Not Your Grandma's Goobers: Designing the Future of Peanut Breeding

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ABSTRACT

The peanut producer has realized a 130% increase in yield since 1969, with production averaging 4,563 kgha^{-1} nationwide for the US in 2017. Advances in agricultural engineering, agricultural practices, and chemicals for pests, diseases and weed management have all contributed to increased peanut production efficiency and profitability. Perhaps greatest contribution to sustainable peanut production has been made by area-targeted peanut breeding programs. Charged with hitting the moving target of a 'perfect peanut cultivar', peanut breeders have managed to deliver to their customers by focusing on developing cultivars with traits of high importance such as disease resistance, high oleic acid content, early maturity, and drought tolerance, while advancing essential traits such as yield and grade. Conventional peanut breeding has provided a continuous supply of improved cultivars over the last 50 years. However, this success may be difficult to exceed if only conventional technologies continue to be used. Fortunately, recent advances in molecular technologies have resulted in the sequencing of both the ancestral and cultivated peanut genomes, opening the door for the mapping of traits and molecular marker development. By extensively phenotyping populations designed for trait mapping, steps can now be taken over the next decade to develop trait-specific markers for use in rapidly mining vast germplasm collections, efficiently identifying useful breeding material, pyramiding traits into cultivars and drastically reducing time and resources required for cultivar development. Future generations of peanut breeders will undoubtedly be well-trained in the use of such markers and will finally have the tools necessary to break through the bottle-neck of the cultivated peanut narrow genetic base. The age of peanut breeding by design may be just around the corner.

Key Words: *Arachis hypogaea,* peanut, future, breeding, review

The U.S. currently ranks 3rd in the world in peanut production behind China and India and produces 10% of the world's crop. Production in the US has risen overall in the last 50 years to a high of 3,200 kg and valued at $1.6 billion reported in 2017 (NASS, 2017). Most of peanut production in the United States has traditionally been located 3 geographic regions: Southeast (Alabama, Florida, Georgia), Southwest (New Mexico, Oklahoma, Texas), and the Virginia-Carolinas (North Carolina, Virginia). Within the last decade, production has also been reported in Arkansas, Mississippi, and South Carolina with the top 10 peanut producing states shown in Figure 1. Because the three peanut production regions vastly differ in aspects biotic and abiotic stressors, peanuts developed in a specific region generally do not perform well in other regions. Therefore, public peanut breeding programs are located strategically within each growing region (Figure 2). Most likely areas of peanut production in the US will remain geographically stable unless shifted by a catastrophic weather event or significant change in the agricultural economic arena.

Public peanut breeding programs have been extremely successful in cultivar development, registering over 100 variety releases since 1969 (Table 1). Since the release of Florunner (Norden et al, 1969) there have been 59 runner-type, 27 virginia-type, 11 spanish-type, 5 valencia-type, and 1 forage-type cultivar releases registered in the U.S. The number of variety releases by peanut market-type is reflected by U.S. peanut production in proportion (Figure 3), underscoring the intimate connection between breeders and producers. Over the last 50 years, peanut yields have more than doubled, increasing from 1,904 kgha^{-1} in 1969 to over 4,480 kgha^{-1} in 2017 (Figure 4). Factors contributing to this increase include precision farming equipment, improved chemicals and advisories for weed and pest control, improved field inoculants and crop rotation practices. Improved peanut cultivars available for commercial production have also contributed to increased yield, disease resistance, oil quality, drought resistance and maturity. In several cases, the release of a disease resistant cultivar has prevented the collapse of the peanut industry in a growing region. For example, the release of Georgia Green in the mid-1990s (Branch, 1996) was largely responsible for saving production in the Southeastern U.S. due to

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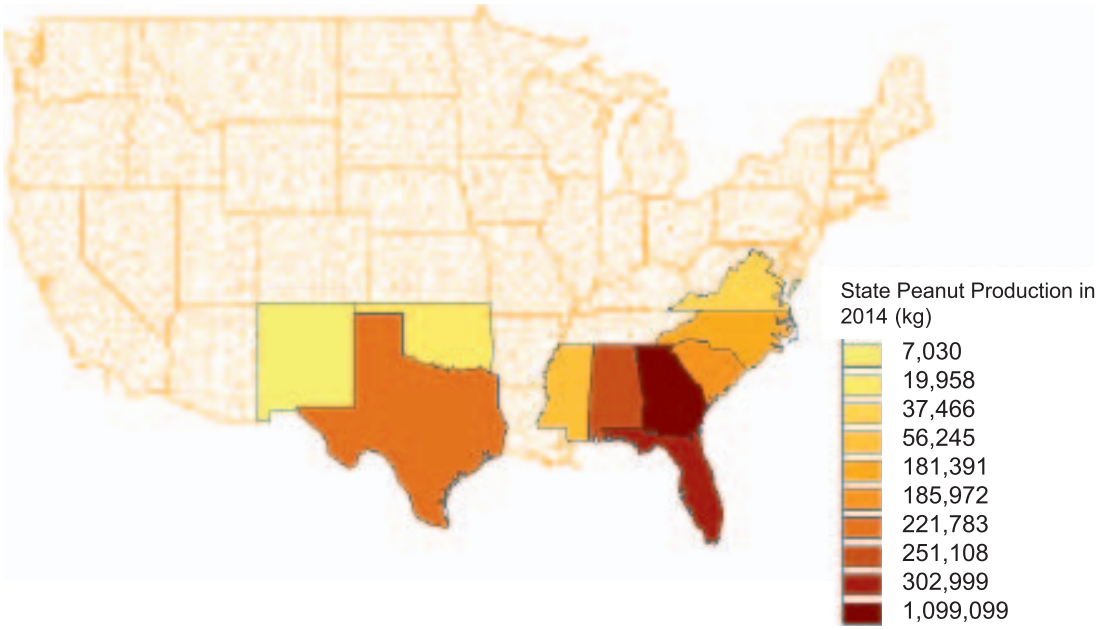

Fig. 1. Top 10 peanut producing states in 2014.

its resistance to the Tospovirus described as *Tomato Spotted Wilt* (Culbreath *et al.*, 1992), a pathogen that still threatens the region today. Timely released cultivars have also shielded Southeastern producers from yield losses due to early and late leaf spot (*Cercospora arachidicola* and *Cercosporidium personatum,* respectively) as well as root-knot nematodes (*Meloidogyne spp.)* and Cylindro-

Fig. 2. Public peanut breeding programs in the United States. (Auburn University, Auburn, AL; University of Georgia, Tifton, GA; University of Florida, Marianna, FL; New Mexico State University, Clovis, NM; North Carolina State University, Raleigh, NC; Texas AgriLife Research: Lubbock, TX, College Station, TX, Stephenville, TX; USDA-ARS locations: Stillwater, Oklahoma, Tifton, Georgia; Virginia Tech: Suffolk, VA.

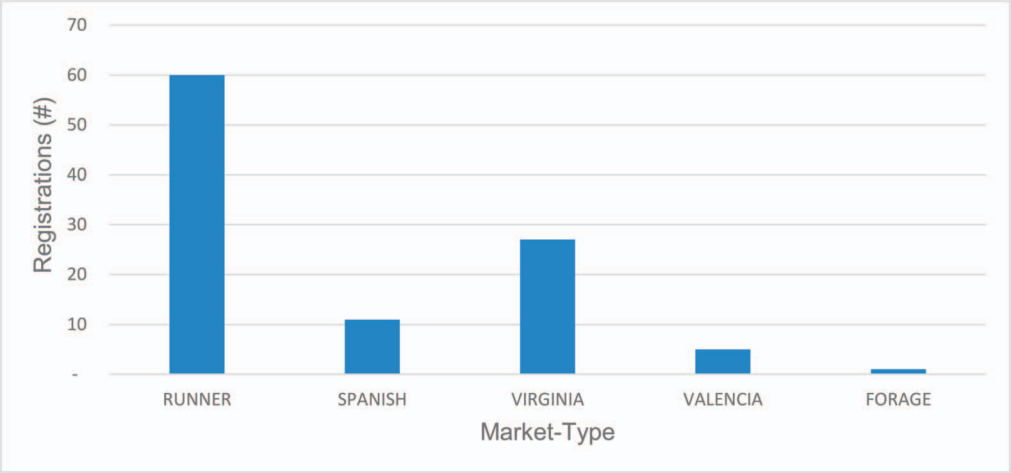

Fig. 3. Registered peanut cultivars by market-type, 1969-2018.

cladium black rot (*Cylindrocladium parasiticum*). Sclerotinia blight on peanut (Sclerotinia minor Jagger) nearly devastated peanut production in the Southwestern U.S., but the release of Tamspan 90 (Smith *et al.*, 1991) and Tamrun 96 (Smith *et al.*, 1998) allowed producers to overcome up to 50% yield losses caused by that disease. The development of disease resistant or otherwise improved peanut cultivars is a never-ending quest because of constantly changing biotic and abiotic stressors. Therefore, peanut breeders face the endless task of continually developing new varieties. The search continues for new and better sources of disease resistance and other value-added traits by phenotyping vast germplasm collections in lengthy and labor-intensive field trials. Incorporation of new beneficial traits into cultivated peanut using traditional breeding methods takes 10-12 years after discovery.

According to a report by the United Nations Department of Economic and Social Affairs, the world population has been predicted to reach 10 billion by 2050, and at current production rates, the world food supply is barely keeping up with demand. What does this mean to future generations of humanity? Although the amount of land available to agriculture in the U.S. has remained constant in the last 50 years, the percentage of the American workforce in agriculture has drastically declined. Fewer generations are choosing to remain on their family's farm, and instead chose to pursue other employment options. The consequence of these actions is that fewer farmers must produce more products. To produce the amount of food

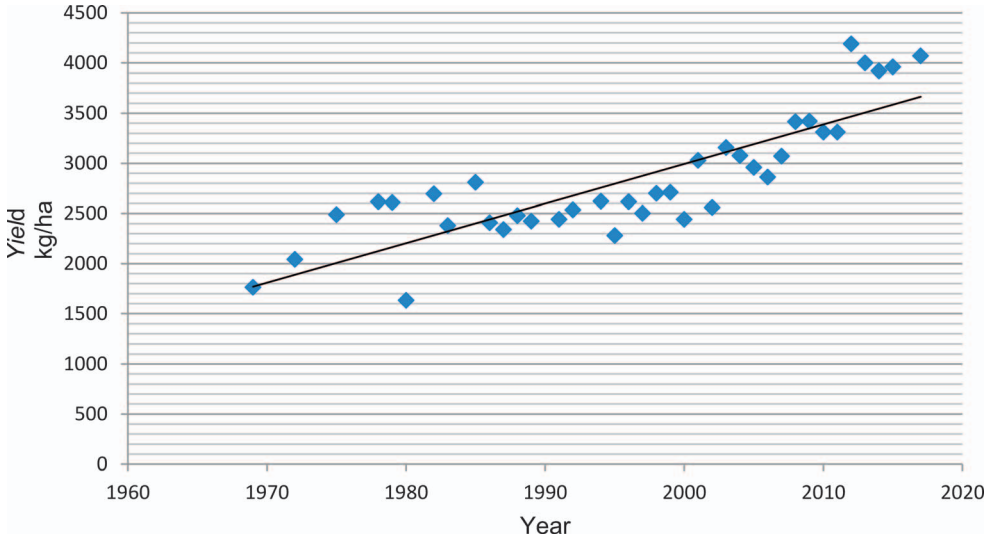

Fig. 4. Growth in yield per acre of peanut cultivars 1969-2017 (y = 39.464x – 77934; R^2= 0.7073; ◆ = average US yield). Yields have increased approximately 130% in the last 48 years.

Table 1. Registered cultivars released by public breeding programs in the U.S. (1969-2018) along with market-type, breeder and trait(s) of interest.

Year of Registration	Cultivar	Type	Breeder	Relevant Trait(s) at Time of Release
1969	Florunner	Runner	Norden et al.	Yield
1972	New Mexico Valencia A	Valencia	Hsi and Finkner	Yield
	Spantex	Spanish	Simpson	Early maturing
	STARR	Spanish	Simpson	Hull thickness, yield
1975	Tamnut 74	Spanish	Simpson and Smith	Yield
1978	Early Bunch	Virginia	Norden et al.	Early maturing
1979	NC 7	Virginia	Wynne et al.	Early maturing
	Toalson	Spanish	Simpson et al.	Hull thickness
1980	New Mexico Valencia C	Valencia	Hsi	Pod size
1982	Sunbelt Runner	Runner	Mixon	Yield
	Virginia 81 Bunch	Virginia	Coffelt et al.	Sclerotinia blight resistance
1983	NC 8	Virginia	Wynne and Beute	CBR resistance
	Pronto	Spanish	Banks and Kirby	Early maturing
1985	Sunrunner	Runner	Norden et al.	Yield
1986	Florigraze	Forage	Prine et al.	Forage
	NC 9	Virginia	Wynne et al.	Early maturing
1987	Georgia Red	Valencia	Branch and Hammons	Yield
	Langley	Runner	Simpson et al.	Early maturing
1988	Southern Runner	Runner	Gorbet et al.	Leaf spot resistance
1989	Okrun	Runner	Banks et al.	Yield
	Spanco	Spanish	Kirby et al.	Yield, uniformity
	Tamrun 88	Runner	Smith and Simpson	Yield
1991	Georgia Runner	Runner	Branch	Yield
	NC 10C	Virginia	Wynne et al.	CBR resistance, pod characteristics
	NC-V11	Virginia	Wynne et al.	Yield
	Tamspan 90	Spanish	Smith et al.	Sclerotinia blight and pod rot resistance
1992	MARC-I	Runner	Gorbet and Knauft	Early maturing
1994	Georgia Brown	Runner	Branch	Yield, small seed, marketed as spanish
	VA-93B	Virginia	Coffelt, et al.	Early maturing
	VA-C-92R	Virginia	Mozingo et al.	Yield
1995	Andru-93	Runner	Gorbet and Knauft	Grade
1996	Georgia Green	Runner	Branch	TSWV resistance, Yield
1997	NC 12C	Virginia	Isleib et al.	Yield, pod characteristics
1997	SunOleic 95R	Runner	Gorbet and Knauft	High-oleic
1998	Georgia Bold	Runner	Branch	Yield
	Southwest Runner	Runner	Kirby et al.	Sclerotinia blight resistance
	Tamrun 96	Runner	Smith et al.	Sclerotinia blight resistance
1999	Gregory	Virginia	Isleib et al.	Pod size
2000	Georgia Hi-O/L	Runner	Branch	High oleic
	Jupiter	Virginia	Banks and Kirby	Pod size
	SunOleic 97R	Runner	Gorbet and Knauft	High oleic
	VA 98R	Virginia	Mozino et al.	Pod and seed characteristics
	Tamrun 98	Runner	Simpson et al.	Sclerotinia blight resistance
2001	COAN	Runner	Simpson and Starr	RKN resistance
	Georgia Valencia	Valencia	Branch	Large pods
2002	C-99R	Runner	Gorbet and Shokes	LLS and TSWV resistance
	Georgia 01R	Runner	Branch	TSWV resistance
	Florida MDR 98	Runner	Gorbet and Shokes	LLS and TSWV resistance
2003	Georgia 02C	Runner	Branch	High oleic, grade, TSWV and CBR resistance
	OLin	Spanish	Simpson et al.	High oleic
	NemaTam	Runner	Simpson et al.	RKN resistance
	Perry	Virginia	Isleib et al.	CBR resistance
	Tamrun OL01	Runner	Simpson et al.	High oleic, Sclerotinia blight resistance
2004	Georgia O3L	Runner	Branch	TSWV resistance
	Wilson	Virginia	Mozingo et al.	Yield, grade
2005	Georgia 04S	Spanish	Branch	Yield, small seeded runner

Table 1. Continued.

Year of Registration	Cultivar	Type	Breeder	Relevant Trait(s) at Time of Release
2006	Andru-II	Runner	Gorbet	High oleic, early maturing
	AT 3081R	Runner	Anderson and Harvey	Yield, TSWV resistance
	Brantley	Virginia	Isleib et al.	High oleic
	Carver	Runner	Gorbet	TSWV, CBR resistance
	CHAMPS	Virginia	Mozino et al.	Early maturing, TSWV resistance
	Georgia 05E	Virginia	Branch	High oleic, ELS, LLS, TSWV resistance
	Tamrun OL02	Runner	Simpson et al.	High oleic
	Tamnut OL06	Spanish	Baring et al.	High oleic, Yield
	Tamrun OL07	Runner	Baring et al.	High oleic, Sclerotinia blight resistance
	Phillips	Virginia	Isleib et al.	Pod characteristics
2007	ANorden	Runner	Gorbet	High oleic, TSWV resistance
	AP-3	Runner	Gorbet	TSWV and white mold resistance
	Georgia 06G	Runner	Branch	Yield, TSWV resistance
	Georgian Greener	Runner	Branch	Yield, TSWV resistance
	GP-1	Runner	Gorbet	High oleic, Yield, TSWV resistance
	Hull	Runner	Gorbet	High oleic, TSWV resistance
	Tifrunner	Runner	Holbrook and Culbreath	TSWV, ELS, LLS resistance
2008	DP-1	Runner	Gorbet and Tillman	TSWV and white mold resistance
	Georgia 07W	Runner	Branch	Yield, TSWV and white mold resistance
	Georganic	Runner	Holbrook and Culbreath	TSWV, ELS, LLS resistance
	Tifguard	Runner	Holbrook et al.	RKN resistance
2009	AP-4	Runner	Gorbet	High oleic, large seeded
	Florida 07	Runner	Gorbet and Tillman	High oleic, seed size, TSWV and white mold resistance
	Georgia 08V	Virginia	Branch	TSWV resistance
2010	Georgia 09B	Runner	Branch	High oleic, TSWV resistance
2011	Bailey	Virginia	Isleib et al.	TSWV, CBR, LLS, Sclerotina blight resistance
	Georgia 10T	Runner	Branch and Culbreath	TSWV resistance
	Titan	Virginia	Balota et al.	Pod and seed size
	York	Runner	Gorber and Tillman	High oleic, LLS, TSWV White mold resistance
2012	Georgia 11J	Virginia	Branch	Pod size
2013	AU-1101	Virginia	Chen et al.	Pod characteristics
	Georgia 12Y	Runner	Branch	TSWV and white mold resistance
	Tamrun OL11	Runner	Baring et al.	High oleic, Sclerotinia blight resistance, grade
	Red River Runner	Runner	Melouk et al.	High oleic, Sclerotinia blight resistance, grade
	Webb	Runner	Simpson et al.	High oleic, Sclerotinia blight and RKN resistance
2014	Georgia 13M	Runner	Branch	High oleic, yield, TSWV resistance
	NuMex 01	Valencia	Puppala and Tallury	High oleic, yield
	Schubert	Spanish	Burow et al.	High oleic, early maturing
	Tamrun OL12	Runner	Burow et al.	Early maturing
2015	Georgia 14N	Runner	Branch	High oleic, RKN, TSWV resistance
	FloRun 107	Runner	Tillman and Gorbet	High oleic, grade
	OLé	Spanish	Chamberlin et al.	High oleic, Sclerotinia blight and pod rot resistance
	Sugg	Virginia	Isleib et al.	CBR, TSWV, Sclerotinia blight, ELS resistance
2017	Georgia 16HO	Runner	Branch	High oleic, Yield, TSWV resistance
	TifNV-High O/L	Runner	Holbrook et al.	High oleic, RKN, TSWV resistance
	TuFRunner 511	Runner	Tillman and Gorbet	High oleic, seed size, grade, yield
	VENUS	Virginia	Chamberlin et al.	High oleic, Sclerotinia blight resistance
2018	Lariat	Runner	Chamberlin et al.	High oleic, Sclerotinia blight resistance

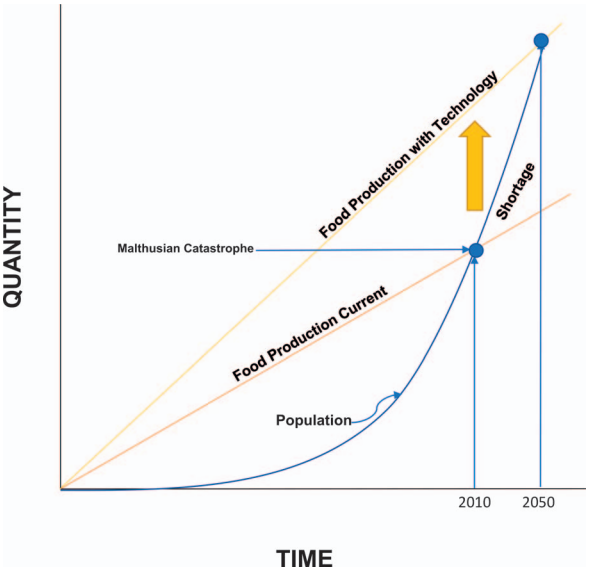

Fig. 5. Current food production vs. future food production in relation to growing world population over time. Orange line predicts boost in production if technology such as precision agriculture and molecular breeding are used (Urbano, 2011).

needed to sustain the world's growing population, much of the additional food will need to come from increases in crop yield rather than increased cropping intensity or land cultivation.

America's peanut farmers help feed the world. Peanuts and peanut products are an important source of protein in countries across the globe, especially those which are underdeveloped, and could contribute greatly to the prevention of human starvation in the future. However, peanut production (along with other food crops) will need to double over the next 30 years to provide ample food for the growing population. Is it possible to double peanut yields in the next 30 years? Researchers predict that a Malthusian Catastrophe (Figure 5) can be avoided in the future by using precision agriculture technology along with molecular breeding to boost farmer's production.

Molecular breeding is described as the application of molecular tools in traditional breeding programs. One example of molecular breeding is marker-assisted selection (MAS) where molecular markers closely associated with a trait of interest are used to select for breeding material and/or advanced breeding lines during early stages of development. This is different from genetic engineering where molecular tools are used to artificially insert beneficial genes into a target genome. MAS, when used in conjunction with traditional breeding methods, increases the efficiency of the development of new cultivars by enabling the breeder to select breeding material containing the trait of interest without having to spend years phenotyping for the trait in the field (Xu, 2010).

Implementation of molecular tools such as MAS in a plant breeding program can greatly increase the efficiency of cultivar development. Early generation selection using MAS allows the breeder to discard many plants with unwanted gene combinations, especially those that lack the essential trait(s) of interest, without years of phenotyping in the field. MAS allows breeders to move fewer breeding lines forward for testing and increases the probability that advanced breeding lines will contain desired traits. These tools also allow foreground and background selection during breeding and backcross population development as well as rapid pyramiding of desired traits within the same cultivar. When used, molecular tools greatly enhance the efficiency and accuracy of breeding program.

MAS has been used successfully in breeding for many other field crops including, but not limited to, *Oryza sativa* (rice) (Collard *et al*., 2008), *Glycine max* (soybean) (Gavioli, 2011), and *Triticum aestivum* (wheat) (Arruda *et al*., 2016). Peanut breeders have been unable to employ MAS in their programs due to a lack of genetic resources required. Pre-requisites to the application of molecular breeding and MAS include a reliable genome sequence, numerous molecular markers on a high-density genetic map, and reliable trait-associated markers. No sequence information for the peanut genome was available until 2016 when the sequences of the diploid ancestors of cultivated peanut were reported by Bertioli *et al.et al*. The sequence of cultivated peanut has recently been determined and is forthcoming. Genetic maps with markers have been generated for peanut and are available for use on PeanutBase (Sudhansu *et al*., 2016), but few reliable trait-associated markers for peanut have been identified. Agronomic traits for which markers have been reported in peanut include high oleic acid content (Chu *et al*., 2009; Barkley *et al*., 2010, 2011). Few molecular markers have been identified in peanut for disease resistance, although markers have been reported for resistance to nematodes (Garcia *et al*., 1996; Chu *et al*., 2007,2016), tomato spotted wilt virus (Liu *et al*., 2015), leaf spot (Varma *et al*., 2005; Mace *et al*., 2006; Mondal and Badigannavar, 2010; Shoba *et al*., 2012; Shirasawa *et al*., 2013; Liu *et al*., 2015), rust (Varma *et al*., 2005; Mace *et al*., 2006; Mondal and Badigannavar, 2010; Shoba *et al*., 2012; Shirasawa *et al*., 2013).

Determination of the peanut genomic sequence was only made possible by significant financial support of the peanut industry for the Internation-

al Peanut Genome Initiative (PGI), a group of scientists from the U.S., China, Brazil, India and Israel whose objectives are to delineate peanut genome sequences, characterize the genetic and phenotypic variation in cultivated and wild peanuts and develop genomic tools for peanut breeding. These investments in research made by the peanut industry moved peanut breeding closer to molecular application. An overwhelming amount of genetic information has now been generated and thousands of molecular markers within the genome have been identified and mapped. A bottleneck now exists between available information and application, and the focus of the PGI must now shift to the identification and implementation of trait-associated molecular markers. Phenotyping of the recombinant inbred line (RIL) populations already developed by the PGI and correlation of that data with genetic data already gathered will provide the information needed to define reliable trait-associated markers and implement the use of those markers in peanut breeding programs throughout the U.S. growing regions.

Once these markers are deployed for use, the breeder must be able to implement their use. Concepts in genomic selection and or marker assisted breeding may not be understood by today's traditional plant breeder, but these techniques are commonly part of the curriculum required for current students of plant breeding. Highly specialized equipment for high-throughput analysis is not available to most plant breeders today, therefore steps must be taken to either provide services and/or equipment for MAS. This action may fall on the shoulders of the peanut industry since breeding programs are normally not well funded by grants, making it difficult to fund MAS. Molecular testing is costly making high-throughput screening difficult for the average peanut breeding program. However, steps are currently underway to make it more affordable for the peanut breeding community.

While the implementation of molecular techniques in breeding programs will increase efficiency and accuracy, they will not replace the breeder's expert eye. Communication with producers and the traditional skills of crossing and selection in the field will remain vital to the successful peanut breeder. However, molecular tools used in concert with traditional techniques will expand the future peanut breeder's toolkit. Peanut breeding-by-design may be the key to achieving increased the cultivar quality and yield necessary to keep pace with expanding world demand.

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