



POPULAR ARTICLE

Maize reimagined: using genomics to grow nutrition and yield together

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Intricacies of the subject

Maize is an important cereal crop for food, feed and nutritional security, but conventional breeding has often focused primarily on yield, with limited attention to grain nutritional quality. This has contributed to the persistence of hidden hunger caused by deficiencies of essential micronutrients and quality proteins. Genomics-assisted breeding provides effective approaches for improving nutritional traits while maintaining yield potential. Marker-assisted selection and marker-assisted backcrossing have facilitated the improvement of provitamin A through favourable crtRB1 and lcyE alleles and enhanced protein quality through the opaque-2 (o2) gene and its modifier genes. For complex traits such as grain iron and zinc concentration, GWAS and genomic selection offer opportunities to identify useful genomic regions and predict breeding values using genome-wide marker information. These approaches can also help reduce linkage drag and identify favourable combinations of yield and nutritional traits. Emerging technologies such as CRISPR/Cas9 genome editing, multi-omics and speed breeding further expand the possibilities for accelerating nutritional improvement in maize. Integrating these tools with conventional breeding, field evaluation and efficient seed

delivery can support the development of biofortified maize that combines improved nutritional value with competitive yield and farmer acceptability.

Introduction

Walk through a maize field in Karnataka or Bihar during grain fill, and you'll see something that looks like agricultural success. Tall, uniform stands. Cobs swelling with kernels. A farmer's calculation of quintals per acre already running in his head. By every metric that mattered to the Green Revolution, this field has done its job. But crack open one of those kernels and look closer. The endosperm is often pale, starchy, and metabolically empty in ways that don't show up on a weighing scale. It can feed a family for a week and still leave a toddler stunted, an anaemic mother exhausted and an entire household technically "food secure" while being nutritionally poor. This is the paradox India has been living with for decades with full stomachs, hidden hunger. The conversation is finally shifting from a Hungry India, obsessed with tonnage, to a Healthy India, where a kilogram of grain is judged by what it delivers, not just how much of it there is. Maize sits right at the centre of this shift. It's the third-largest cereal crop in the country, increasingly



consumed as food, feed, and now poultry ration, and it happens to be genetically flexible enough to carry meaningful nutritional upgrades. The catch has always been the same one that haunts every breeding program: can you fix the nutrition without wrecking the yield farmers actually get paid for?

The hidden hunger problem

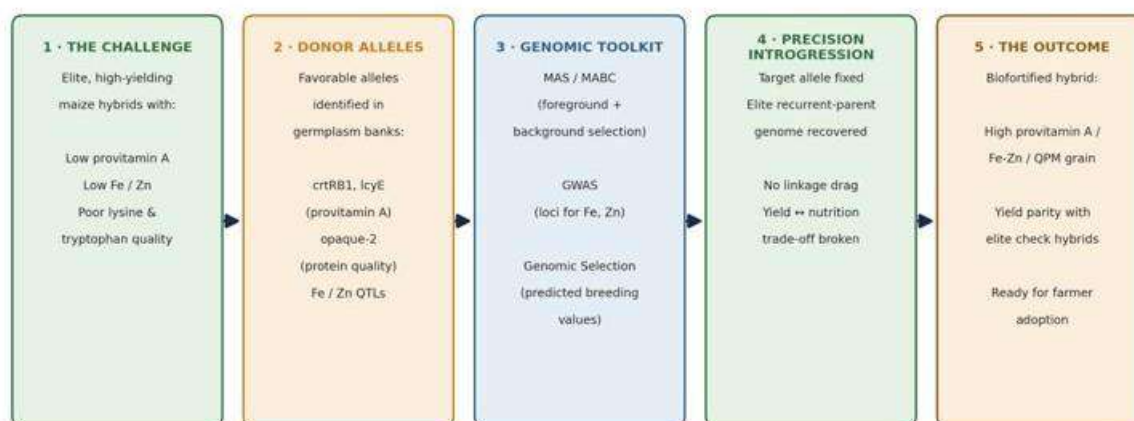
Hidden hunger is a deceptively gentle term for a brutal reality. It refers to micronutrient deficiencies that don't announce themselves the way a famine does no visible signs, just a slow erosion of immunity, cognition, and growth. Vitamin A deficiency remains a leading cause of preventable childhood blindness in India. Iron deficiency drives anaemia rates that are still uncomfortably high among women and children. Zinc deficiency quietly undermines immune function and stunts growth. And the protein maize traditionally offers poor in lysine and tryptophan the amino acids a growing child actually needs which is where Quality Protein Maize, or QPM, enters the picture. Conventional breeding could, in theory, fix all

of this. It has, in fact, delivered real progress over the decades. But conventional selection for a trait like kernel provitamin A content is slow and unreliable, because the biochemical assay needed to measure carotenoid levels is destructive, expensive, and has to be repeated across generations. You can't just look at a cob and know its beta-carotene content. Each backcross generation demands lab time, and each cycle of selection can take a full season. Stack that against the six to eight generations typically needed to introgress a trait into an elite background, and you're looking at a program that could easily eat up a decade by which point the "elite" recipient line may no longer be elite at all. Nutritional breeding needed a shortcut. Genomics gave it one.

The genomic toolkit: current trends

Marker-Assisted Selection and Marker-Assisted Backcrossing (MAS/MABC) turned the provitamin A story around almost single-handedly. The discovery that a specific favourable allele at the crtRB1 gene could triple or quadruple provitamin A concentration in the kernel without needing a biochemical

Figure 1. A graphical overview of the genomics-assisted biofortification pipeline in maize



assay at every step was a genuine breakthrough. Breeders could now genotype seedlings with a simple marker test, identify which plants carried the favourable crtRB1

allele, and discard the rest before wasting field space or time on them. Add the lcyE gene, which controls the branch point in the carotenoid pathway between the beta and



alpha branches, and you get a stacking strategy: favourable alleles at both loci push flux firmly toward beta-carotene accumulation. CIMMYT and Indian public-sector programs, including ICAR-IIMR, have used exactly this pairing to convert popular hybrid backgrounds into biofortified versions without starting from scratch. QPM improvement tells a similar story. The opaque-2 (o2) gene, when introgressed alongside modifier genes that restore normal kernel hardness, converts a soft, chalky endosperm into one with roughly double the lysine and tryptophan of ordinary maize, while keeping the kernel texture farmers and millers expect. Markers linked to o2 let breeders confirm the recessive allele is homozygous without waiting for a full protein assay, cutting years off conversion timelines. Iron and zinc are a tougher problem, because they aren't controlled by one or two genes with large effects instead, they're quantitative traits, shaped by dozens of loci each contributing a small amount, and heavily influenced by soil and environment. This is exactly the kind of complexity where Genome-Wide Association Studies (GWAS) earn their keep, scanning diverse maize panels to flag genomic regions associated with grain Fe and Zn concentration. And because no single marker will ever capture that kind of polygenic architecture, Genomic Selection (GS) has become the more practical tool going forward with using genome-wide marker data to predict breeding values for micronutrient density before a single kernel is harvested, compressing selection cycles and letting breeders juggle multiple traits at once rather than chasing them sequentially.

Breaking the negative correlation

Here's the part that used to keep breeders up at night: nutrient density and yield have historically pulled in opposite directions. Push hard on protein or micronutrient accumulation

in the grain, and total starch and therefore yield can quietly slip. This isn't superstition; it reflects real resource allocation trade-offs within the developing kernel. Genomics doesn't wave a magic wand over this problem, but it does something almost as valuable: it lets breeders be precise instead of blunt. Traditional introgression by phenotypic selection often dragged along large chunks of donor chromosome linkage drag carrying undesirable genes right alongside the target trait, silently depressing yield in the recovered lines. Marker-assisted backcrossing solves this through foreground and background selection simultaneously: foreground markers confirm the target allele is present, while background markers across the rest of the genome confirm that everything else has been recovered from the elite, high-yielding recurrent parent. The result is a converted line that is genetically almost identical to its high-yielding parent, plus the one nutritional upgrade not a compromise between two parents' worth of traits. Genomic selection adds another layer of untangling. By modelling yield and nutrient density as separate but simultaneously predicted traits, breeders can identify the rare recombinant individuals where the genetic correlation has effectively been broken the lines that carry favourable, non-deleterious alleles for nutrition without the yield-penalizing baggage historically linked to them. It's less about fighting biology and more about being selective enough to find where biology already offers an exit.

Future prospects: the next frontier

MAS and GS are the current workhorses, but the tools coming up behind them are sharper still. CRISPR/Cas9 genome editing offers something backcrossing never could: the ability to tweak a gene in place, in an already-elite background, without introducing a single base pair of unwanted donor DNA. Editing regulatory regions of carotenoid pathway



genes, or fine-tuning opaque-2 modifiers directly, could deliver biofortification in a fraction of the generations MABC requires as assuming India's regulatory environment for gene-edited crops continues to evolve. Multi-omics integration through layering transcriptomics, metabolomics, and genomics together is starting to reveal not just which genes matter, but which regulatory networks control nutrient flux under real field stress, which is a very different question from what a single-trait GWAS can answer. Speed breeding, using extended photoperiods and controlled environments to force multiple generations per year, is a logistics innovation more than a genomic one, but paired with genomic selection it means the years-long introgression pipeline of the past could realistically shrink to a handful of seasons.

The way forward

None of these matters if it stays in a research paper. Biofortified maize succeeds or fails on a farmer's field, and farmers adopt hybrids for one reason above all others yield parity with

what they're already growing. Every genomics tool discussed here exists, in the end, to protect that non-negotiable condition. That means public breeding institutions and private seed companies need to keep working the same problem from both ends: public programs doing the discovery-stage marker work and germplasm conversion, private partners scaling hybrid seed production and distribution. Policy needs to catch up too faster varietal release pathways for biofortified hybrids, procurement incentives that reward nutrient density the way MSP currently rewards volume, and public awareness campaigns that help consumers actually recognize and value an orange-kerneled, provitamin-A-rich maize instead of assuming it's simply a different, lesser crop. The technology to grow nutrition and yield together, in the same cob, already exists. What's left is largely a question of institutional will getting these converted hybrids out of trial plots and into the hands of the farmers who'll decide, season after season, whether Healthy India and productive India can finally be the same field.

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