



Press release - 17 April 2020

## Oak genomics proves its worth

**Some 18 months after the full pedunculate oak genome sequence was published by a French consortium led by INRAE and CEA, some initial results based on this genomic resource have been written up in a series of articles in 16 April 2020 issue of the *New Phytologist*. These new results help clarify the oak's evolution, from the deep roots of its diversification through the more recent evolution of the European white oaks, and identify key genes involved in its adaptation to certain environments or resistance to pathogens.**

The keystones of forest ecosystems, trees – especially oaks- are also model organisms for determining the ecological and evolutionary processes responsible for plant diversification and adaptation to the environment.

Of the 10 articles published in the journal *New Phytologist*, seven were co-signed by INRAE researchers, including four based on cooperation between the UMR BIOGECO in Nouvelle-Aquitaine, France, and its long-standing partners such as Morton Arboretum in Chicago or the Genoscope at the CEA's François Jacob Institute of Biology.

Through those articles and the data generated by the CEA-Jacob Genoscope, researchers brought to light several issues:

- by reviewing the knowledge gained on the oak's early and recent evolution, they uncovered evolutionary mechanisms that allowed oaks to colonise the Northern Hemisphere (*Kremer et Hipp, 2020*);
- in view of recent discoveries made through genomics, they summarised, in an opinion article, the oak's traditional use as a symbol to represent its main features such as longevity, cohesiveness and robustness (*Leroy et al. 2020a*); they also proposed an oak conservation strategy designed to facilitate these sessile, long-lived organisms' adaptation to global change (*Cannon et Petit, 2020*).

Finally, publication of a series of research articles shines a positive light on the forward-looking review work being carried out on oak genome sequencing.

### **A closer look:**

#### **> 56 million years of oak evolution engraved in their genome**

By sequencing a portion of the genetic heritage of 260 oak species for an international consortium coordinated by Mortum Arboretum, INRAE researchers and their colleagues first showed that such species had diversified several different times throughout the continents of the Northern Hemisphere and that their rate of diversification increased in response to migration into new environments (Hipp *et al.* 2020). They also discovered that in terms of this diversification time-scale, there was no genome region that could be used to differentiate between those oak species.

#### **> When natural selection leaves its mark within the genome**

Researchers also pinpointed the genes that help trees adapt to their environment and those that bring about the particular intrinsic characteristics of each species.

To do that, they sequenced the genomes of 18 sessile oak populations sampled in contrasting environments, at different latitudes and altitudes in Europe (from southeastern France to northern Germany and from the foothills of the Pyrenees to stands at more than 1600 metres, and with regards to three other inter-fertile European white oak species (pedunculate, pubescent and Pyrenean). Their simulations supported the premise that these species had long been isolated from each other and that, following the last Ice Age, they exchanged a large amount of genetic information through hybridization, apart from a few specific genomic regions that could be described as "impermeable to inter-species gene flow".

It was those specific areas of the genome (and the genes that those areas contain) that researchers identified and described (Leroy *et al.* 2020b). In other genome regions, however, inter-species exchanges have been very intense, allowing the spread of certain genetic adaptations to particular environmental conditions. For example, some sessile oak populations found in environments that are very cold for the species have benefited from adaptations that originally came from the pedunculate oak, i.e. a species that is better adapted to such environmental conditions (Leroy *et al.* 2020c).

#### **> The genetic foundations of resistance to a major oak parasite**

INRAE scientists have also begun to decrypt the molecular basis of the pedunculate oak's resistance to the mildew pathogen that causes a chalky white coating on the leaves typically seen in the springtime.

Although this Ascomycetes fungus comes from Asia and has only been in Europe for about 100 years, certain oak genotypes display high levels of resistance to the disease even though they did not co-evolve with it. In particular, researchers identified the genes that code proteins involved in extracellular signalling, which sets off an immune response, in two genomic regions (Bartholomé *et al.* 2020).

This research only represents a sampling of the extensive work underway at the UMR BIOGECO in Bordeaux. For example, mention could be made of: (i) a study on the genetic determinants for biosynthesis of the specialised metabolites involved in oak defences against plant-eating insects, (ii) work on the molecular mechanisms involved in production of the compounds that contribute to the organoleptic qualities of wine that is aged in oak barrels, and (iii) the possibility of using DNA extracted from the ancient remains of dead wood (such as wood in the posts of the prehistoric lake dwellings found around Alpine lakes) so as to access the genome of trees that lived thousands of years ago. This research offers the prospect of gaining a better understanding of forest ecosystems' recent evolution and studying their ability to adapt to climate change.

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