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 kg ha⁻¹ in 1969 to over 4,480 kg ha⁻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
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 South-eastern 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-
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
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                                |
| 1972                 | Spantex  | Spanish  | Simpson                    | Early maturing                       |
| 1972                 | 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                       |
| 1980                 | New Mexico Valencia C | Valencia | Hsi                        | Pod size                             |
| 1982                 | Sunbelt Runner | Virginia | Coffelt et al. | Sclerotinia blight resistance |
| 1983                 | NC 8     | Virginia | Wynne and Beute            | CBR resistance                       |
| 1985                 | Sunrunner| Runner   | Norden et al.              | Yield                                |
| 1986                 | Florigraze| Forage  | Prine et al.               | Forage                               |
| 1987                 | Georgia Red | Valencia | Branch and Hammons         | Yield                                |
| 1987                 | Langley  | Runner   | Simpson et al.             | Early maturing                       |
| 1988                 | Southern Runner | Runner | Gorbet et al. | Leaf spot resistance |
| 1989                 | Okrun    | Runner   | Banks et al.               | Yield                                |
| 1991                 | Georgia Runner | Runner | Branch                     | Yield                                |
| 1991                 | NC 10C   | Virginia | Wynne et al.               | CBR resistance, pod characteristics  |
| 1991                 | NC-V11   | Virginia | Wynne et al.               | Yield                                |
| 1992                 | MARC-I   | Runner   | Gorbet and Knauft          | Early maturing                       |
| 1994                 | Georgia Brown | Runner | Branch                     | Yield, small seed, marketed as spanish |
| 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                                |
| 1999                 | Southwest Runner | Runner | Kirby et al. | Sclerotinia blight resistance |
| 2000                 | Georgia Hi-O/L | Runner | Branch                     | High oleic                           |
| 2000                 | Jupiter  | Virginia | Banks and Kirby           | Pod size                             |
| 2000                 | SunOleic 97R | Runner | Gorbet and Knauft          | High oleic                           |
| 2000                 | VA 98R   | Virginia | Mozino et al.              | Pod and seed characteristics         |
| 2001                 | Tamrun 96| Runner   | Simpson et al.             | Sclerotinia blight resistance        |
| 2001                 | COAN     | Runner   | Simpson and Starr          | RKN resistance                       |
| 2002                 | Georgia Valencia | Valencia | Branch                   | Large pods                           |
| 2002                 | C-99R    | Runner   | Gorbet and Shokes          | LLS and TSWV resistance              |
| 2002                 | Georgia 01R | Runner | Branch                     | TSWV resistance                      |
| 2003                 | Georgia 02C | Runner | Branch                     | High oleic, grade, TSWV and CBR resistance |
| 2004                 | Georgia 03L | Runner | Branch                     | TSWV resistance                      |
| 2005                 | Wilson   | Virginia | Mozino et al.              | Yield, grade                         |
| Year of | Cultivar | Type | Breeder | Relevant Trait(s) at Time of Release |
|---------|----------|------|---------|------------------------------------|
| Registration | | | | |
| 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 |
|        | Hull Runner | Gorbet | High oleic, Yield, 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 |
|        | 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 |
| 2011   | Georgia 11J Virginia | Branch | Pod size |
|        | 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 | 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 |
|        | 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 |
| 2015   | Sugg Virginia | Isleib et al. | CBR, TSWV, Sclerotinia blight, ELS resistance |
|        | Georgia 16HO Runner | Branch | High oleic, Yield, TSWV resistance |
|        | TilNV-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 |
| 2017   | Lariat Runner | Chamberlin et al. | High oleic, Sclerotinia blight resistance |

**Note:** The table continues with similar entries for years 2018 and 2019.
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 reported for peanut 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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