Advanced-Generation Seed Orchard Designs

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Abstract

Over 30 years of seed orchards establishment and management, the spatial configurations of clones remained unchanged creating a paradoxical state. This is characterized by static seed orchard designs in an environment of constant changes driven by advancement in breeding programs with the majority entering their advanced generations phase. Additionally, the vast accumulation of knowledge pertaining to reproductive biology, ecology and output have changed our perception and assisted in rejecting of some seed orchards' myth. Advanced generations breeding programs feature complicated relatedness structures, combinations of backward and forward selections, desire to capitalize on proportional deployment or exploiting assortative mating etc. We propose two novel seed orchard designs applicable to first and advanced generations where these issues are considered. The first design combines the benefits of randomization and systematic arrangement of ramets and their clones after considering their regional proximity to neighboring clones from the same parent (called Randomized, Replicated, Staggered Clonal-Row (R^2SCR)) facilitating easy crop harvest. The second design (Minimal Inbreeding) utilizes global assignment of clonal ramets within the entire orchard with the objective to minimizing potential inbreeding in the seed crop. Many modifications to both designs are available, making them flexible, yet efficient in delivering genetic gain to operational forestry.

Introduction

During the initial phase of forest tree breeding, seed orchards have evolved as special-purpose plantations to facilitate mass production of genetically improved seeds. During the same period, number of special orchard layouts has been developed (see Giertych 1975 for a review) with a primary goal – to maximize the gain-conversion efficiency between breeding programs and operational forestry. At this initial stage, breeding programs started out with initial unrelated individuals' selections from wild stands, thus relatively simple orchard layouts served well its purpose. Fifty years later, the genetic statuses of breeding programs' have changed considerably with increased relatedness and inbreeding coupled with greater selection differentials and the emergence of new ideas for seed orchard structures such as proportional clonal deployment to maximize gain while managing diversity (Lindgren and Matheson 1986) and clonal-rows facilitating ease of harvesting without appreciable build-up of inbreeding (El-Kassaby 2003; El-Kassaby et al. 2007). Multi-generational breeding programs offer the opportunity to select material across generations, supported by the development and implementation of efficient genetic evaluation techniques with interested desire in combining specific parents with desirable properties. Additionally, advances in reproductive biology (e.g. Erickson and Adams 1989, Adams and Birkes 1991, Perry and Knowles 1990, Xie et al. 1991, Mitton 1992, El-Kassaby et al. 1994, O'Connell et al. 2004), including better understanding of mating systems, pollination biology, fertility variation, and contamination as well as the recent emergence of new breeding strategies (called "Breeding-Without-Breeding") that integrates classical breeding and pedigree reconstruction methods (El-Kassaby et al. 2006) with its specialized seed orchards (breeding arboreta) designs that maximizes the outcrossing rate among parents. All these factors individually and in concert made it possible to consider new seed orchard designs.

In order to develop appropriate seed orchard design suitable to advanced generations, one needs to identify relevant criterions, such as the acceptable overall outcrossing rate and/or the desire to perform crosses among numbers of specific parents, integration of related and inbred trees originating either from the same or different generations, separation of specific parents, different orchard's shapes/configurations, proportional deployment etc. In the same time, it is obvious that neither design will be optimal in every situation, due to year-to-year variability in reproductive output; however, some species-specific reproductive patterns (e.g. pollen dispersion) and environmental conditions (e.g. prevailed wind direction) should be considered during the establishment of advanced generation seed orchards.

Regional Assignment

El-Kassaby & Lstibůrek (in preparation) developed the "Randomized, Replicated, Staggered Clonal-Row (R^2SCR)" design that combines the advantages of systematic and randomized designs. This design allows each clone's rows to be separated by a predetermined radius, thus minimizing mating among ramets in a specific row with others of the same clone and maximizing mating among unrelated clones through: 1- staggering of rows (i.e., each clone is surrounded by 4 different neighbors), and 2- changing the neighbors at each replication. Additionally, a predetermined isolation zone could be created to separate genetically related individuals (i.e., exclusion zone among related clones). This design evolved from earlier work by El-Kassaby (2003) and El-Kassaby et al. (2007) that aimed to: 1- maintaining a relatively simple layout, thus facilitating selective seed harvest by individual clones and 2- reducing the effective selfing rate and correlated mating (Figure 1).

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z
1	23	7	25	19	8	5	6	22	27	8	1	25	21	22	13	14	1	28	5	13	10	23	22	15	6	7
2	23	7	25	19	8	5	6	22	27	8	1	25	21	22	13	14	1	28	5	13	10	23	22	15	6	7
3	23	7	25	19	8	5	6	22	27	8	1	25	21	22	13	14	1	28	5	13	10	23	22	15	6	7
4	23	14	25	16	8	1	6	13	27	19	1	9	21	11	13	18	1	4	5	9	10	27	22	14	6	10
5	23	14	25	16	8	1	6	13	27	19	1	9	21	11	13	18	1	4	5	9	10	27	22	14	6	10
6	23	14	25	16	8	1	6	13	27	19	1	9	21	11	13	18	1	4	5	9	10	27	22	14	6	10
7	18	14	28	16	12	1	5	13	11	19	24	9	6	11	2	18	26	4	11	9	21	27	4	14	2	10
8	18	14	28	16	12	1	5	13	11	19	24	9	6	11	2	18	26	4	11	9	21	27	4	14	2	10
9	18	14	28	16	12	1	5	13	11	19	24	9	6	11	2	18	26	4	11	9	21	27	4	14	2	10
10	18	4	28	22	12	9	5	28	11	4	24	3	6	14	2	27	26	20	11	22	21	17	4	28	2	25
11	18	4	28	22	12	9	5	28	11	4	24	3	6	14	2	27	26	20	11	22	21	17	4	28	2	25
12	18	4	28	22	12	9	5	28	11	4	24	3	6	14	2	27	26	20	11	22	21	17	4	28	2	25
13	10	4	26	22	15	9	18	28	2	4	25	3	20	14	7	27	3	20	14	22	15	17	6	28	13	25
14	10	4	26	22	15	9	18	28	2	4	25	3	20	14	7	27	3	20	14	22	15	17	6	28	13	25
15	10	4	26	22	15	9	18	28	2	4	25	3	20	14	7	27	3	20	14	22	15	17	6	28	13	25
16	10	5	26	7	15	17	18	5	2	10	25	23	20	16	7	26	3	17	14	16	15	24	6	7	13	21
17	10	5	26	7	15	17	18	5	2	10	25	23	20	16	7	26	3	17	14	16	15	24	6	7	13	21
18	10	5	26	7	15	17	18	5	2	10	25	23	20	16	7	26	3	17	14	16	15	24	6	7	13	21
19	21	5	20	7	28	17	16	5	11	10	6	23	19	16	12	26	5	17	28	16	21	24	12	7	11	21
20	21	5	20	7	28	17	16	5	11	10	6	23	19	16	12	26	5	17	28	16	21	24	12	7	11	21
21	21	5	20	7	28	17	16	5	11	10	6	23	19	16	12	26	5	17	28	16	21	24	12	7	11	21
22	21	15	20	13	28	14	16	3	11	12	6	8	19	18	12	25	5	20	28	6	21	2	12	10	11	8
23	21	15	20	13	28	14	16	3	11	12	6	8	19	18	12	25	5	20	28	6	21	2	12	10	11	8
24	21	15	20	13	28	14	16	3	11	12	6	8	19	18	12	25	5	20	28	6	21	2	12	10	11	8

Figure 1. An example of the "Randomized, Replicated, Staggered Clonal-Row (R^2SCR)" seed orchard design showing the separation among replicated clonal-rows of the same clone (i.e., regional separation) and the staggered nature of rows (see position occupied by clone #7).

A user-friendly computer program was developed to implement this scheme under a specific scenario without the need to understand the mathematics of the model. As stated above, regional clonal assignment requires the selection of specific separation zones prior to the randomization and the length of row (must be even to allow perfect overlap between rows). A number of feasible solutions is generated by the program along with the relevant fit-statistics and this number is correlated with the number of initial iterations selected (i.e., the higher the iteration number, the higher the resultant solutions). Input parameters include the number of clones, seed orchard size, length of rows, separation zones, physical configuration and either balanced or proportional deployment option is desired. A computer program is available from YAE.

Global Assignment

Theoretically, this represents the most efficient seed orchard design with respect to the minimization of inbreeding in seed orchard crop ("Minimum-Inbreeding" design) (Lstibůrek and El-Kassaby, in preparation). There are no separation zones in this design since a given location of a particular ramet is considered in relation to all other locations in the orchard. In some cases apparent inbreeding is not completely avoided (proximity between two ramers of the same clone) but the resulting layout leads to a minimum inbreeding in seed orchard's crop considering all other feasible layouts (Figure 2).

Optimum layout is a result of separating clones and their ramets on the orchard's grid to minimize selfing and mating among relatives, where the degree of genetic relatedness proportionally affects the level of separation. Complicated pedigree relationships can be easily accommodated by this design, allowing the flexibility to differentially "penalize" different relationships, thus considering closely biological properties of a given species. The outcrossing rate within this orchard is maximized. Computer program is available from ML.

Conclusion

Most seed orchards are established in outdoor conditions with trees planted to a given layout. Reproductive output differs among years, thus no design is truly optimum. Here we propose two innovative designs suitable to advanced-generation seed orchards that are easy to implement. While the first design offers simple scheme to facilitate selective seed harvest by clone, and minimizes the impact of selfing and correlated matings, the second orchard's layout uses a global assignment and leads to theoretically minimum levels of inbreeding in seed orchard's crop, while maximizing the outcrossing rate.

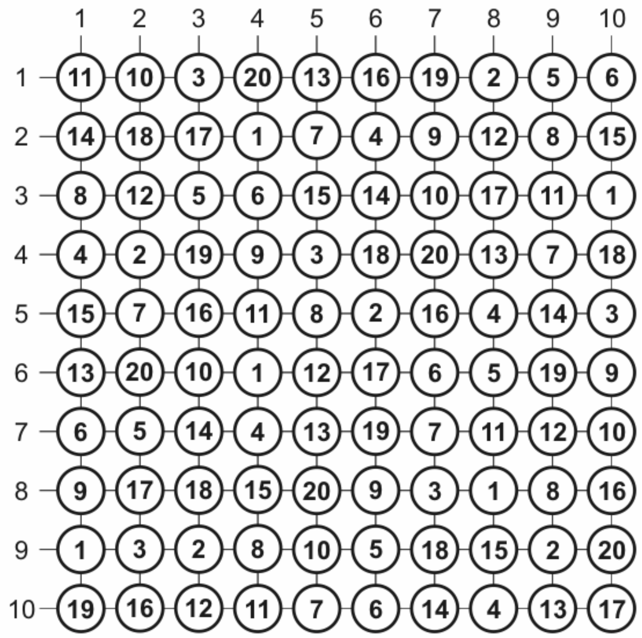

Figure 1. An example of the "Minimum Inbreeding" seed orchard design showing separation among replicated ramets of the same clone and the global separation and randomization among 20 clones each with 5 ramets.

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