

Seed Yield Prediction Models of Four Common Moist-Soil Plant Species in Texas

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ABSTRACT

Seed production by moist-soil plant species often varies within and among managed wetlands and on larger landscapes. Quantifying seed production of moist-soil plants can be used to evaluate wetland management strategies and estimate wetland energetic carrying capacity, specifically for waterfowl. In the past, direct estimation techniques were used, but due to excessive personnel and time costs, other indirect methods have been developed. Because indirect seed yield models do not exist for moist-soil plant species in east-central or coastal Texas, we developed direct and indirect methods to model seed production on regional managed wetlands. In September 2004 and 2005, we collected *Echinochloa crusgalli* (barnyardgrass), *E. walterii* (wild millet), *E. colona* (jungle rice), and *Oryza sativa* (cultivated rice) for phytomorphological measurements and seed yield modeling. Initial simple linear and point of origin regression analyses demonstrate strong relationships ($P < 0.001$) among phytomorphological and dot grid methods in predicting seed production for all four species. These models should help regional wetland managers evaluate moist-soil management success and create models for seed production for other moist-soil plants in this region.

KEYWORDS: barnyardgrass, east-central Texas, jungle rice, moist-soil plants, moist-soil wetlands, rice, seed yield, wild millet

INTRODUCTION

Moist-soil managed wetland habitats are often effective at providing high quality foraging habitat for wintering and migrating waterfowl through moist-soil management techniques that focus upon intentionally manipulating wetland hydrology to encourage

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germination and growth of native, annual-seed producing plant species that provide essential nutritive value (i.e., carbohydrates, amino acids, and proteins; Low and Bellrose 1944; Fredrickson and Taylor 1982; Haukos and Smith 1993; Loesch and Kaminski 1989; Bowyer et al. 2005). Moist-soil managed wetlands are often primary foraging habitats that may elevate waterfowl carrying capacity during winter, even in spatially limited habitats (Anderson and Smith 1999; Taylor and Smith 2005). The overarching goal of waterfowl managers using moist-soil management techniques is to maximize the production of naturally occurring moist-soil plants (Fredrickson and Taylor 1982; Moser et al. 1990; Lane and Jensen 1999; Strader and Stinson 2005; Taylor and Smith 2005) by manipulating wetland seed bank and vegetative structure (i.e., disking, mowing, and inundation) and hydrology (via regulated drawdown and inundation) that create germination conditions suitable for desirable moist-soil wetland plants (Fredrickson and Taylor 1982; Reinecke et al. 1989; Lane and Jensen 1999; Strader and Stinson 2005; Taylor and Smith 2005; Collins et al. 2013). Consequently, maximizing annual moist-soil plant seed production is typically a high management priority, whereby obtaining accurate estimates of seed production (i.e., seed yield) is desirable for waterfowl habitat evaluation (Laubhan and Fredrickson 1992; Gray et al. 1999a, 1999b; Sherfy and Kirkpatrick 1999; Naylor et al. 2005).

Seed yield can be estimated directly as the product of plant density and average seed mass per plant measured in quadrats extrapolated over the entire area of interest (Haukos and Smith 1993; Anderson and Smith 1998, 1999; Smith et al. 2004; Anderson 2007). However, this direct estimation technique can be time consuming and costly (Laubhan and Fredrickson 1992; Gray et al. 1999b; Sherfy and Kirkpatrick 1999; Anderson 2007).

Consequently, indirect methods have been developed (i.e., phytomorphological and dot grid methods) to predict seed yield of desirable moist-soil plant species using regression modeling (Laubhan and Fredrickson 1992; Gray et al. 1999b, 1999c; Sherfy and Kirkpatrick 1999; Anderson 2007). Such techniques also require field measurements of stem density, but typically require fewer samples and less field time (Laubhan and Fredrickson 1992; Gray et al. 1999b, 1999c; Sherfy and Kirkpatrick 1999; Anderson 2007). These indirect seed yield-modeling techniques have improved model precision and accuracy using easily obtained, parsimonious combinations of field-generated data.

Estimates of moist-soil seed production are useful to Joint Venture partners of the North American Waterfowl Management Plan (NAWMP) (U.S. Fish and Wildlife Service and Canadian Wildlife Service 1986) for calculating annually variable duck-use-days (Reinecke et al. 1989; Naylor et al. 2005) and track temporal changes in wetland food abundance. Such data allow managers to better plan for habitat and foraging needs of wintering waterfowl (Naylor et al. 2005) and promote regionally suitable and important moist-soil species. However, models may produce biased predictions outside of the region of development and some variables are frequently subject to multicollinearity (Gray et al. 1999c). As such, several studies have emphasized the need for development of regionally specific seed yield models, as relevant phytomorphological features may not be universal for predicting seed yield, because plant morphology and seed production may vary spatiotemporally (Reinecke et al. 1989; Mushet et al. 1992; Gray et al. 1999c).

Beyond regionality, empirical evidence indicates that locally or regionally specific management practices can strongly influence germination and growth of important moist-soil plant species, whereby seed production can be highly variable within and among wetlands subjected to similar management techniques (Laubhan and Fredrickson 1992;

Sherfy and Kirkpatrick 1999; Gray et al. 1999b; Anderson 2007). In response to this information gap regarding regionally specific estimates of seed production, this research was designed to (1) estimate seed production estimates developed using phytomorphological and dot grid methods on *Echinochloa crusgalli* (barnyardgrass), *Echinochloa walteri* (wild millet), *Echinochloa colona* (jungle rice), and *Oryza sativa* (cultivated rice) produced in moist-soil managed wetlands within two geographic areas in Texas.

STUDY AREA

Research was conducted on four sites: Richland Creek Wildlife Management Area (RCWMA), Big Woods (BW), Trinity and Pettigrew Ranch (TPR), and Mad Island Marsh Preserve (MIMP). RCWMA (31°13'N, 96°11'W) is located 40 km southeast of Corsicana, Texas, between Richland-Chambers Reservoir and the Trinity River in Freestone and Navarro counties. Both the BW and the TPR sites are private ranches located within a 25 km radius of RCWMA and occur within the Trinity River Basin. RCWMA, BW, and TP were combined to make the middle Trinity River site. The Nature Conservancy of Texas' MIMP occurs on the upper Texas coast in Matagorda County, Texas (28°6'N, 95°8'W) southeast of Collegeport, Texas on the eastern portion of West Matagorda Bay (Smeins et al. 1992; Collins 2012).

METHODS

Phytomorphological method. Samples for all four focal species (barnyardgrass, wild millet, jungle rice, and cultivated rice) were collected to construct models using the phytomorphological technique (Laubhan and Fredrickson 1992) by randomly placing a 0.0625-m² quadrat (i.e., 25 cm x 25 cm) in monotypic stands of each focal species at each study site August and September 2004 and 2005.

Upon ocular inspection of the focal species sample, the following morphological features were measured on the most "average" plant within each quadrat: plant height (TH) (cm), inflorescence height (SHH) (cm), inflorescence diameter (DI) (cm), and total number of inflorescences present (TSH) (*n*) (Laubhan and Fredrickson 1992; Gray et al. 1999b; Sherfy and Kirkpatrick 1999). Inflorescence volume (IV) (cm³) was calculated using the following equation:

$$IV = \pi \frac{(DI/2)^2 SHH}{3} \quad (1)$$

*following Laubhan and Fredrickson (1992)

After field data were collected following Laubhan and Fredrickson (1992), each inflorescence within each quadrat was clipped, placed into a brown paper bag, and air dried for at least two weeks at room temperature (20° C) to a constant mass (g). Once dry, all seeds were threshed off the rachis and measured to the nearest 0.1g (i.e., initial wet seed mass), oven dried at 50° C for > 24 hrs, and then remeasured to nearest 0.1g. Finally, mean seed mass on each inflorescence per sample quadrat (SSHD) was calculated by dividing total grams of seed mass by total number of inflorescence (i.e., 14 (g)/quadrat with 14 inflorescence present = 1(g)/inflorescence).

Dot grid method. Samples used for regression model construction using the dot grid technique (Gray et al. 1999c) were collected by randomly clipping a single inflorescence of focal species (i.e., barnyardgrass, wild millet, jungle rice, and cultivated rice) at the same time and within the same representative monotypic stand as data were collected for phytomorphological method. Once clipped, inflorescences were immediately placed into a plant press, where care was taken to separate inflorescence pedicels to avoid seed overlap. Samples were pressed at room temperature (20° C) for ≥ 7 days. Once dry, each inflorescence was overlaid on a dot grid (9 dots/cm²) and the number of dots partially or completely obscured by seeds or seed parts were counted following Gray et al. (1999c). Once all dots obscured were summed, inflorescences were removed, all seeds were threshed off the rachis, and measured to the nearest 0.1 g, oven dried at 50° C for 24 hrs, and then remeasured to the nearest 0.1g after drying.

Data analyses. To develop species-specific models using phytomorphological and dot grid methods, simple and multiple linear regression were used employing both the no-intercept (i.e., point of origin) and intercept option following prior research (Laubhan and Fredrickson 1992; Sherfy and Kirkpatrick 1999; Gray et al. 1999b, 1999c; Anderson 2007). Dry seed mass per plant (dependent variable [γ]) was regressed against external phytomorphology (i.e., total inflorescence height, number of inflorescences present, inflorescences volume, etc.) or number of dots obscured to predict species specific seed production. For model construction, the RCWMA, BW, and TPR were combined as the Middle Trinity River Valley sites. Use of the no-intercept method (i.e., point of origin) for model development followed Laubhan and Fredrickson (1992), which forces the regression line through the origin, and allows a value of 0 for all single independent variables. This approach was used to be consistent with previous work. Assumptions of residual, normality, and homoscedasticity were tested using the Shapiro-Wilks' test and residuals were plotted against predicted values of seed mass (Myers 1990; Bowerman and O'Connell 1993). If assumptions were violated ($P < 0.05$), then data transformation (i.e., ln of the dependent variable) occurred to normalize data. Eigenvalue and condition indices were used to check for collinearity if ≥ 2 independent variables were present in selected models (Gray et al. 1999b). If collinearity was present, a single independent variable was removed (Gray et al. 1999b). Final model selection was based upon the best combination of the following criteria: greatest adjusted coefficient of determination (R^2_{adj}), greatest predicted R^2 , lowest residual mean square (S2), and Mallow's Cp statistic (Gray et al. 1999b).

RESULTS

Seed yield models: phytomorphological method. Regression models for all four focal species contained all or a combination of plant height, total number of inflorescence, inflorescence volume, inflorescence height, and average inflorescence mass. Inflorescence diameter and inflorescence volume were positively correlated ($r = 0.86$, $P < 0.001$) for all species and models. Therefore, inflorescence volume replaced inflorescence diameter in all models. Mallow's Cp statistic was always approximately equal to the number of parameters in models for both model structure sets. Collinearity diagnostics were within acceptable limits for all regression analysis. Analyses were successful in developing valid seed yield production models for all four focal species, where models explained 93-98% of the variation in seed biomass, depending upon species and variable inclusion (Table 1).

Table 1. Regression equations for estimating seed biomass (g) of 4 moist-soil plants using phytomorphological measurements collected on Richland Creek Wildlife Management Area (Freestone County, Texas), Big Woods (Freestone County, Texas), Trinity and Pettigrew Ranch (Freestone County, Texas) and Mad Island Nature Preserve (Matagorda County, Texas) August 2004 and 2005.

Species	n	Equation	F	R ²	P
Barnyard Grass ¹	168	Y = 0.0163(TH) + 0.29501(TSH) + -0.4329(SSHH)	292.01	0.90	< 0.001
Barnyard Grass ²	32	Y = 0.01785(TH) + 0.41626(TSH) + -1.05019(SSHH)	557.60	0.98	< 0.001
Wild Millet ¹	76	Y = 0.00682(TH) + 0.40688(TSH) + -0.91945(SSHD)	263.17	0.97	< 0.001
Jungle Rice ²	25	Y = 0.02787(TH) + 0.28309(TSH) + -0.96071(SSHH)	125.63	0.96	< 0.001
Rice ²	34	Y = 0.48262(TH) + 1.98994(TSH) + 0.63947(SHH) + -89.1609(SSHH)	400.14	0.98	< 0.001

¹ Middle Trinity River Valley Collection Sites

² Mad Island Nature Preserve Collection Site

Table 2. Regression equations for estimating seed biomass (g) of four moist-soil plants using dot grid estimates collected on Middle Trinity River and Mad Island Nature Preserve site(s) August 2004 and 2005.

Plant Species	n	Regression Equation	F	R2	P
Barnyardgrass ¹	135	(0.00309 x dots)	1791.43	0.93	<0.001
Barnyardgrass ²	31	(0.00275 x dots)	174.54	0.85	<0.001
Wild Millet ¹	40	(0.00233 x dots)	1382.14	0.97	<0.001
Jungle Rice ²	32	(0.00377 x dots)	181.22	0.90	<0.001
Rice ²	22	(0.01217 x dots)	470.94	0.95	<0.001

¹ Middle Trinity River Valley Collection Sites

² Mad Island Nature Preserve Collection Site

For the collective Middle Trinity River Valley sites the barnyard grass regression equation accounted for 93% of the variation in seed mass ($F = 582.42$; 4,160 df; $P < 0.001$; $R^2 = 0.93$). For barnyardgrass from the MIMP site, the regression equation accounted for 93% of the variation in seed mass ($F = 130.87$; 3, 31 df; $P < 0.001$; $R^2 = 0.93$). For wild millet at the collective Middle Trinity River, the regression equation accounted for 93% of the variation in seed mass ($F = 391.87$; 1, 75 df; $P < 0.001$; $R^2 = 0.93$). At the MIMP, the jungle rice regression equation accounted for 98% of the variation in seed mass ($F = 309.24$; 3, 25 df; $P < 0.001$; $R^2 = 0.98$). At the MIMP, the cultivated rice regression equation accounted for 98% of the variation in seed mass ($F = 552.11$; 4, 30 df; $P < 0.001$; $R^2 = 0.98$) (Table 1).

Seed yield models: dot grid method. For the collective Middle Trinity River sites, the number of dots partially or completely obscured by barnyardgrass seeds or seed parts explained 93% of the variation in barnyardgrass seed biomass ($F = 1791.33$; 1, 134 df; $P < 0.001$; $R^2 = 0.93$) (Table 2). For barnyardgrass collected at the MIMP, the number of dots partially or completely obscured by barnyard grass seeds or seed parts, explained 85% of the variation in barnyard grass biomass ($F = 174.54$; 1, 30 df; $P < 0.001$; $R^2 = 0.85$) (Table 2). For wild millet at the collective Middle Trinity River sites, the number of dots partially or completely obscured by wild millet seeds or seed parts, explained 97% of the variation in wild millet seed biomass ($F = 1382.14$; 1, 39 df; $P < 0.001$; $R^2 = 0.97$) (Table 2). For jungle rice samples collected at the MIMP, the number of dots partially or completely obscured by jungle rice seeds or seed parts explained 90% of the of the variation in jungle rice seed biomass ($F = 181.22$; 1, 20 df; $P < 0.001$; $R^2 = 0.90$) (Table 2). For cultivated rice samples collected at the MIMP, the number of dots partially or completely obscured by cultivated rice seeds or seed parts explained 95% of the of the variation in cultivated rice seed biomass ($F = 470.94$, 1, 21 df; $P < 0.001$; $R^2 = 0.95$) (Table 2).

DISCUSSION

Seed yield prediction models developed during this study were consistent with other research (Gray et al. 1999b, 1999c; Laubhan and Fredrickson 1992; Sherfy and Kirkpatrick 1999; Anderson 2007), where both the phytomorphological and dot grid techniques satisfactorily explained much of the variation in seed biomass of focal plant species. Laubhan and Fredrickson (1992) found plant height and volume explained 88% of barnyardgrass seed mass, slightly more parsimonious than the three-variable (i.e., total height, inflorescence height, and average mass per inflorescence) model for the Middle Trinity River sites. However, model success was better where 90% of the variation was explained by these three variables. The MIMP model for barnyardgrass performed better, and was a two-variable model that included inflorescence height and average mass per inflorescence and explained 93% of the variation. Gray et al. (1999b), using multiple linear regression analyses on phytomorphology, found that plant height, volume, and pedicel number explained 95% of model variation for barnyardgrass. Although these studies produced slightly different models than the current study, they are perhaps more similar than first glance would indicate as inflorescence volume is likely correlated with other inflorescence measures. However, such variability among models and in phytomorphology as a whole for this focal species highlights the previous call for regional and site specific predictive seed yield model development (see Laubhan and Frederickson 1992; Gray et al. 1999b).

Anderson (2007) examined wild millet seed production using predetermined variables, without a stepwise approach for model development. This approach regressed plant height,

volume, pedicel numbers, and impoundments, and found that these variables explained 77% of wild millet seed biomass, while another model showed plant height, inflorescence volume, and pedicel number explained 76% of seed biomass variation. Both models accounted for less seed biomass variance than the best point of origin models developed in this study for both barnyardgrass and wild millet. Moreover, pedicel number was never an included variable in any model for any focal species in this study.

Gray et al. (2009) examined moist-soil seed heads using desktop and portable scanners using estimated seed-head area to estimate production, and reported that their models explained 87-98% of the variation in seed production. Specifically for barnyard grass and wild millet, 97% and 98% of the variation was explained using scanners, although processing time was not much greater than taking phytomorphological measurements in the field. They estimated that processing time averaged 15-45 seconds across species, but wild millet was nearly 2 minutes/plant for the portable scanner. In contrast, our field collection took on average a minute per plot, which consisted of recording morphological measurements, clipping seed heads, and moving onto the next plot.

Inconsistency in variable inclusion (see Laubhan and Fredrickson 1992; Gray et al. 1999b; Anderson 2007) among studies provides evidence of regional variability in plant phytomorphology, perhaps due to variable hydrological or management regimes, genetic variation, soil conditions, or growing season duration. Seed production apparently varies dramatically widely within and among species and even localized variation within impoundments (i.e., moist-soil wetlands, units, etc.) that might provide local sources of variation (Gray et al. 1999b, 1999c; Laubhan and Fredrickson 1992; Sherfy and Kirkpatrick 1999; Anderson 2007). Accounting for both local and regional variation within species may be difficult to capture without intensive sampling throughout a given study area and region (see Laubhan and Fredrickson 1992; Gray et al. 1999c; Naylor et al. 2005). However, if samples are collected from representative stands of focal species, regardless of moist-soil management strategies, seed yield models should reflect local and/or regional conditions and water management approaches. Beyond models developed using the phytomorphological technique, the Gray et al. (1999c) dot grid technique also performed well for the focal species in this study. In comparison, Gray et al. (1999c) reported seed biomass variance explanation of 91-96% for five moist-soil species, where the number of barnyard grass seeds or seed parts obscuring dots explained 95% of seed biomass variance. Anderson (2007) also evaluated the dot grid approach and reported an 85% wild millet seed biomass variance explanation. In this study, the dot grid models developed for wild millet performed better ~97% variance explanation in seed biomass using point of origin.

MANAGEMENT IMPLICATIONS

While the accuracy and precision of the dot grid method are adequate at predicting seed production, the phytomorphological method developed by Laubhan and Fredrickson (1992) is more than suitable because of its relative data collection ease. This technique also produces accurate and precise regression models to accurately estimate temporal and spatial changes in seed production. This will permit waterfowl managers to independently estimate seed production in individual moist-soil managed wetlands and evaluate the impacts of management practices on seed production of individual plant species temporally and spatially. During the course of this study other techniques have been published (Naylor et al. 2005; Gray et al. 2009), which emphasizes to waterfowl managers to explore all techniques available and determine which

published technique fits the needs of their area to explain the spatial and temporal variation often seen on local and regional scales.

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