PHASESPACE DESIGN LAB / CURRENT INVESTIGATIONS

Can We Increase Potato Protein Without Losing the Potato?

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IN BRIEF

An extra helping of protein sounds like a simple improvement to a potato, until one asks what kind of protein, where it accumulates, and what might have to change to make it. Our goal is at least **10% more edible true-protein yield** without losing the potato's yield, cooking qualities, storability, or safety. We have followed genetic approaches and microbial partnerships into sweet potato, cassava, yam, and mashua, and encountered a surprisingly wide range of reported protein concentrations among Colombian *papa criolla* genotypes. Our own work so far consists of a literature and environmental scan, comparative evidence curation, and screening calculations, not a newly field-tested high-protein potato. We are especially interested in where acquired nitrogen goes, and how much its route into tuber protein depends on the potato, its microbial companions, or their interaction.

A familiar potato, and a surprisingly elastic number

The turn that changed the project came from a potato already familiar to Colombian cooks. In a study of whole, boiled tubers, researchers examined 113 genotypes of *Solanum tuberosum* Group Phureja, the group to which many Colombian *papas criollas* belong. Across the collection, the highest reported crude-protein concentration was nearly ten times the lowest. This unexpected spread made us wonder how much protein a potato can accumulate before we introduce any new intervention at all.[1]

One accession, CCC-76, reached 17.2 ± 0.3 grams of reported protein per 100 grams of dry tuber; another, NC-8, reached 16.7 ± 0.7. The collection as a whole ranged from 1.8 to 17.2, while commercial controls reached 3.1–9.5.[1] These are **crude protein estimates**, derived from total nitrogen, not direct measurements of the protein molecules present. Even so, the variation is striking. Does one potato acquire more nitrogen? Does it move a larger share into the tuber? Does it convert that nitrogen into useful protein more effectively? Or does a microbial partner help it do some of this work?

That was not quite where we began. Our original question was whether a potato might deliver **at least 10% more edible tuber true protein per hectare**, while retaining its characteristic yield, starch and dry matter, cooking behavior, storability, disease resilience, and food safety. We started by thinking about genes and storage proteins. A little later we encountered bacteria that supply or mobilize nitrogen. Later still, high-protein Andean genotypes made it difficult to avoid the possibility that the potato itself was already doing much of the relevant work.

A note about the word “protein”

“More protein” can mean more protein per gram of dry tuber, more protein per fresh serving, or more protein from a hectare of land. These are different achievements. A genotype with greater protein concentration but fewer marketable tubers may provide less edible protein overall. Nitrogen analysis creates another ambiguity: nitrate, free amino acids, and other non-protein nitrogen can contribute to a Kjeldahl or Dumas result, even when the analytical convention translates total nitrogen into “crude protein” using a conversion factor.

Our primary outcome is therefore **edible true-protein yield (kg/ha)**, accompanied by measured protein composition and amino-acid quality. In practical terms, that yield is the marketable fresh-tuber yield multiplied by the edible fraction, the dry-matter fraction, and the true-protein fraction of dry matter. Alongside it we would measure total and marketable tuber yield, starch, reducing sugars, glycoalkaloids, cooking texture, storage losses, and disease responses. This is what “without losing the potato” means operationally. A result is interesting only if both the nutritional numerator and the ordinary uses of the crop survive inspection.

Three quite different precedents

A 2010 study by Chakraborty and colleagues expressed an amaranth seed albumin, AmA1, in seven potato genetic backgrounds. The authors reported approximately 24–60% higher nitrogen-derived total-protein values in selected transgenic tubers, accompanied by protein-expression and proteomic evidence, changes in several essential amino acids, and moderate yield gains in promising lines.[2] This tells us that a potato tuber can accommodate a substantially altered protein economy. It does not settle the culinary, storage, regulatory, or cultivar-transfer questions for our project.

A second approach came from work by Tahir Naqqash, Asma Imran, Sohail Hameed and their colleagues, associated chiefly with NIBGE in Faisalabad and later also with Bahauddin Zakariya University in Multan. TN09 was not a one-off isolate. In 2016, the collaborators reported potato-rhizosphere strains TN10, TN14, TN36, TN38 and TN42, testing their plant-growth-promoting traits and nitrogen-fixing activity. The names show that the TN series extended at least to TN42; they do not establish how many isolates were collected or how many remain viable. TN09 is therefore one investigated member of a wider experimental effort rather than a solitary lucky strain.[14]

In the 2022 TN09 paper itself, two *Azospirillum* strains, TN03 and TN09, were isolated from potato-associated material; both showed nitrogen-fixing traits, and pot experiments using nitrogen isotopes supported biological nitrogen fixation. Microscopy placed TN03 mainly outside root cells and TN09 within them.[3] In two field sites, the treatment with TN09 and a reduced fertilizer dose was associated with 13.93–15.59% greater tuber dry weight and 10.44–10.57% higher tuber nitrogen concentration **relative to the study’s uninoculated, zero-nitrogen negative control**. Multiplying those published percentage changes yields an exploratory *tuber-nitrogen-yield proxy* of roughly 25.8–27.8%. This is a Phasespace arithmetic proxy, not a directly measured protein result, and it should not be attributed to the bacterium alone: the inoculated treatment also received fertilizer.[3]

A separate two-year Polish field study applied a foliar preparation containing *Methylobacterium symbioticum* (BlueN) to potato. Mean tuber yield was about 6.1% higher, and the authors reported increased tuber dry matter, total nitrogen, and nitrogen removed with harvested tubers, together with reduced nitrate concentration.[4] Again, the finding is about yield and tuber nitrogen, not a direct assay of true protein. It gives us an alternative to a root-associated diazotroph and a pleasingly practical comparison against ordinary fertilization.

These precedents are useful precisely because they do not all say the same thing. AmA1 changes tuber composition more directly. TN09 and BlueN approach the problem through nutrient access and possible nutrient transfer. None licenses the claim that ten percent more **edible true protein** has already been achieved by a microbial route.

Following nitrogen through other storage organs

We then began asking what other plants store underground and who helps them do it. Sweet potato offers unusually direct evidence of endophytic nitrogen fixation: Ueda and Yano exposed plants to isotopically labeled nitrogen gas and detected labeled nitrogen in some bacterial cells using Raman spectroscopy.[5] This is an unusually concrete observation of capability inside the plant. It does not by itself tell us how much of the nitrogen reaches storage-root protein, but it moves the conversation from speculation to an observed process.

Cassava provides a different kind of evidence. Researchers isolated an endophytic *Curtobacterium* strain, A02, with nitrogenase activity; inoculated plants showed increased root biomass, reported as 17.6% above controls, along with changes in plant nitrogen.[6] Water yam produced a useful negative result. A Japanese research group assembled a five-member synthetic community from native nitrogen-fixing bacteria associated with *Dioscorea alata*. Their inoculation measurably reorganized the root and rhizosphere communities, yet did **not** significantly improve plant growth or nitrogen content in the reported experiment.[7] The microbes arrived; the hoped-for agronomic benefit did not. Colonization, nitrogen fixation, host uptake, and storage-organ allocation cannot be treated as one event.

There may also be ways to improve the partnership rather than either partner. Work in rice has shown that increasing root-secreted apigenin can encourage diazotroph recruitment and biofilm formation under nitrogen limitation.[8] In a 2026 study, *Bacillus velezensis* BRI3 produced surfactin that stimulated *Stutzerimonas stutzeri* A1501 biofilms, with a 3.2-fold enhancement of nitrogen-fixation activity and 2.3-fold greater rhizosphere colonization in the reported system.[9] Neither demonstration establishes a potato treatment. Both illustrate possible interface functions: recruitment, attachment, persistence, and microbial cooperation. We are interested in whether useful pieces of these partnerships can be made available to potato without having to transplant an entire foreign ecology.

Mashua, and the limits of a tempting number

Mashua (*Tropaeolum tuberosum*) led us back into the Andes. A 2018 Ecuadorian study reported 18.25% protein for an accession called Poza Rondador, collected in Chimborazo, compared with 11.19% for a yellow accession. The researchers grew six accessions at Cevallos; Poza Rondador had a long, 282-day crop cycle.[10] The study used Dumas nitrogen analysis, but the published account does not adequately identify the conversion to protein or the analytical weight basis. Two later reviews even assign different fresh- versus dry-weight bases to the same reported value.[11] For now this is a reason to find the accession and its analytical records, not a reliable figure to place comfortably on the same scale as Phureja.

We have not found convincing direct evidence that mashua's reported protein concentration is caused by a nitrogen-fixing partner. Its close relative *Tropaeolum majus*, however, supports diverse root endophytes. In one Brazilian study, co-inoculation with *Bacillus thuringiensis* CAPE95 and *Paenibacillus polymyxa* CAPE238 increased early plant growth and changed root bacterial diversity. [12] That is evidence about a relative's microbial interface, not proof about mashua tubers. The distinction is part of what makes the comparison useful: different crops may contribute different portions of the problem.

Back to papa criolla

The Colombian Phureja result remains close to our original purpose because it involves a potato rather than an imported storage-organ strategy. A 2025 study measured nitrogen-use characteristics in 100 Phureja accessions and five commercial varieties under contrasting nitrogen supply and identified genomic associations with several nitrogen-use traits.[13] It gives us a second kind of observation alongside the earlier composition survey: not simply which tubers contain nitrogen, but which genotypes acquire, use, and distribute it differently.

What we do not yet possess is an authoritative crosswalk demonstrating that CCC-76 and the lower-protein comparison CCC-83 are represented in that later experiment, or accession-level nitrogen-use values for the pair. Nor do we have microbiome data specifically comparing them. A later study of the Universidad Nacional working collection grew CCC76 and other Phureja accessions in replicated field plots at Marengo.[15] This establishes field cultivation, but not CCC-76's complete sanitation or propagation history. If microbiological cleaning had occurred and a high-protein phenotype persisted under controlled, standardized communities, that would strengthen a host-genetic interpretation; field propagation also allows plants to acquire microbial partners again.

Several explanations remain open. CCC-76 may acquire nitrogen unusually well; it may direct a greater share to the tuber; it may favor protein synthesis over non-protein nitrogen; a particular microbiome may amplify these processes; or combinations may differ by soil and nitrogen availability. The ratio between two crude-protein percentages is not, by itself, a ratio between two rates of microbial nitrogen fixation.

What we have actually done

Our work to date has combined a literature and environmental scan, comparative evidence curation, and modest computational tests. The current *storage_organ_partnerships* registry was built from studies of potato, sweet potato, cassava, yam, and other storage-organ crops. Through run 33v26e it contained **21 records**, including ten manually curated search canaries, five newly promoted records from an already reviewed backlog, and six fresh promotions from the next search cycle. These are indexed **evidence cases**, not 21 independent confirmations of higher tuber protein. A grain-biological-control false positive has since been identified for scope repair.

One early calculation multiplied changes in tuber dry weight and tuber nitrogen concentration from the TN09 paper. This exposes how strongly the choice of outcome and comparator affects interpretation. We also explored uncertainty in the conversion from total tuber nitrogen to true protein. A previous sensitivity pass reported 100,000 draws and favorable results under its assumptions; however, its original executable and complete sampling specification have not been recovered, so we do **not** present it as a reproducible simulation finding. The reproducible quantity presently available is the simpler arithmetic proxy, with its limitations stated above.

It is also worth being exact about simulators. The biological workflow here is currently a comparison and evidence-integration instrument, not a mechanistic potato twin. Models such as DSSAT/SUBSTOR-Potato, OpenSimRoot, and CPlantBox have been considered as possible future components, but they have **not** been executed as one validated model of tuber protein allocation in this project. No new microbial inoculation experiment or true-protein assay has yet been conducted by Phasespace as part of this work.

A test that would teach us something either way

An attractive first study would compare high- and low-reported-protein Phureja accessions, if their identities and planting material can be confirmed, with a commercial control. Under matched high- and reduced-nitrogen conditions, the plants could receive either no added microbe, a well-characterized potato-native partner, or that partner with a separately tested recruitment or persistence treatment. Replication, soil histories, contamination control, and microbiome measurements would be essential. Isotope evidence could help distinguish nitrogen fixation from other microbial benefits.

The measurements would begin with marketable tuber yield, true protein in the harvested edible tissue, protein fractions and amino-acid composition, and the starch and food-quality measures that keep a potato a potato. Root colonization and microbial activity would be measured independently of host nitrogen assimilation. A positive result would reveal a productive pairing; a negative result might show that an apparently successful microbiome interface does not improve tuber allocation, as in the water-yam consortium. Either would narrow the space of useful designs.

We are particularly curious whether a high-protein Phureja line retains its phenotype when its microbial community is standardized, whether the same microbial partner benefits different potato genotypes unequally, and whether nitrogen added to a tuber becomes patatin or another useful protein fraction rather than simply enlarging the pool of non-protein nitrogen. The most immediate missing result is modestly stated: **true protein in harvested tubers, measured alongside yield, starch, nitrogen source, and microbial history**. That is where several of the paths we have followed might meet, or diverge again.

Sources and methodological notes

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Method note. Numbers attributed to published studies are reported as those authors present them. The 25.8–27.8% TN09 tuber-nitrogen proxy is a Phasespace multiplication of two published treatment contrasts, not a measured protein effect. Registry counts describe our literature workflow. Proposed experiments and simulators are not completed experiments. Bibliographic identities and the principal attributed results were independently checked against journal and publisher records on 14 October 2026.