In rice grown in the United States from 1981 to 2011, yields
562 increased 47% (2.5 t ha^{-1}) at an average of 86 kg ha^{-1} annually. These yield gains have occurred due to
563 improved traits such as a semidwarf habit, disease resistance, specific cultivars, herbicide tolerance, and
564 F_1 hybrids (Moldenhauer et al., 2013). In Australian wheat, Brennan & Bialowas (2001) found that, on
565 average, 54% of the genetic gain was due to yield improvement alone, excluding external factors other
566 than varieties
567 While in countries such as the U.S., Australia, and Brazil, wheat or maize mechanized cropping
568 establishment and harvest systems have contributed to 40% of the yield improvement as mentioned
569 above, in Southeast Asia, application of fertilizers, such as nitrogen for rice crop establishment, and
570 harvesting generally, are not mechanized at the farmer level (Okasha & Hegazy 2020). Even among
571 breeding programs, mechanization is either minimal or lacking completely for crop establishment.
572 Evaluations of breeding lines and varieties under experimental plot trials established using variable,
573 manual crop establishment methods, manual methods of fertilizer applications and harvests conducted
574 under inconsistent moisture conditions could contribute to lower genetic gain in rice.
575 These studies, while recognizing that there has been genetic gain in IRRI's irrigated rice breeding program,
576 have clearly demonstrated that there is a need for further improvement of genetic gain for yield in rice
577 because OECD/FAO (2019) has estimated a need for a 40 million ton increase in rice required by 2028. A

higher level of genetic gain for yield is critical along with traits for mitigating effects of climate change (e.g., flood and drought tolerances) and managing abiotic stress in soils. Studies have shown that, for every 1-degree Celsius increase in temperature, there is a yield reduction of up to 10% with a reduction in economic growth by 1.3% (Wassmann & Jagadish, 2014). Interestingly, the Peng study et al. (2000) recorded much higher yields in 1998 compared to Study 1 (2013–2014) and Study 2 (2016–2017). While there is also a case for improvements in agronomic practices without much need for additional inputs from farmers, there is an important need for breeding programs to develop breeding strategies with available resources to improve yield and other desired traits to increase realized genetic gains for yield and other consumer-desired traits.

A major difficulty for rice is that, unlike other crops such as maize and wheat, rice is consumed directly as a grain and so consumer and value chain stakeholder preferences and market demand must also have consideration beyond genetic gain for yield when selecting new varieties. In this regard, studies such as those by Laborte et al. (2015) would assist in assessment of consumer needs in rice producing countries. Therefore, while it is important to have genetic gain for yield in rice varieties, it is also important to select for a combination of multiple traits required for not only yield, but climate resilience and quality traits as well. This simultaneous trait selections would help in improving the performance of varieties on the farm, increasing adoption by farmers of the improved varieties, and ensuring marketability due to alignment with consumer desires.

The studies in this paper do not focus on recommending an ideal breeding method to increase yield genetic gain in rice as comparison was not done using varieties developed by different breeding methods. The varieties used in these studies were developed using different methods over a long period defined as an “Era”. Studies comparing different breeding method generated varieties would require using rice varieties in multi environments across multiple years in addition to being resource-intensive.

Utilization of available molecular tools for selection of diverse improved parents and development of a new generation of crosses will lead to a better certainty of the presence of desired genes and prediction of performance of those crosses. Implementation of single-seed decent methods, either in the field or in the glasshouse, will reduce costs of a breeding program while also improving the program's speed and agility. Heffner et al. (2010), in their studies comparing marker-assisted selections (MAS) and genomic selections (GS) in wheat and maize, indicated that, even at lower genomic estimated breeding values (GEBVs) for complex traits, the expected annual gain from genomic selections in maize was three times that from MAS and in winter wheat twice that from MAS therefore genomic selections can accelerate genetic gain due to shorter breeding cycles. Voss-Fels et al. (2019) in their paper on accelerating genetic gain using genomic selection stated that, genomic selection in crops offers a way to reduce breeding cycles, especially when combined with molecular tools, and rapid generation advancement. This is quite specific to crops and breeding programs and needs continued research. Apart from reduction in breeding cycles, plant breeding programs can fast-track the outputs of the varieties by utilizing methods such as selection index and utilize economic weights for selections of parents (Batista et al., 2018). Details of various aspects of developing a selection index for plant breeding have been described by Céron-Rojas & Crossa (2018).

For all practical purposes, studies such as 'Era" studies or analysis of historical data sets need to be conducted at regular intervals utilizing best practices to assess genetic gain of the new varieties using in multi-location trials under climate change scenarios in the major rice-producing environments. This will enable breeding programs to develop strategies for release of enriched varieties that are used by the farmers for better adoption and increased profitability. Assessments need to be done to estimate the required target population of environments for early breeding line selections for yield, pest and disease resistances and tolerances. Consumer-desired grain quality traits under multi environment trials of advanced lines must also be assessed. Simulated studies may provide genetic gain to be targeted by

breeding programs to develop crossing plans and strategies to ensure target is reached with necessary population structures in the breeding programs. Assessment of realized genetic gain at the farm level will also provide a critical feedback loop that breeders will require to make necessary improvements for faster breeding cycles and catering to changing markets and demands. To that end, it is critical that necessary investments be made for both early breeding line evaluations in Target Population of Environments (TPEs) as well as advanced breeding lines in the TPEs. Since IRRI itself does not release varieties directly but instead nominates varieties to the NARES partners in the national variety-release systems, it should be emphasized that research collaboration on a sustained basis will require continual funding and longer-term engagement to meaningfully achieve genetic gain in farmers' fields.

Abbreviations in alphabetical order

CIMMYT: International Maize and Wheat Improvement Center

DS: Dry seasons

EBVs: Estimated breeding values

FAO: Food and Agriculture Organization

FLW: Flowering time

GEBV: Genomic estimated breeding value

GS: Genomic selections

IRRI: International Rice Research Institute

INGER: International Network for Genetic Evaluation of Rice

MAS: Marker-assisted selections

MET: Multi Environment Trials

OECD: Organization for Economic Cooperation and Development

PH: plant height

SES: Standard evaluation system

649 TN: Number of productive tillers

650 TPE: Target Population of Environments

651 WS: Wet seasons

652 RCBD: Randomized Complete Block Design

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Declarations

Ethics approval and consent to participate

Not Applicable

Consent for Publication

Not applicable

Availability of Data and Material

All datasets supporting the conclusions of this article are included in this article (and its additional information files). The datasets used and/or analysed during the current study are also available from corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests

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Authors' contribution

SV is the corresponding author. SV conceived and designed the experiments and organized all analysis for Studies 1 and 2. BCYC conceived and designed the experiments and provided the data for analyses for Study 1. SV contributed to majority of the writing of the article, submission for internal reviews, revisions

and interpretation of the data and preparation of tables and figures for manuscripts. SV was assisted by AG for all the statistical analyses narrative writing and development of figures and tables. BCYC assisted with the writing, revisions and provided all data for the study 1. AG conducted all data analyses for studies 1 and 2. SV also organized and edited and revised the manuscript for submission. SV for study 2 fully organized the conduct of the work in the field, collection, collation of data and assisted by AP. BCYC, designed the study 1, contributed to the work in the field, organized the collection, collation of data for study 1 supported by MRI and VL. All authors read and approved the final manuscript.

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