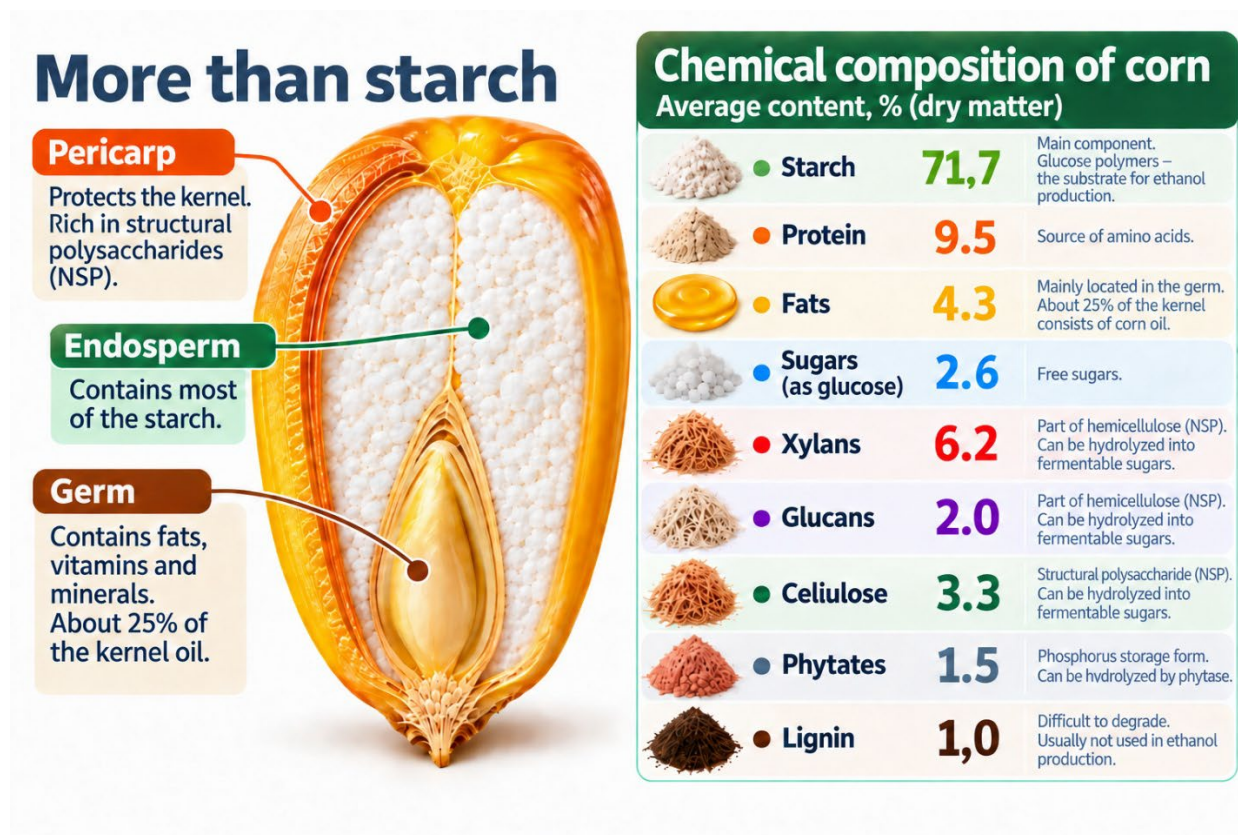


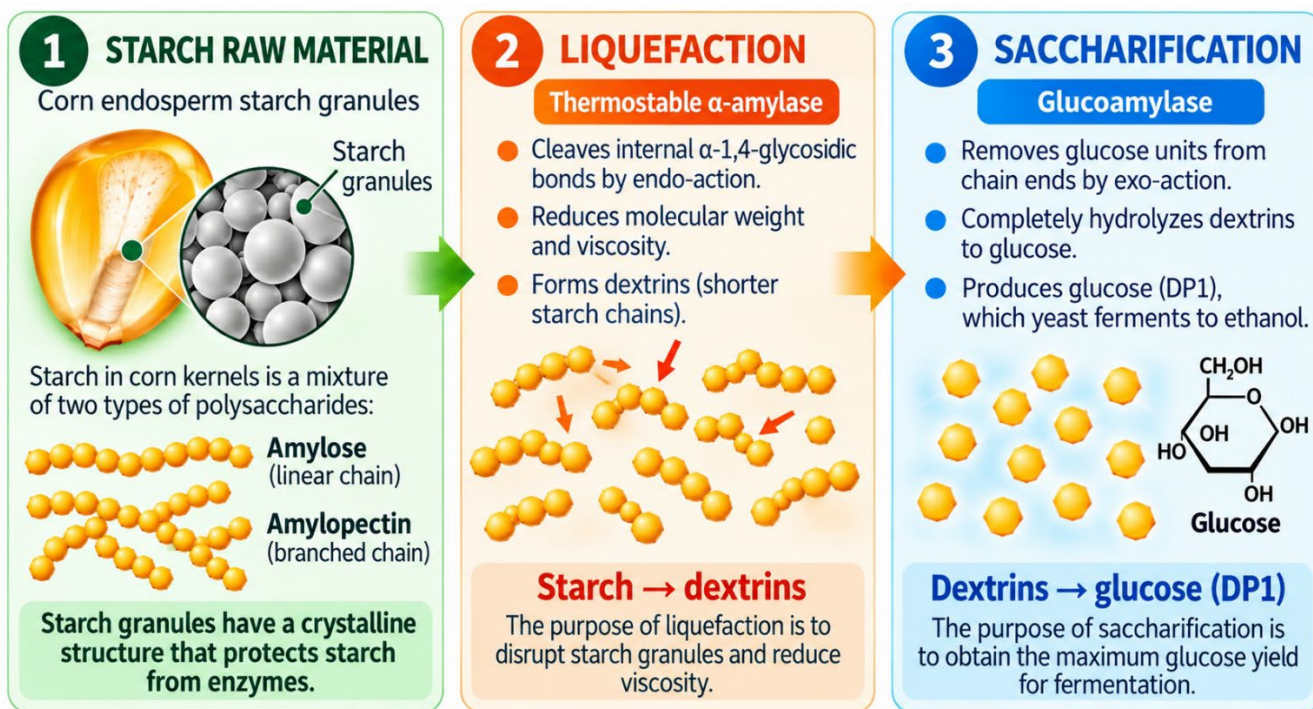
Maximizing grain value in ethanol production

Corn represents the largest share of raw-material costs in grain ethanol production. Therefore, the goal should be not only to convert starch into ethanol, but also to obtain as much value as possible from every tons of corn entering the plant. This requires understanding the structure and chemical composition of the whole corn kernel. The endosperm contains mainly starch and protein, with starch being the most important fraction for ethanol production. The pericarp protects the kernel and is rich in structural non-starch polysaccharides (NSP). The germ contains oil, vitamins and minerals. The key idea is simple: corn is much more than starch, and the ethanol producer has already paid for all these kernel components.



All these chemical components, except lignin, can potentially be utilized in the ethanol production process while also facilitating processing and reducing production costs, because some grain components create technological constraints because of their complex chemical structure and functional properties.

1. Starch is the main component of corn, accounting for about 72% of the kernel. It is a glucose polymer, and the amount of glucose is directly related to ethanol yield. Two principal enzymes are sufficient for the core conversion: alpha-amylase for starch liquefaction and glucoamylase for dextrin saccharification. These enzymes are fundamental to ethanol production and are well known throughout the industry.

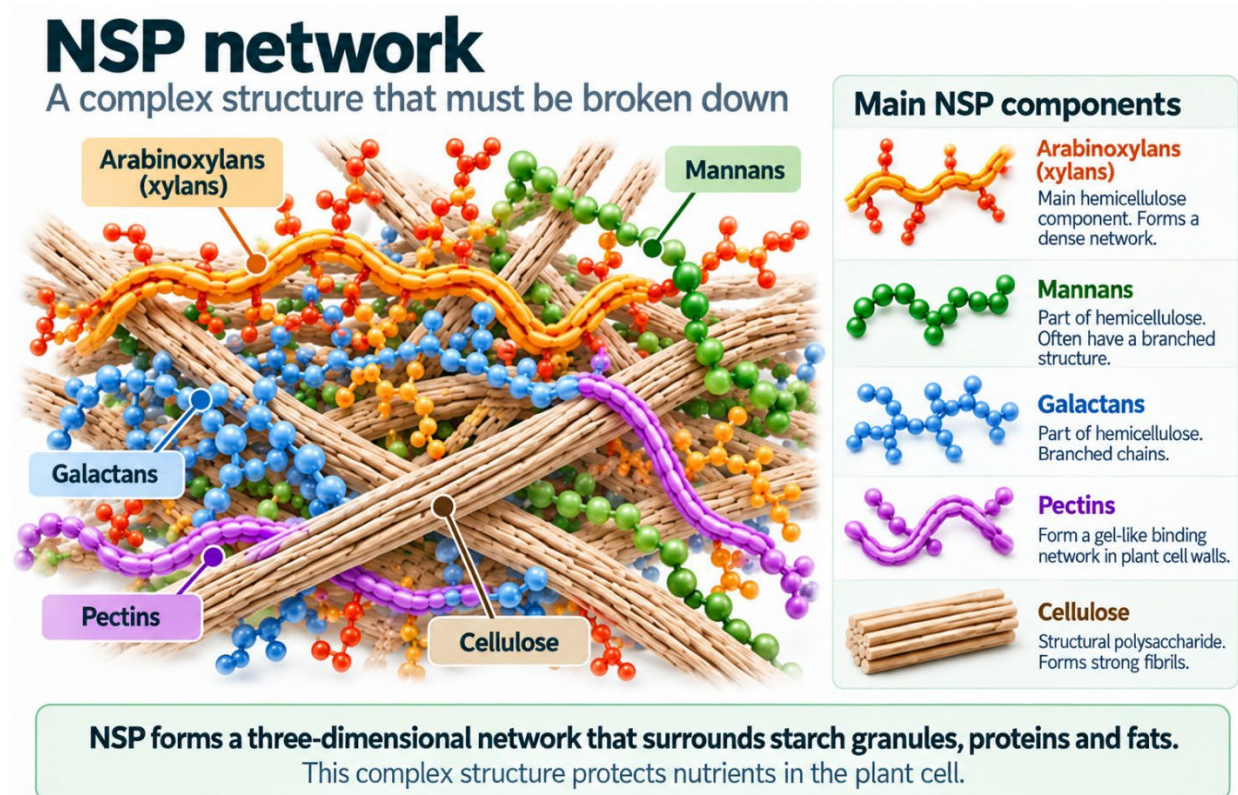


However, complete conversion of starch to glucose is not a simple process and is not always easy to achieve under industrial conditions. The natural purpose of any grain is to germinate and grow into a plant; therefore, the nutrients required for germination are securely embedded within complex grain structures. In the corn kernel, starch granules are embedded in a complex starch-protein endosperm matrix.



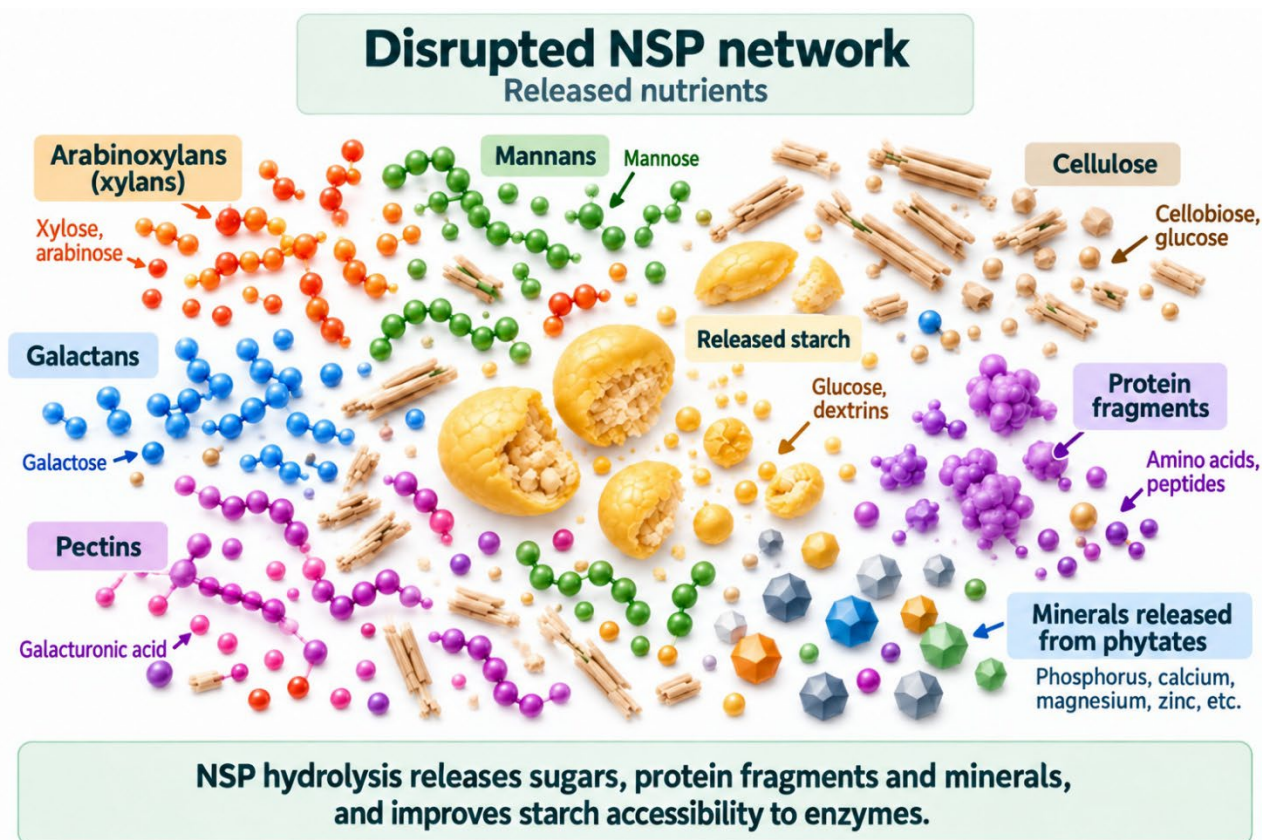
Starch granules in the corn endosperm matrix

This endosperm matrix is additionally covered and protected by a complex network of non-starch polysaccharides (NSP), consisting mainly of cellulose and hemicelluloses.

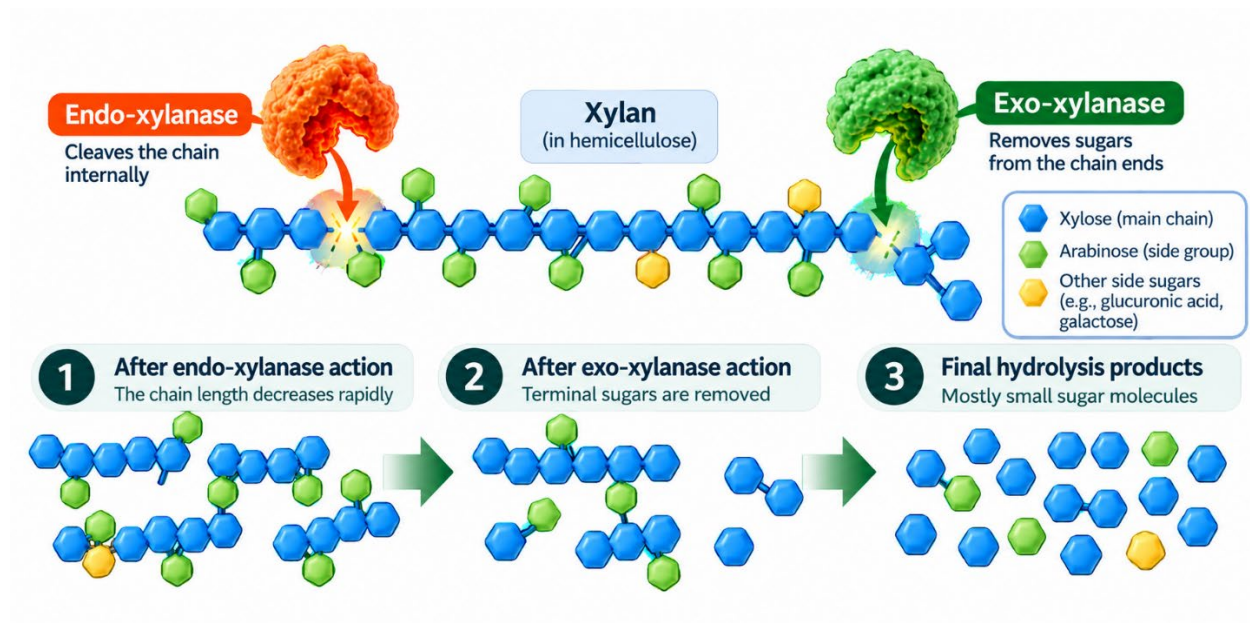


The NSP network limits enzyme access to starch and proteins and hinders the release of other kernel components, including oil. It binds large amounts of water and increases mash viscosity. High viscosity complicates mixing, pumping and other processing operations, increases energy and water consumption, and limits dry-matter concentration and therefore plant throughput. However, NSP are structurally complex polysaccharides composed of polymers containing different sugars, including xylans, beta-glucans, galactans, mannans, pectins and cellulose. With appropriate enzyme treatment, some of the sugars released from these polymers may become available to yeast and contribute to ethanol production. Effective NSP hydrolysis is therefore not only an important tool for overall process optimization, but also a potential source of additional fermentable sugars.

Effective disruption of the NSP network requires a broad set of enzymes acting synergistically. These enzymes must remain active under specific process conditions. Thermostable enzymes – alpha-amylase, phytase and NSP-degrading enzymes – are especially valuable already during liquefaction, when starch is hydrolyzed to dextrins, phytates are degraded and the NSP network is disrupted. As a result, mash viscosity decreases and other enzymes gain better access to starch and proteins.



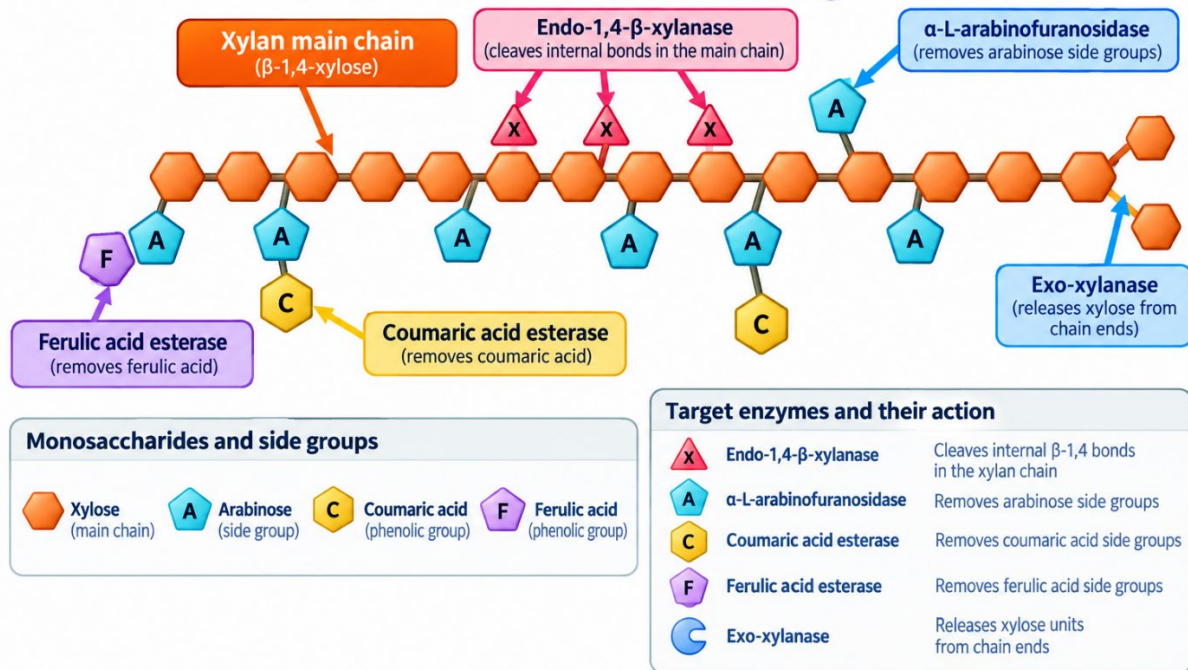
Hydrolysis of complex polysaccharides requires not only different enzymes, but specifically synergistic endo- and exo-acting enzymes. Endo-enzymes cleave polymer chains internally, rapidly reducing the degree of polymerization and viscosity. Exo-enzymes act from the ends of polymer chains and further degrade the resulting fragments into smaller carbohydrates. The combination of these activities enables deep and extensive NSP hydrolysis.



Non-starch polysaccharides (NSP) – cellulose and hemicelluloses – have very different three-dimensional structures and degrees of branching. This determines the need for different enzymes. It is necessary not only to cleave the main polymer backbone, but also to remove side groups. Different enzymes are required for each of these tasks.

Xylan structure

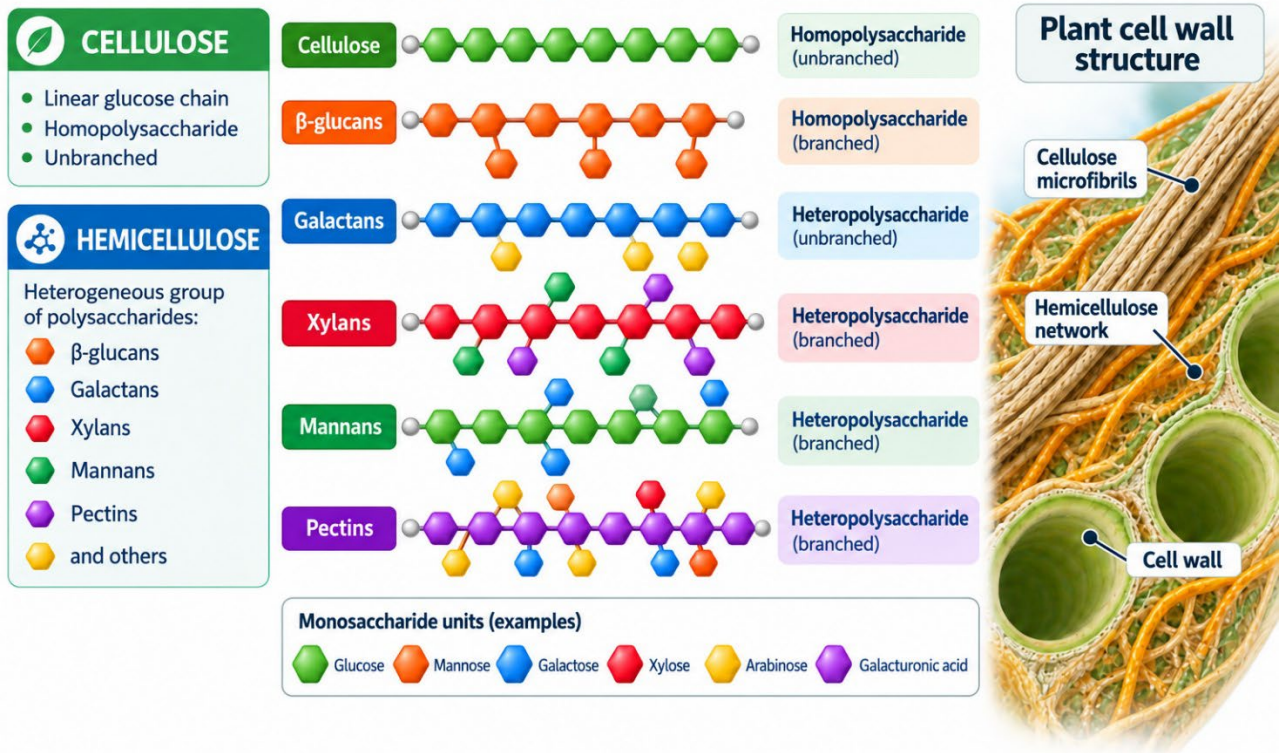
Main chain, side groups and the enzymes that degrade them



Non-starch polysaccharides (NSP) – cellulose and hemicelluloses – differ in their composition.

Cellulose is a linear glucose homopolysaccharide, whereas hemicelluloses are a heterogeneous group of polysaccharides that includes xylans, beta-glucans, galactans, mannans, pectins and others. Their backbones and side groups differ; therefore, complete hydrolysis of the NSP network requires many synergistically acting enzymes, not only xylanase, cellulase or beta-glucanase.

Plant cell wall polysaccharides (NSP)

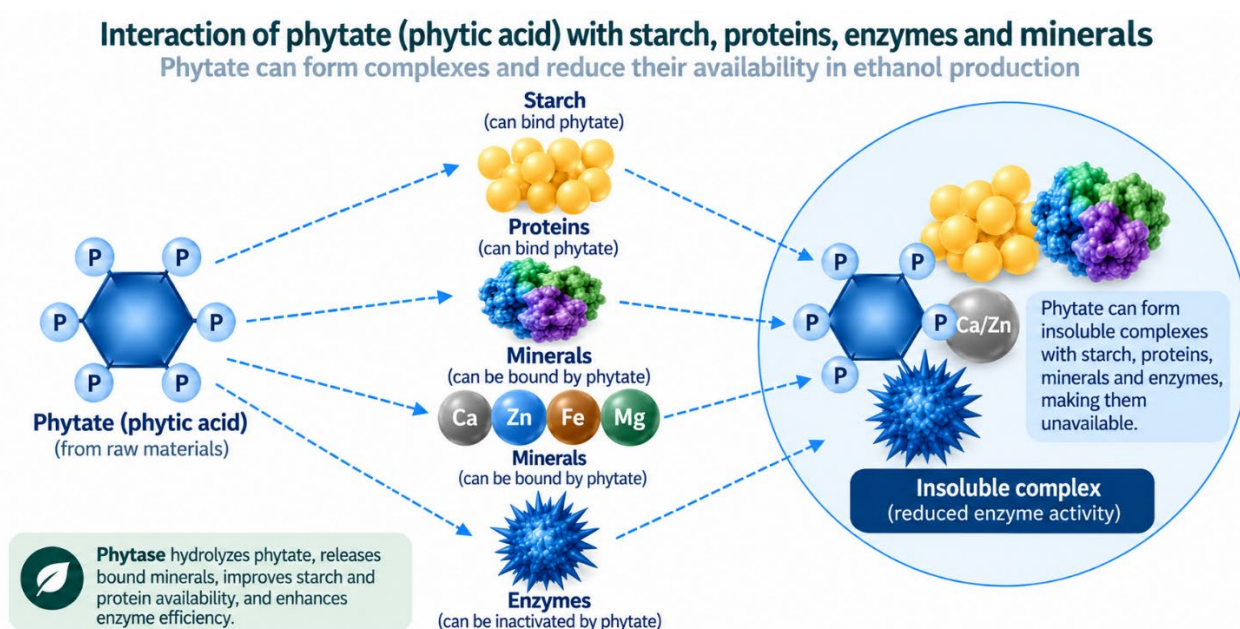


An effective NSP-degrading system therefore includes endo- and exo-cellulases, xylanases, beta-glucanases, mannanases, pectinases, galactosidases and other activities. Together they disrupt the NSP network, reduce water binding and viscosity, improve enzyme access to starch and proteins, and release additional sugars. These sugars are not equivalent to glucose, but some can be fermented to ethanol. Conventional *Saccharomyces cerevisiae* efficiently ferments glucose, whereas utilization of pentoses such as xylose and arabinose depends on the yeast strain and process conditions. Thus, some sugars released from NSP may make an additional contribution to ethanol formation, but the actual contribution must be evaluated according to the resulting sugar profile and the yeast used. Nevertheless, the primary benefit of NSP hydrolysis is improved accessibility of starch and proteins to hydrolytic enzymes, lower mash viscosity and greater overall process efficiency.

2. Proteins account for about 10% of the kernel and are another valuable corn component as well as part of the complex starch-protein matrix. Proteases hydrolyze proteins into smaller peptides and amino acids, weakening the protein fraction surrounding starch granules and improving starch accessibility to alpha-amylase and glucoamylase. Protein hydrolysis to amino acids also improves yeast nutrition by providing additional nitrogen. Protease therefore provides two benefits: improved yeast nutrition during fermentation and greater starch accessibility to amylolytic

enzymes. Fungal alpha-amylase can additionally hydrolyze residual dextrins during fermentation after the liquefaction stage.

3. Phytates are another important grain component. Their concentration in grain is relatively low – up to about 2% – but their interactions with other grain nutrients and enzymes are important. Phytates can interact with minerals, proteins, starch and enzymes, reducing their availability or effectiveness. Proper use of phytase in ethanol production hydrolyzes phytates, releases bound minerals and inorganic phosphate, and may reduce phytate-related process constraints. Lower phytate levels in DDGS may also increase the nutritional value of this co-product.



The Suntaq International Limited approach to ethanol production is focused not only on starch conversion, but also on broader utilization of grain components – transformation of starch, NSP, proteins and phytates, reduction of process constraints, and generation of greater value from every tonne of corn. A complete enzyme package is therefore proposed:

- **LiqueStar EX** – a thermostable alpha-amylase combined with a thermostable phytase. This combination enables efficient starch liquefaction and simultaneous initiation of phytate hydrolysis in a single process stage.
- **Fermentase THX** – a combination of glucoamylase and trehalase. Glucoamylase hydrolyzes dextrins to glucose, while trehalase hydrolyzes trehalose to glucose, making this carbohydrate fraction available for yeast fermentation. In the fermentation process, trehalose originates mainly not from corn starch but from the yeast itself. *Saccharomyces*

cerevisiae synthesizes trehalose from glucose as a reserve and protective carbohydrate. During ethanol fermentation, yeast is exposed to various stresses – high ethanol concentration, osmotic stress caused by high solids and sugar levels, temperature stress and nutrient limitation. Under these conditions, trehalose may accumulate in yeast cells. Thus, part of the glucose is not immediately converted to ethanol but is used for trehalose synthesis. Later, particularly when yeast cells die or lyse, some trehalose may enter the fermentation medium. This is where the trehalase activity in Fermentase THX becomes relevant.

- **Grainzyme NL** – a concentrated, thermostable NSP-degrading enzyme complex whose description lists numerous synergistically acting enzyme activities, including endo-xylanase, exo-xylanase, beta-glucanase, cellulase, mannanase, pectinase and galactosidase. Its purpose is to disrupt the complex structural polysaccharide (NSP) network, reduce mash viscosity, improve starch and protein accessibility, and release additional sugars. Its broad operating pH and temperature range allows the product to be applied at different process stages depending on specific production conditions.
- **SQzyme PSL** – an acid protease for protein hydrolysis.
- **SQzyme FAL** – a fungal alpha-amylase for dextrin control in the mash.

This complete enzyme system includes activities targeting starch, proteins, NSP, phytates and yeast breakdown products (trehalose), supporting a broader objective: not only producing ethanol from starch, but maximizing utilization of all major corn-kernel fractions.

Why is this important?

Grain is too valuable a raw material to be viewed only as a source of starch. The producer has already paid for the whole kernel, so it is important to consider how each fraction can contribute to ethanol yield, plant throughput, energy and water consumption, and co-product value.

An integrated enzyme strategy can open grain structures, improve the accessibility of starch and nutrients, reduce process constraints and help recover value that would otherwise remain inaccessible within the grain structure or pass into DDGS. The objective is not to use more enzymes. The objective is to obtain measurable technical and economic benefits from every ton of grain processed.

Not more enzymes, but more value from the same ton of grain. Maximizing grain utilization means greater process efficiency, better raw-material utilization and higher economic value from every ton of corn.