**Pasta food: the DNA sequence reveals the secrets of a long evolution process from neolithic to modern breeders**

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**GENERAL INTRODUCTION** Durum wheat is one of the most important food crops for human consumption in the world, and it is used mainly for pasta production. The origin of this crop dates back about 10,000 years ago in the Fertile Crescent, the cradle of civilization between Euphrates and Tigris rivers, when domesticated emmer wheat was selected by humans from wild emmer wheat. Then, domesticated emmer wheat evolved, through breeder selection, to make the modern durum wheats that we grow today for making pasta. Although the first evidence of durum wheat dates to 7,000 years ago, it established as a prominent crop only 2,000 years ago. The evolution of wheat has been a human-driven process, from the neolithic farmers who selected domesticated plants much more productive and performing than wild plants, to modern breeders who release modern durum wheat cultivars. Studying modern durum wheat is as important as studying wild relatives. This way, beneficial alleles left behind in the breeding process, but useful to improve modern varieties, can be rescued. Moreover, structural features of the wild genome can help in understanding the evolution of this important crop.

**INTRODUCTION TO STUDY**

A recent study released the sequence of the durum wheat genome, provided a comparison with the genome of its wild emmer wheat ancestor, and discovered the evolutionary changes that have led to the development of modern durum wheat.

**METHODOLOGY & RESULTS & CONCLUSION** An international team of scientists has, for the first time, completed the high-quality genome of durum wheat for the cultivated variety “Svevo”. This was a very challenging task given that the genome sequence is very repetitive, is made of two separate but very similar genomes that can be difficult to tell apart, and is three times larger than the human genome (nearly ten Giga of DNA bases). The DNA sequence assembly is made up of chunks called scaffolds that have been assigned and ordered to represent all 14 durum wheat chromosomes. To know how many and which genes are expressed in durum wheat, the RNA was also sequenced; this led to the discovery of 66,559 high confidence genes. Identification of the genes was critical, as many of the traits important for crop yield and pasta quality are controlled by these genes. Equipped with the gene annotations and genome sequence, researchers and breeders now have powerful tools at their fingertips to improve durum wheat.

The genome sequence for durum wheat provides a common reference to understand and compare all past, present, and future durum wheat research. For example, previous research identified 2,191 regions in the durum wheat genome that were important for different wheat traits, such as grain yield and quality, and resistance to diseases. These regions were projected onto the genome, resulting in a meta-analysis for many traits of importance for durum wheat. The density and distribution of these regions matches the gene density distribution, and that is a powerful tool which will help to identify the genes responsible for these traits.

As another example, we used the reference genome to compare the genomes of nearly 2,000 wheat lines to identify regions and genes that may have changed throughout the evolutionary history of durum wheat. A deep analysis of genetic diversity and structure was performed for the large panel, comprised of lines belonging to different subspecies from wild emmer wheat to modern cultivated varieties of durum wheat. The analysis identified distinct DNA signatures that have been critical to the evolution and breeding of durum wheat, and which combination of genes is driving a particular signature. A loss of genomic diversity in durum wheat compared to its wild wheat relative was uncovered, and these areas of loss of diversity were mapped in order to precisely recover beneficial genes lost during centuries of breeding.

One gene that has been lost during domestication and breeding coded for a cadmium transporter. In most modern durum wheats, the cadmium transporter gene is defective. This causes cadmium to build up in the grain, particularly in soils that have lots of the metal present. Too much cadmium can be detrimental to human health, breeders are therefore working towards reducing cadmium in the grain. It turns out that the transporter for cadmium is functional in the wild emmer ancestor and became defective during domestication. By using the genome sequences as a guide, we were able to determine that the cadmium gene was clearly functional in wild emmer wheat, then the non-functional version of the gene spread into modern durum wheats. The cadmium transporter gene is now just the beginning of a new age of gene discovery; with the newly available genome sequences, we expect there to be a lot of new exciting research emerging that describes genes that can be used for durum wheat improvement.

**Original Article:**

Maccaferri M, Harris N S, Twardziok S O, Pasam R K, Gundlach H, Spannagl M, Ormanbekova D, Lux T, Prade V M, Milner S G, Himmelbach A, Mascher M, Bagnaresi P, Faccioli P, Cozzi P, Lauria M, Lazzari B, Stella A, Manconi A, Gnocchi M, Moscatelli M, Avni R, Deek J, Biyiklioglu S, Frascaroli E, Corneti S, Salvi S, Sonnante G, Desiderio F, Marè C, Crosatti C, Mica E, Özkan H, Kilian B, De Vita P, Marone D, Joukhadar R, Mazzucotelli E, Nigro D, Gadaleta A, Chao S, Faris J D, Melo A T O, Pumphrey M, Pecchioni N, Milanesi L, Wiebe K, Ens J, MacLachlan R P, Clarke J M , Sharpe A G , Koh C S, Liang K Y H, Taylor G J, Knox R, Budak H, Mastrangelo A M, Xu S S, Stein N, Hale I, Distelfeld A, Hayden M J, Tuberosa R, Walkowiak S, Mayer K F X, Ceriotti A, Pozniak C J and Cattivelli L. Durum wheat genome highlights past domestication signatures and future improvement targets. *Nature Genetics*. 2019; VOL 51 pp. 885–895. doi:10.1038/s41588-019-0381-3.