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THE BARLEY MUTANT HAPPY UNDER THE SUN 1 (HUS1): AN ADDITIONAL CONTRIBUTION TO PALE GREEN CROPS

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There is a need for ground-breaking technology to boost crop yield and its processing into materials of economic interest.

As well as grains, barley plants produce an almost equivalent amount of straw that one time was considered as a worthless product. The upward demand for renewable materials makes straw, and especially barley straw characterized by the largest content of carbohydrates among cereals, a valuable product for its potential conversion into biofuels and other eco-friendly products. One possible solution could be the realization of a dual-purpose crop ideotype, that produce likewise a large amount of grains and straw. Novel crops with enhanced photosynthesis and assimilation of green-house gasses, such as Carbon Dioxide (CO2) and Ozone (O3), and tailored

straw suitable for industrial manufacturing will be the foundation of a radical change. A way to increase the biomass production is tuning the photo-protection mechanism that control photosynthesis. Decreasing the light harvesting chlorophyll antenna size could lead to diminish the excess of light absorption avoiding photo-damage to the plant and boost energy flux for photochemistry. Pale-green leaves appear to perform better under high light conditions or high density cultivation and contribute to reflect a significantly larger proportion of incoming solar radiation, mitigating the local temperature.

The hus1 (happy under the sun 1) mutant has been isolated by forward genetics approach within the HorTILLUS chemical mutagenize population, searching for plants with improved photosynthetic performance. hus1 plants are characterised by showing a pale phenotype of the leaves, a reduced antenna size and an improved photosynthetic performance respect to Sebastian control plant. Segregation analysis performed on the F2 population obtained by crossing hus1 with Morex indicates that the hus1 phenotype is caused by a monogenic recessive allele. Using exome capture sequencing of DNA, the putative SNP mutation, that causes a premature stop codon, has been identified in the Arabidopsis thaliana homologous CHAOS gene (Chloroplast Signal Recognition Particle 43), that codifies a stromal chaperone that transfers the antenna proteins from the chloroplast stroma to the thylakoid membranes. Besides a detailed molecular and physiological characterization of the mutant grown under controlled greenhouse conditions, we show that the agronomic performance of hus1 plants, in terms of total biomass production and grain yield under standard field conditions, is comparable to that of control plants. These features make hus1 one of the most promising candidates for the EU-funded BEST-CROP project, which expects to improve barley productivity by 15-20% without modification of the harvest index, and to tailor barley straw to the needs of the circular bioeconomy.