Beyond a reference genome: pangenomes and population genomics of underutilised and orphan crops for future food and nutrition security

**Mark A. Chapman1,\*****, Yuqi He2 and Meiliang Zhou2,\***

1 Biological Sciences, University of Southampton, Life Sciences Building 85, Highfield Campus, Southampton, SO17 1BJ, UK;

2 Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Room 405, National Crop Gene Bank Building, Zhongguancun South Street No. 12, Haidian District, Beijing, 100081, China; ORCID:.

\* For correspondence: m.chapman@soton.ac.uk (MAC) and zhoumeiliang@caas.cn (MZ).

ORCID:

MAC: 0000-0002-7151-723X; YH: 0000-0001-9920-9653; ML: 0000-0001-5175-3684

Brief heading and social media: MAC at the Centre for Underutilised Crops can be followed on Twitter @CUCsoton

**Summary**

Underutilised crops are, by definition, under-researched compared to staple crops yet come with traits that may be especially important given climate change and feeding a globally increasing population. These crops are often stress tolerant, combined with unique and beneficial nutritional profiles. Whilst progress is being made by generating reference genome sequences, in this Tansley Review, we point out how this is only the very first step. We advocate that going ‘beyond a reference genome’ should be a priority, as it is only at this stage one can identify the specific genes and the adaptive alleles that underpin the valuable traits. We sum up how population genomic and pangenomic approaches have led to the identification of stress and disease tolerant alleles in staple crops and compare this to the small number of examples from underutilised crops. We also demonstrate how previously underutilised crops have benefitted from genomic advances and that many breeding targets in underutilised crops are often well-studied in staple crops. This cross-crop population level resequencing could lead to an understanding of the genetic basis of adaptive traits in underutilised crops. This level of investment may be crucial for fully understanding the value of these crops before they are lost.

**Keywords:** Crop Improvement,Food security, Genomics, Pangenome, Population genomics, Reference genome, Underutilised crops

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**1. Introduction**

In 2020, at least 720 million people (≥9.9% of the world’s population) faced hunger; an increase on previous years, and the greatest percentage of the total population since 2010 (FAO et al. 2021). With ongoing climate change, the increasing global population, and the COVID19 pandemic, the number of people facing hunger is expected to rise significantly. It is increasingly recognised that achieving Sustainable Development Goal (SDG) 2 (“Zero Hunger”) by 2030 is in doubt (Global Panel on Agriculture and Food Systems for Nutrition 2020). To overcome this challenge, one of the most favourable approaches is to breed new germplasm to face these stresses. Crop breeders have identified germplasm (either local varieties or crop wild relatives [CWRs]) with beneficial traits, and introgressed the adaptive alleles into elite varieties. Although substantial efforts and many successes have been made to breed climate resilient crops, yield has started to plateau because of negative effects of extreme weather events in at least some years and in some parts of the world (Zhao et al. 2017). Homogenization of diets and the increasing consumption of calorie-rich yet nutrition- deficient crops has also lead to an increase in hidden hunger, a significant factor threatening human health (Khoury *et al.* 2014; [Dawson *et al.*, 2019](#_ENREF_6)). A greater understanding of the effect of environmental stresses on crop quality, for example nutrient content and composition is also needed.

Staple crops are limited in their tolerance of a changing climate, forcing researchers and breeders to start to investigate new pathways to ensure future food security. Underutilised crops (sometimes known as semi-domesticated, orphan and/or forgotten crops) are locally important crops grown in limited regions with low-input conditions. They are currently impossible or inefficient to be produced at large-scale due to low yield, anti-nutrient content, consumer preferences, harvestability, or other properties. Because of the diverse nutrient and local adaptations, these crops are often locally important or vital, and represent a broad gene pool for future crop improvement. Examples include high iron, zinc and calcium content in tepary bean and bambara groundnut (Chibarabada et al. 2017), tolerance of drought stress in lablab, horsegram and cowpea (Ewansiha and Singh 2006; Muchow 1985), and tolerance of heat in amaranth and cassava (Kuo et al. 1992). Thus, underutilised crops have significant potential to aid food security (Massawe et al. 2016; Mabhaudhi et al. 2017; Li et al. 2020b; Siddique et al. 2021). However, some of underutilised crops are becoming abandoned due to globalisation, migration and other economic forces and therefore are at risk of loss of diversity, or complete loss of the crop, or the loss of associated indigenous knowledge (Mabhaudhi et al. 2017).

This review will summarise advances made in major crops, and how genome sequencing has brought about a step-change in agricultural research. We also discuss some crops which could have been described as underutilised only *c*. 30 years ago but have become more mainstream, and the genomics-assisted research that has taken place. Beyond this, we discuss the benefits of venturing ‘beyond a reference genome’, i.e., resequencing, population genomics and pangenomics, and what advantages this can bring. We encourage the research community to incorporate underutilised crops into wider research and to envisage the benefits that come from this increased investment.

**1.1 Genomics and its contribution to agricultural improvements**

For staple crops, notable successes have been made using genomic-related approaches to uncover the genes responsible for important phenotypes.

*1.1.1 Genome-wide Association Study (GWAS)*

GWAS relies on genome-scale data (dense single nucleotide polymorphisms [SNPs] or whole genome sequences) to associate genomic variation with trait variation (Liu and Yan 2019). Typically, the analysis of hundreds of varieties/lines is necessary to generate sufficient power to resolve quantitative trait loci (QTL), as well as to ensure rare causative variants are included (e.g., Xing et al. 2015). This breadth of variation encompasses orders of magnitude more recombination than QTL mapping therefore can resolve even small-effect QTL and with typically greater resolution. Thousands of GWAS have been reported and do not only cover the staple cereals, for example cucumber, peach, sesame and lettuce (Liu and Yan 2019), however GWAS of crops that fit the definition of underutilised are in their infancy (see section 2.2).

*1.1.2 Nested-Association Mapping (NAM)*

NAM involves the development of multiple mapping populations sharing one parent, circumventing in part the issues related to traditional QTL mapping approaches only covering the variation present in two parents and the low power to tightly define QTL due to limited recombination events (McMullen et al. 2009). With this increased power (Bouchet et al. 2017), resources are being developed for a range of crops, and have provided candidate genes for a range of agronomic traits, for example flowering time in maize (Buckler et al. 2009), barley (Maurer et al. 2015) and sorghum (Bouchet et al. 2017), and plant architectural traits in maize (Brown et al. 2011) and durum wheat (Kidane et al. 2019). Many of these studies have confirmed previous work as well as identified novel QTL for follow-up, however, are currently restricted to only the main crops.

*1.1.3 Pangenomes*

It has become increasingly clear that across varieties of a crop, presence/absence variation is common; this means that any one reference genome contains only a subset of the species’ genome, potentially lacking causative loci (Della Coletta et al. 2021). Sequencing and assembling multiple varieties and adding novel genomic regions to the reference results in the pan-genome. Genes present in all accessions as ‘core’ and others ‘dispensable’. In some cases, half or less of some crop genomes are core (Gordon et al. 2017; Wang et al. 2018; Haberer et al. 2020), although these values are highly dependent on the number of accessions sequenced, and whether wild relatives are examined. This rare variation can underlie loci of agronomic importance, for example a flavour-related gene in tomato (Gao et al. 2019). Pangenomics has also revealed some important evolutionary genomic insight; core maize genes exhibit much greater expression than dispensable genes (Haberer et al. 2020), and dispensable regions tend to have higher transposable element (TE) content than core regions (e.g., Gao et al. 2019).

Most of the above studies have focussed on agronomic traits such as yield and its associated components (flowering time, plant stature and size), however because of ensuing climate change, a concerted effort to increase the study of climate change resilience phenotypes, for example root traits and stress response would be prudent. Whilst some studies have investigated this, for example using NAM to explore drought adaptive phenotypes in barley (Pham et al. 2019) and maize (Li et al. 2016), these are comparatively rare.

**1.2 Genome-assisted advances in staple crops**

Here we focus on rice and maize as two of the most widely grown staple crops, collectively grown on 360 M ha in 2019 (<http://faostat.fao.org>; accessed August 2021), to highlight how genomic advances have led to significant crop improvement for hundreds of millions of consumers.

*1.2.1 Genomic advances in rice*

Rice is one of the most important crops providing staple food for more than half of the world population. Due to the relatively small genome size (430 Mb), co-linearity with other cereals, a high efficiency genetic transformation system, and abundant genetic resource, rice has become a model grass species equivalent to the eudicot *Arabidopsis*. Significant efforts have been made to assemble and annotate the rice genome, for the *japonica* subspecies (cv. Nipponbare; Goff et al. 2002) and the *indica* subspecies (93-11; Yu et al. 2002). Compared to *Arabidopsis*, rice exhibits a gradient in GC content, which means a large proportion of rice genes have no obvious homolog in *Arabidopsis* (Yu et al., 2002).

Rice is an excellent candidate for population genomic analysis because of its extremely strong population structure and the large extent of LD owing to self-pollination. Resequencing of 527 rice landraces clearly separate the two cultivated subspecies and further divided these by latitudinal photoperiod and temperature clines (Huang et al. 2010). Genome analysis of 446 wild rice (*Oryza rufipogon*) accessions and 1083 cultivated varieties has identified a population of *O. rufipogon* in southern China where it appears that the domestication into the *japonica* subspecies took place; from there, hybridisation with local wild rice formed *indica* rice which spread into Southeast and South Asia (Huang et al. 2012). Combining genomic and phenotypic data through GWAS, a variety of loci associated with agronomic traits in rice have been identified (Supplementary Table 1).

Whilst mapping short sequence reads of other varieties onto one of the reference genomes can allow these types of analyses, this means that genomic regions absent from the reference will be ignored. Therefore, more recently the genomes of other varieties with beneficial agronomic traits (Zhao et al. 2018; Choi et al. 2020), weedy rice (Sun et al. 2019) and other species of *Oryza* (Li et al. 2020a) have been sequenced and assembled, forming a potential rice pangenome resource. A rice pangenome initiative, involving the comparison of 16 *de novo* assembled genomes from the main population genomic groups (sequenced and assembled using long reads and optical mapping, hence are described as ‘platinum’ genomes), showed that an average of 33.7 Mb of genome was absent among all pairwise comparisons (Zhou et al. 2020). This highlights how using one reference will only ever describe variation in a subset of the entire crop’s (pan)genome. It is worth noting that the majority (nearly 90%) of the presence/absence fraction of the rice pangenome is made up of TEs indicating these are more evolutionary labile, however the remaining 10% contains potentially protein-coding loci. These genome resources will promote evolutionary studies and the identification of adaptive genetic variation in rice.

*1.2.2 Genomic advances in maize*

Maize was domesticated from teosinte in southwestern Mexico *c*. 10,000 years ago. From its wild progenitor, maize has evolved a strikingly different morphology, forming an unbranched plant with large cobs and sweet naked kernels (Doebley 1990; Matsuoka et al. 2002). Since then, maize has been continuously improved, and an array of hybrid lines suitable for modern agricultural practice have been developed. In the past century, maize yield has increased eight-fold due to the increase of yield per plant and plant density adapted by harnessing heterosis. The ancestor genome of maize experienced a tetraploid intermediate stage (n=20), and then a series of chromosome fusion led to diploidisation and the recovery of the chromosome number n=10 (Schnable 2015). Thus, the maize genome is very large (Gaut and Doebley 1997) and is especially known for its array of TEs, indeed it is from maize that McClintock first hypothesised that some genetic elements could be mobile (McClintock 1950).

Using bacterial artificial chromosome and fosmid clones, the genome of maize variety B73 was assembled, and revealed that long-terminal repeat retrotransposons (LTRs) account for 74% of genome. Proliferation of the LTRs was the primary reason why the maize genome is so expanded relative to other grasses (Schnable et al. 2009). Resequencing of 17 wild relatives, 23 traditional landraces and 35 improved maize lines and mapping back to the B73 reference genome suggested that introgression from wild relatives could be responsible for diversity recovery in maize post-domestication and identified genes with diverse biological functions having been under selection during domestication (Hufford et al. 2012).

Although significant advances have been made in maize genome sequencing and population genomics, GWAS in maize is a challenge because the linkage disequilibrium (LD) decays within 2 kb. The development of the large NAM panel (McMullen et al. 2009) has significantly increased the efficiency of GWAS in maize, and loci associated with multiple agronomic traits have been identified (Supplementary Table 2).

Using single-molecule real-time sequencing and high-resolution optical mapping, an improved B73 genome was more recently assembled (Jiao et al. 2017). Due to significant structural variation among inbred lines, the genome of B73 alone is not sufficient to fully explain the variation among other inbred lines. Thus, the genome of other inbred lines including PH207 (Hirsch et al. 2016), W22 (Springer et al. 2018), Mo17 (Sun et al. 2018), HuangZaoSi (Li et al. 2019), small-kernel (Yang et al. 2019) and B73-Ab10, a variant of B73 containing Abnormal chromosome 10 (Liu et al. 2020b), have been assembled. This and other ongoing work will facilitate the understanding of maize genome diversity, as well as the breeding and improvement of maize.

**2. Genomics of underutilised crops to-date**

The genetic improvement of underutilised crops is, in part, constrained by limited genome resources. Recent developments in genome technology and the reduction of sequencing costs means genome-scale research is no longer limited to major food crops (Table 1).

**2.1 Reference genome sequences for underutilised crops and cross-crop comparisons**

The Poaceae (grasses) is the second largest plant family, with *c*. 12,000 species. Besides the staple crops rice, maize, wheat, and sugarcane, and some previously common cereals such as barley, oats and rye, the Poaceae also contains many underutilised crops, including sorghum, foxtail millet, finger millet and broomcorn millet that all use C4 photosynthesis, in which photorespiratory losses induced by hot and arid environments are reduced. The conversion of C3 rice and wheat towards C4 photosynthesis is a long-standing biotechnological goal. Comparative genomics has revealed that genes involved in C4 carbon fixation are all present in C3 plants (Zhang et al. 2012), and therefore the C4 pathway might have evolved from ancestral C3 isoforms. The panicoid grasses maize and sorghum show greater conservation of these genes compared to the pooid grasses rice and *Brachypodium* (Bennetzen et al. 2012). Further, a tandem duplication of the carbonic anhydrase Caβ subfamily, which hydrates atmospheric CO2 to bicarbonate in the mesophyll, was found in C4 plants, potentially vital for C4 evolution (Zhang et al. 2012). Genome comparisons between underutilised C4 crops and the staple C3 crops in the Poaceae will provide new suggestions for the evolution C4 photosynthesis, with the potential to improve the photorespiration efficiency and subsequent drought tolerance of other underutilised and staple crops.

The Fabaceae is the third-largest plant family, including many agronomically important grain and forage species. Legumes can improve soil fertility through the fixing of atmospheric nitrogen via root nodule-specific bacteria. The discovery of many genes involved in nitrogen fixing has been aided through the study of underutilised legume genomes (Jain et al. 2013; Lu et al. 2018; Zhuang et al. 2019). In addition, the legumes also contain species with unique nutritional features; for example, adzuki bean, widely cultivated in Asia, is referred to as the “weight loss bean” due to its sweet taste but low caloric and fat content. Genomic comparison to other legumes found that adzuki bean has fewer starch and fatty acid biosynthesis genes, which could play a role in its unique nutritional profile (Yang et al. 2015).

Several underutilised crops are advocated as worthy of investment because of their extreme stress resilience, often greater than staple crops (Cullis and Kunert 2017; Massawe et al. 2015). Further comparative genomics in the Poaceae has identified numerous gene family expansions associated with stress tolerance in underutilised crops, and these might explain the high stress resistance in underutilised crops. Drought tolerant foxtail millet and sorghum (compared to drought susceptible rice and maize) contain expansions of stress response genes, including those encoding cytochrome P450 proteins, expansins, lipid transfer proteins, and several others, as well as miRNA169 targeting drought stress-associated transcription factor nuclear factor-YB (Paterson et al. 2009; The International Brachypodium Initiative 2010). Tef, a drought tolerant cereal mainly distributed in Ethiopia, contains a tandem duplication of the nucleotidase/phosphatase *SAL1*, a gene family involved in drought tolerance, relative to other grasses investigated (Cannarozzi et al. 2014). Pearl millet possesses more members of cutin, suberin, wax biosynthetic and metabolite transporter genes, which might be responsible for the heat and drought tolerance in this underutilised crop (Varshney et al. 2017b). The number of BTB ubiquitin E3 ligases is greater in grasses than *Arabidopsis* and one subgroup, the BTB-BACK subgroup, was only expanded in the underutilised cereal broomcorn millet (Zou et al. 2019) which may contribute to the excellent stress tolerance. Clearly, genome comparison of these underutilised crops will provide a new pool of stress targeted genes for well-studied main crops. Similar results were found in the genus *Dioscorea*, in which draft genomes have been assembled for two yam species (Tamiru et al. 2017; Siadjeu et al. 2020), and phylogenetic analyses show that *Dioscorea* has more bulb-type lectin genes than the Poaceae and *Arabidopsis*, with potential roles in the insecticidal properties of Guinea yam (Tamiru et al. 2017).

In sum, reference genomes of underutilised crops can help resolve the genetic basis of agronomic traits, especially as a (sometimes unique) resource for improving the photorespiratory efficiency, nutritional value and stress tolerance of related major food crops currently challenged by climate change.

**2.2 Population genomics** **in underutilised crops**

Population genomics of underutilised crops can help researchers understand population structure and domestication history, as well as aid in identifying candidate genes modulating key agronomic traits through GWAS and to develop molecular markers for marker-assisted breeding (MAB; Figure 1).

*2.2.1 Identifying crop wild relatives and untapped resources*

The combination of genome resequencing and phylogenetic analysis enables us to better understand the population structure and identify wild relatives. For example, resequencing of 994 pearl millet lines identified four main clusters and pinpointed a West African origin of the crop (Varshney et al. 2017b). Resequencing of 166 fonio millet accessions and 17 proposed progenitors found a significant separation between cultivated and wild accessions, and the cultivated accessions were genetically closest to wild accessions from Southern Togo and West Guinea (Abrouk et al. 2020). Further, diversity of the grain size gene *GS5* was significantly reduced in fonio millet cultivars (with larger grains than the wild progenitor) suggesting human selection on this locus during domestication. Resequencing of 510 accessions of Tartary buckwheat from the entire global distribution identified three major clades and indicate two geographically distinct domestication events (Zhang et al. 2021). Similar investigations in other underutilised crops have identified wild relatives and genetic sub-populations of the domesticates, for example adzuki bean (Yang et al. 2015), lupin (Wang et al. 2021a; Hufnagel et al. 2020), and coix (Liu et al. 2020a). Resequencing of Guinea yam and its potential wild relatives resolved a hybrid origin from a cross between the wild rainforest species *D. praehensilis* and the savanna species *D. abyssinica* (Sugihara et al. 2020).

*2.2.2 GWAS and selection analyses*

The high-density single nucleotide polymorphism (SNP) data obtained from population-scale genome resequencing can be used to identify the genetic basis of adaptive traits through GWAS and selection analyses. From this, genetic markers can be designed and used for MAB. Beyond breeding, genetic modification-type approaches can be used to insert the candidate genes from a stress tolerant or otherwise novel underutilised crop into a susceptible or trait-lacking staple crop.

Seed size and weight are some of the most important traits of many crops, affecting price and milling qualities. GWAS of 368 cowpea accessions found candidate genes involved in endosperm development, embryo development and cell elongation associated with seed size, some of which also play a role in common bean (Lo et al. 2019). Similar analyses in castor bean identified candidate genes for seed traits that differentiate the wild and cultivated types (Xu et al. 2021). Recently, GWAS of Tartary buckwheat identified a mutation in the GCC cis-element of an *AP2* transcription factor associated with grain weight (Zhang et al. 2021).

Underutilised crops can possess multiple agronomic traits which are not present in staple crops, therefore present untapped resources for traits such as abiotic tolerances and novel nutrients. GWAS has been used to identify genes involved in tuber quality in cassava (Zhang et al. 2018b) and anthocyanin content in mungbean (Noble et al. 2018). Regarding stress tolerance, genes involved in lateral root development, stress tolerance and phosphorus use efficiency of mungbean have been identified (Reddy et al. 2020).

Comparing wild and domesticated cassava genomes has identified selective sweeps in genes involved in photosynthesis, starch accumulation and stress response (Wang et al. 2014). Extending this to other crops will facilitate the development of markers associated with domestication related traits. Candidate genes identified in underutilised crops through GWAS can help improve the quality and stress tolerance of not only the underutilised crops, but related staple crops, to better suit the needs of human beings in a changing climate.

Extended population genomics, for example using reduced representation technologies can be used to link genetic markers to agronomic traits, without knowing the precise genetic basis of the trait. Markers linked to several diverse agronomic traits in foxtail millet have been identified using these approaches, for example coloration, leaf size and shape, grain yield and weight, and flowering time (Upadhyaya et al., 2015; Jaiswal et al., 2019). Similarly, QTL mapping approaches at sufficient density can provide marker-trait associations, for example markers associated with yield and flowering in pea (Annicchiarico et al. 2017) and dormancy in groundnut (Kumar et al. 2020).

Genomics-assisted breeding of underutilised crops has been limited due to the lack of molecular markers linked to traits of interest, however the recent recognition of the importance of underutilised crops and the development of genome technology has clearly started to remedy this. The use of these markers to accelerate breeding (i.e., genomic selection) has been shown for a handful of underutilised crops (Ye and Fan 2020).

**2.3 Genetic transformation and gene editing in underutilised crops**

In recent years, genetic engineering has been widely used to elucidate gene function and for crop improvement. Compared with traditional hybridisation and crossing of varieties, genetic engineering could deliver agronomically useful traits into plant faster and in a more targeted manner. *Agrobacterium*-based transformation systems are widely used for genetic transformation in plants, facilitating the integration of foreign gene copies into the host plant’s genome. Although *Agrobacterium* transformation has been successfully used for transformation in several major crops, the inherent limitations associated with resistance to *Agrobacterium* infection and their recalcitrance to *in vitro* regeneration limit the transformation of many orphan crops. At present, *Agrobacterium*-mediated transformation has only been successfully transformation in shoot apex explants of finger millet ([Ceasar & Ignacimuthu, 2011](#_ENREF_4)) and foxtail millet ([Ceasar *et al.*, 2017](#_ENREF_3)), callus derived from mature seeds of finger millet ([Hema *et al.*, 2014](#_ENREF_9)), green millet ([Martins *et al.*, 2015a](#_ENREF_15); [Nguyen *et al.*, 2020](#_ENREF_19)), sorghum ([Zhao *et al.*, 2000](#_ENREF_24); [Belide *et al.*, 2017](#_ENREF_2)) and foxtail millet ([Santos *et al.*, 2020](#_ENREF_20)), embryonic axis explants of pigeonpea ([Ghosh *et al.*, 2017](#_ENREF_8)), germinated seedlings of chickpea ([Senthil *et al.*, 2004](#_ENREF_21)), and hairy roots of chickpea ([Aggarwal *et al.*, 2018](#_ENREF_1)) and buckwheat ([Mi *et al.*, 2020](#_ENREF_18)). Still, the recalcitrant tissue culture efficiency and occasional and unpredictable chimerism hinder the efficiency of these tissue culture-based methods.

Recently, using the floral-dip *Agrobacterium*-mediated transformation method, the wild ancestor of foxtail millet, green millet, was successfully transformed ([Martins *et al.*, 2015b](#_ENREF_16)). This is a significant advance because millets are model C4 grasses, and green millet it diploid, with a rapid life cycle, small genome size, simple growth requirements and high transformation efficiency.

Despite ongoing challenges of carrying out gene editing in even the best studied crops (Yang, 2020), CRISPR/Cas9-based gene editing has been conducted in underutilised crops with relatively high tissue culture efficiency, including green millet ([Weiss *et al.*, 2020](#_ENREF_23)) and sorghum ([Jiang *et al.*, 2013](#_ENREF_11); [Che *et al.*, 2018](#_ENREF_5)). These approaches will provide the necessary technical support for improving the efficiency of confirming the function of unique genes and the development of advantageous varieties of underutilised crops.

**3. The way forward**

**3.1 The successful transition from underutilised to mainstream**

In the past 20 years, a few previously underutilised crops, such as quinoa, chickpea and pigeonpea have seen a significant boost in research and recognition. For these crops we have seen a parallel 20% to 500% increase in the area grown worldwide between the 1960s and 2010s (<http://faostat.fao.org>; accessed August 2021). Chickpea and pigeonpea were among the first underutilised crops to have their genomes sequenced (Varshney et al. 2012; Varshney et al. 2013) with the (tetraploid) quinoa genome being made available more recently (Jarvis et al. 2017). Clearly the availability of genome sequence was a major stepping-stone in resolving the genetic basis of adaptive and agronomic phenotypes in these crops.

Using pigeonpea as an exemplar, this crop was recognised as worthy of significant investment in the 1970s, with the Pigeonpea Genomics Initiative (PGI) established in 2006 (Varshney et al. 2010). After genome sequencing (Varshney et al. 2012), significant advances have been made identifying genomic regions underlying adaptive traits which could be crossed between varieties using MAB (Varshney et al. 2017a); for example markers associated with sterility mosaic disease (Saxena et al. 2017a) and fusarium wilt (Saxena et al. 2017b). Genomic analysis has revealed less genes involved in lipid biosynthesis in pigeonpea than in soybean, and more cellulose synthesis genes, which together might underlie the biochemical and morphological differences between pigeonpea and other legumes (Singh et al. 2012). In addition, a pigeonpea gene involved in disease resistance was cloned and transferred to soybean, conferring resistance to Asian soybean rust (Kawashima et al. 2016), which would have been impossible without using the pigeonpea genome sequence.

More recent GWAS of nearly 300 pigeonpea accessions (Varshney et al. 2017a) identified dozens of associations and provides significant resources for MAB (Bohra et al. 2020). Pigeonpea is probably the only underutilised crop for which a pangenome has been sequenced (Zhao et al. 2020); this has 55,512 genes, compared to the reference genome (Varshney et al. 2012), which has only 53,612 (when annotated in exactly the same way as the pangenome). Using this pangenome, novel GWAS associations have been identified (Zhao et al. 2020) which were absent using the single reference genome (Varshney et al. 2017a). This further highlights the additional insights that can be made when a pangenome is made available.

Chickpea is grown and consumed worldwide, but 30 years ago could have been considered underutilised. Although productivity has steadily increased, the development of accessions with greater yield, improved nutrition and stress resistance are essential to meet the increasing demands. Comparative genomics of legumes has identified a lack of some resistance and nodulation genes, potential reasons for the low stress resistance (Jain et al. 2013; Varshney et al. 2013). Resequencing panels have identified genetic groups of cultivars (primarily the desi and kabuli types), identified the origin of the crop, and uncovered genes involved in drought tolerance and heat stress response through GWAS (Varshney et al. 2013; Varshney et al. 2019).

Several other previously underutilised crops are seeing a revolution in their investigation, suggesting they are on the path to escaping some of the reasons they were previously underutilised. The following examples are case studies of crop species early on this trajectory and provide ideas to circumvent issues such as large genomes and examples of crops with unique attributes which have received investment.

For species with polyploid genomes, investigations of related diploids can shed light on agronomic traits. Oat is nutritional crop containing abundant calcium, dietary fibre (especially β-glucan), and unsaturated fatty acids ([Joyce *et al.*, 2019](#_ENREF_12)). Due to the cholesterol-lowering properties and the antidiabetic effect of β-glucan, oat has been widely used to adjuvant treatment of diabetes and cardiovascular disorders. The rotation of oat with other crops can improve soil structure and reduce diseases in other crops. This disease resistance has been attributed to the production of avenacins, specialised antifungal metabolites. Oat is allohexaploid, with a relatively large, highly repetitive, and rearranged genome, thus brings challenges for genome assembly. The current sequencing has mainly focussed on wild diploid oats. For example, through genome assembly of the diploid extant progenitors, candidate genes regulating flowering time and disease resistance were identified ([Maughan *et al.*, 2019](#_ENREF_17)). Genome assembly of other diploid accessions identified a 12-gene cluster responsible for avenacin biosynthesis, and this cluster was located in a subtelomeric region which may have formed since oat diverged from other crops ([Li *et al.*, 2021](#_ENREF_14)). These results shed light on the evolution of oat and will help breeding oat varieties with modified and improved health benefits.

For other underutilised crops, they bring qualities and traits which are lacking in mainstream staple crops, and as such significant investment has begun to begin their escape from being underutilised. Quinoa is one example, a crop of the Chenopodiaceae, which has been cultivated for approximately 7000 years. Its diverse environmental adaptability means it is grown from the sea level of Chile to altitudes above 4500m in Bolivia ([Suárez-Estrella *et al.*, 2018](#_ENREF_22)). Due to its extraordinary balance of essential amino acids, and abundant vitamins, minerals, dietary fibre and unsaturated fatty acids, it was recognized as a complete food and has attracted the attention of the scientific community ([Filho *et al.*, 2017](#_ENREF_7)). However, quinoa contains bitter and astringent anti-nutritional factors such as saponins. Although these substances are health-promoting, their bitter taste still limit the utilization of quinoa (Suárez-Estrella et al., 2018). Thus, selection of genotypes with low saponin content is one of the most important quinoa breeding objectives for the future. In addition, due to the outcrossing nature, genome assembly of quinoa was not trivial, requiring repeated self-pollination to reduce heterozygosity (Yasui et al., 2016a). Analysis of the subsequently assembled quinoa genome (Yasui et al. 2016a) identified expansions of gene families involved in lysine, vitamins, polyphenol and betalain synthesis, as well as ABA signalling, which together may relate to the unique nutritional and anti-nutritional factors profile and abiotic stress tolerance in quinoa (Yasui et al. 2016a; Zou et al. 2017).

Another example of an underutilised crop with novel attributes is buckwheat, a pseudocereal originating from and domesticated in China more than 4000 years ago (Zhang et al., 2021). This crop possesses outstanding nutritional profile (especially flavonoids) and an excellent ability to grow under adverse climatic and soil conditions. The main cultivated species are common buckwheat and Tartary buckwheat. Similar to quinoa, being outcrossing makes genome sequencing of common buckwheat more challenging and required repeated self-pollination to reduce heterozygosity (Yasui et al. 2016b). In contrast to common buckwheat, the sequencing of Tartary buckwheat was relatively simple because of a smaller genome and being predominantly a selfer. Comparative genomics using the chromosome-scale Tartary buckwheat genome, revealed a whole-genome duplication event after buckwheat divergence from sugar beet with some evidence this might play a role in buckwheat tolerance of extremely harsh environments (Zhang et al. 2017). Genome resequencing of Tartary buckwheat identified two independent domestication events, in southwestern and in northern China, which has resulted in the diversity of modern Tartary buckwheat varieties (Zhang et al., 2021). Candidate genes responsible for flavonoid biosynthesis were also identified and will help buckwheat breeding with improved health and medical benefits.

Given these findings from the significant investment and the ongoing work in representative orphan crops (Roorkiwal et al. 2020), we feel encouraged that the resources and investment needed for these crops to be elevated to the national stage are in place. However these are only the tip of the underutilised crop iceberg; dozens of underutilised crops have a single reference genome, and in some cases small resequencing panels (Table 1) but significant population and GWAS resources or pangenomes are absent for the vast majority.

**3.2 What do we need and why?****The advantages of going beyond a reference genome**

To efficiently breed improved varieties of underutilised crops we need to have reliable linkage between genetic markers and traits of interest. Markers identified in a single QTL mapping experiment may not be reliable given many QTL are only expressed in some environments (genotype x environment interaction) and do not always tightly define the genomic region (therefore the QTL spans dozens or hundreds of genes). More precision can be gleaned from LD mapping approaches (Thornsberry et al. 2001), including GWAS, which requires extensive panels of germplasm and high marker density. A reference genome is an asset to begin to understand important and adaptive phenotypes in underutilised crops, yet it is becoming clear that significant advances in breeding improved varieties are only possible when the genomic variants are identified, thus requiring a population of genomes and potentially a pangenome.

*3.2.1 Quality trait-marker linkage*

One main advantage to having population level sequencing is to tie this to trait data using GWAS-type approaches. This is an efficient way to start to narrow down the genetic basis of quantitative traits such as yield, seed and organ size, plant stature and so on, all traits which need to be optimised to ensure a crop is cost-effective to be grown at scale (Figure 2). A reference genome is an asset, but without the resequencing (or high-density SNP genotyping), GWAS cannot be done. Examples of GWAS-style analyses in the underutilised crops cowpea, castor bean, Tartary buckwheat, cassava and mungbean are given above.

Using reduced-representation technology (e.g., genotyping-by-sequencing, or restriction site-associated DNA sequencing) is an efficient way to screen large numbers of genetic loci throughout the genome at lower cost than resequencing. The downside being that unless LD extends for very long distances, most markers will be so widely spaced that they will be too far from the underlying causative loci to be associated. Nevertheless, these approaches have yielded marker-trait associations (MTAs) in some underutilised crops and pave the way for more in-depth analyses. For example, in Proso millet (*Panicum milaceum* L.) 13 MTAs for seven traits were resolved, however no MTAs were found for another nine traits (Boukail et al. 2021). In foxtail millet, 81 MTAs for ten traits were resolved, however most did not pass false discovery rate correction (Jaiswal et al. 2019), and in Kersting’s groundnut, ten MTAs for five traits were resolved (Akohoue et al. 2020). It is important to bear in mind that because of the marker spacing, partly due to the location of cut sites in the genome, and partly because of uneven sequencing coverage across loci (Beissinger et al. 2013), these studies are likely to only report a subset of genomic loci involved in the traits of interest.

*3.2.2 Cross-crop analyses*

Whilst underutilised crops may lack some desirable traits (fast growth, ease of harvest, high harvest index), or have additional phenotypes that are unwanted (antinutrients, perenniality), significant advances have been made in understanding the genetic basis of many of these traits in other crops (Figure 2). Thus, where these traits have been studied in detail, there may be candidate genes that can be followed up if population resequencing or pangenomic data are available in the underutilised crop.

Several underutilised crops would benefit from having more predictable flowering/fruiting or being adapted to novel environments where the daylength is different. The legume lablab is typically a short-day plant therefore expansion outside its native tropical latitudes is unlikely to be successful (Sennhenn et al. 2017). Bambara groundnut, another tropical underutilised legume, is typically short-day although a few semi-improved varieties can be grown further from the equator, however it is acknowledged that this is still a barrier to more widespread adoption (Mayes et al. 2019). Daylength response (and therefore flowering time) is relatively well-studied in staple crops, including rice, maize and the typically long-day legumes, lentil and pea (Weller et al. 2012; Itoh and Izawa 2013; Hung et al. 2012), offering candidate genes for the development of underutilised cereal and legume varieties for adaptation to non-native latitudes. Candidate genes, or genomic regions, underlying annual vs perennial growth have been identified in Brassicaceae species (Kiefer et al. 2017; Heidel et al. 2016); this is another trait which might help the adoption of underutilised crops.

An often-cited reason for the poor adoption, or decline in use, of underutilised crops is their antinutrient content. Antinutrient factors (ANFs) inhibit the uptake of beneficial minerals and vitamins, therefore a high nutrient crop with high ANF content will have low nutrient bioavailability. This is especially the case in legumes where several ANFs have been identified that affect iron, zinc and protein uptake. Whilst cooking and fermentation can reduce the presence of these compounds (e.g., (Samtiya et al. 2020)) these take time or energy (e.g., fuel for cooking). However, ANFs are usually vital for crop disease resistance, therefore breeding for high ANF during the growth period coupled with low ANF in the maturation period would clearly be advantageous. Progress has been made understanding the genetic basis of these traits (Sparvoli and Cominelli 2015; Campion et al. 2013) therefore opening the door for understanding the genetic basis of these traits in underutilised crops.

There are other traits which make underutilised crops less attractive as a choice for a farmer or the consumer, for example poor shelf-life, unpleasant taste, or lengthy cooking times (and an increase cost for fuel). Genes involved in shelf life in tomato have been elucidated (Casals et al. 2012; Zhang et al. 2018a), along with QTL for alkaloid content in lupin (Rychel and Książkiewicz 2019), and for seed hardness, and therefore cooking time, in legumes (Sandhu et al. 2018; Diaz et al. 2021).

Relatedly, many underutilised crops are known for their extreme resilience phenotypes. Any analysis of the genetic basis of drought or heat tolerance in any underutilised crops, likely requiring population sequencing for e.g., GWAS, will be of significant value to other more mainstream crops. This could resolve novel alleles or even undercover novel genes and pathways involved in these climate-change relevant tolerances. The sequencing of one reference genome of an underutilised crop cannot offer this.

Population level resequencing mapped to one reference will not be able to examine the fraction of the genome that is only present in some accessions (presence-absence variation lacking from the sequenced reference which would only be identified in a pangenome). This problem could be underestimated for underutilised crops where variation in genome size might not be recognised; for example, the underutilised legume lablab was likely domesticated twice (Maass et al. 2017; Robotham and Chapman 2015), and the two gene pools differ in genome size by ~20% (MAC, unpublished).

*3.1.3 Next steps*

We propose that efforts should be made to not only generate a reference genome but carry out population level sequencing and pangenomics. In parallel we encourage the continued collection and long-term archiving of seed resources, and addressing the challenges associated with archiving the required indigenous knowledge associated with these under-investigated species (Kamenya et al. 2021; Mabhaudhi et al. 2017). Researchers should make data free to use, and collaborations between institutes worldwide encouraged to expedite the production of results and limiting unnecessary overlap and wasted resources.

Whilst the cost and time implications of multiple reference genomes, resequencing, and collecting global germplasm are not trivial, we believe that, given the climate crisis and the need to fast-track the development of mainstream and novel crops, this is the most reliable way to ensure that underutilised crops are investigated in the depth at which reliable and meaningful data can be used. It is likely that some underutilised crops hold vital genetic variants to help the human population combat food insecurity in the next few decades; this genetic erosion is under-investigated even in staple crops (Khoury et al. 2022). Without fully investigating underutilised cropgenomes, we do not know where these variants lie, and if we delay too long, we may lose alleles, varieties and crops entirely.

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**Author contributions**

MAC, YH and MZ researched the topic and wrote the manuscript.

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**Table S1. List of important traits dissected by GWAS in rice**

**Table S2. List of important traits dissected by GWAS in maize**

**Table 1 – Underutilised crops for which reference genomes are available. Crops are organized into families (subfamilies) and the genome statistics are given.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Species** | **Common name** | **Chromosome No.** | **Estimated genome size** | **Sequencing method1** | **Scaffold N50** | **Number of contigs** | **Assembled scaffolds size** | **References** |
| Poaceae (Pooideae) | *Secale cereale* | Rye | 2n=2x=14 | 7.92 Gb | H2000 | 9.4 Kb | 1,581,707 | 2.80 Gb | Bauer et al. 2017 |
| *Aegilops tauschii* | Wheat (D-genome) | 2n=2x=14 | 4.36 Gb | H2000 | 58.0 Kb | 179,145 | 4.23 Gb | Jia et al. 2013 |
| Poaceae(Chloridoideae) | *Eleusine coracana* | Finger millet | 2n=4x=36 | 1.45 Gb | H4000, N500 | 23.7 Kb | 525,759 | 1.20 Gb | Hittalmani et al. 2017 |
| 1.5 Gb | NS500, PB | 905.3 Kb | 2,812,919 | 1.20 Gb | Hatakeyama et al. 2018 |
|  | *Eragrostis tef* | Tef | 2n=4x=40 | 772 Mb | H2000, 454 | 85.0 Kb | 　 | 672 Mb | Cannarozzi et al. 2014 |
| 622 Mb | PB, H4000, Hi-C | 1.6 Mb | 1344 | 576 Mb | VanBuren et al. 2020 |
| Poaceae(Panicoideae) | *Setaria italica* | Foxtail millet | 2n=2x=18 | 510 Mb | GAII | 12.3 Mb | 　 | 397 Mb | Bennetzen et al. 2012 |
| 490 Mb | GAII, H2000 | 1.0 Mb | 16,903 | 423 Mb | Zhang et al. 2012 |
|  | *Setaria viridis* | Green millet | 2n=2x=18 | 500 Mb | PB, H2000 | 11.2 Mb  | 75 | 395 Mb | Mamidi et al. 2020 |
| 401 Mb | ONT, NS500 | 19.5 Mb | 44 | 397 Mb | Thielen et al. 2020 |
|  | *Cenchrus americanus* | Pearl millet | 2n=2x=14 | 1.79Gb | H2000, PB | 885.0 Kb | 175,708 | 1.79 Gb | Varshney et al. 2017b |
|  | *Panicum miliaceum* | Broomcorn/Proso millet | 2n=4x=36 | 887 Mb | PB, X-ten, BN, Hi-C | 8.24 Mb | 1308 | 848 Mb | Shi et al. 2019 |
| 1 Gb | X-ten | 89 Kb | 171,982 | 823 Mb | Ott et al. 2018 |
| 923 Mb | PB, H2500 | 46.7 Mb | 5,541 | 855 Mb | Zou et al. 2019 |
|  | *Echinochloa crus-galli* | Barnyard millet | 2n=6×=54 | 1.38 Gb | H2000, PB  | 1.8Mb | 　 | 1.27 Gb | Guo et al. 2017 |
| PB, H4000 | 4.1 Mb | 　 | 1.34 Gb | Ye et al. 2020 |
|  | *Digitaria exilis* | Fonio millet | 2n=4×=36 | 893Mb | H2500, No6000, Hi-C, BN | 10.7 Mb | 29,155 | 716 Mb | Abrouk et al. 2020 |
| PB, H3000, H4000 | 1.73 Mb | 3329 | 761Mb | Wang et al. 2021b |
|  | *Coix lacryma-jobi* | Adlay/Job's tears | 2n=2×=20 | 1.68 Gb | H2000 | 　 | 　 | 　 | Cai et al. 2014 |
| PB, H2500 | 2.24 Mb | 4519 | 1.62 Gb | Guo et al. 2020 |
| PB, H2500 | 594.3 Kb | 13,691 | 1.28 Gb | Kang et al. 2020 |
| PB, H2000, BN, Hi-C | 14.0 Mb | 3321 | 1.73 Gb | Liu et al. 2020a |
|  | *Sorghum bicolor* | Sorghum | 2n=2x=20 | 730Mb | BAC | 35 Mb | 12,873 | 679 Mb | Paterson et al. 2009 |
| BAC, H2500 | 68.7 Mb | 2688 | 655 Mb | McCormick et al. 2018 |
| Fabaceae | *Cajanus cajan* | Pigeonpea | 2n=2x=22 | 833 Mb | BAC, GAII, H2000 | 516.1 Kb | 173,708 | 606 Mb | Varshney et al. 2012 |
| BAC, 454 | 14.0 Kb | 332,766 | 511 Mb | Singh et al. 2012 |
|  | *Cicer arietinum* | Chickpea | 2n=2x=16 | 738 Mb | BAC, GAII, 454 | 77.3 Kb | 　 | 520 Mb | Jain et al. 2013 |
| BAC, H2000, BAC | 40.0 Mb | 62,619 | 532 Mb | Varshney et al. 2013 |
| 454, GAII | 39.9 Mb | 182,734 | 510 Mb | Parween et al. 2015 |
|  | *Vigna radiata* | Mungbean/ Green gram | 2n=2×=22 | 543Mb | H2000, 454 | 1.52 Mb | 180,372 | 431 Mb | Kang et al. 2014 |
|  | *Vigna. angularis* | Adzuki bean | 2n=2×=22 | 542 Mb | H2000 | 1.3 Mb | 25,426 | 467 Mb | Yang et al. 2015 |
| 612 Mb | H2000, 454 | 703 kb | 36,516 | 443 Mb | Kang et al. 2015 |
|  | *Vigna unguiculata* | Cowpea | 2n=2×=22 | 640 Mb | H2000, BAC, PB | 16.4 Mb | 765 | 519 Mb | Lonardi et al. 2019 |
|  | *Lupins albus* | White lupin | 2n=2x=50 | 584 Mb | PB, H2000, Hi-C | 18.7 Mb | 3171 | 474 Mb | Xu et al. 2020 |
| PB, H3000, BN | 17.4 Mb | 　 | 451 Mb | Hufnagel et al. 2020 |
|  | *Lupinus angustifolius* | Narrow leafed lupin | 2n=2x=40 | 　 | H2500 | 703.2 KB | 14,379 | 609 Mb | Hane et al. 2017 |
|  |  |  | 　 | PB, H2000 | 30.8 Mb | 123 | 616 Mb | Wang et al. 2021a |
|  | *Vigna mungo* | Blackgram | 2n=2x=22 | 574 Mb | X-ten and ONT | 1.4 Mb | 　 | 475 Mb | Jegadeesan et al. 2021 |
|  | *Trifolium subterraneum* | Subterranean clover | 2n=2x=16 | 540 Mb | H2000, M, 454 | 287.6 Kb | 101,010 | 472 Mb | Hirakawa et al. 2016 |
| BN | 1.4 Mb | 264 | 512 Mb | Kaur et al. 2017 |
| Polygonaceae | *Fagopyrum esculentum* | Common buckwheat | 2n=2x=16 | 1.2 Gb | H2000 | 25.1 Mb | 　 | 1.18 Gb | Yasui et al. 2016b |
|  | *Fagopyrum tataricum* | Tartary buckwheat | 2n=2x=16 | 540 Mb | H2000, H2500, M, PB, GBS | 550.7 Kb | 8778 | 489.3 Mb | Zhang et al. 2017 |
| Amaranthaceae | *Chenopodium quinoa* | Quinoa | 2n=4x=36 | 1.5Gb | H2500, PB | 86.9 Kb | 110,092 | 1.1 Gb | Yasui et al. 2016a |
| PB, BN | 3.8 Mb | 4232 | 1.18 Gb | Jarvis et al. 2017 |
| H2500, PB | 1.2 Mb | 10,795 | 1.3 Gb | Zou et al. 2017 |
| Euphorbiaceae | *Manihot esculentum* | Cassava | 2n=2x=36 | 746 Mb | H2000, 454, BAC | 67 Kb | 　 | 432 Mb | Wang et al. 2014 |
| *Ricinus communis* | Castor bean | 2n=2x=20 | 320 Mb | Plasmid, Sanger | 561.4 Kb | 25,800 | 325 Mb | Chan et al. 2010 |
| Convolvulaceae | *Ipomoea batatas* | Sweet potato | 2n=6x=90 | 4.4 Gb | H2500, N500, H4000, 454 | 200.7 Kb | 35,919 | 836 Mb | Yang et al. 2017 |
| Dioscoreaceae | *Dioscorea dumetorum* | Trifoliate yam | 2n=2x=36 | 322 Mb | H1500, ONT | 3.2 Mb | 1172 | 485 Mb | Siadjeu et al. 2020 |
| *Dioscorea rotundata* | White Guinea yam | 2n=2x=40 | 579 Mb | H2500, BAC | 2.1 Mb | 4723 | 594 Mb | Tamiru et al. 2017 |

1 Sequencing approaches are abbreviated as follows: 454, Roche 454; BAC, Bacterial Artificial Chromosome sequencing; BN, BioNano; GAII, Illumina Genome Analyzer II; H, Illumina Hiseq; Hi-C, high-throughput chromosome conformation capture; M, Illumina Miseq; N500, NextSeq 500; No6000, Novaseq6000; ONT, Oxford Nanopore Technologies; PB, PacBio; X-ten, Illumina X-ten.

**Figure 1 – Schematic diagram highlighting the main sequencing and breeding approaches discussed in this article.** Firstly (left), by comparing the reference genomes of underutilised crops and staple/main crops, genome variants responsible for superior agronomic traits (such as specific resistance and nutrient quality or quantity) of underutilised crops could be explored. In addition (right), the combination of genome resequencing and phenotyping through genome wide association study could help identifying candidate genes responsible for agronomic traits of underutilised crops. Through genetic transformation or genome editing, the function of these candidate genes could be verified. Finally, by associating genomic data to phenotypic information of different accessions, germplasm resources can be effectively screened and bred by means of molecular marker-assisted breeding and crossing, to improve the resistance and nutritional value of underutilised crops in addition to staple crops.

**Figure 2 – Schematic diagram highlighting common breeding targets for any crop, and whether the genetic basis has been investigated in underutilised crops (UCs) and/or staple crops.** ANF, Anti-nutrient factor.

Fig 1

Fig 2

