



Molecular Plant Identification

Technical White Paper

Identifying Plants, Weeds and Trees

Plants, weeds and trees are traditionally identified based on various characteristics, such as the shape and size of leaves, flower colour, petal shape, the presence of nuts or berries, stem colour as well as a number of additional physiological features. In the case of many plant species, this requires many years of experience and can be extremely difficult during winter and early spring when plants have no foliage or are not flowering.

The identification of invasive plants such as Himalayan balsam is relatively easy during summer, due to its characteristic appearance and bright pink flowers. However, in order to eradicate this invasive species, control measures need to be carried out during the winter months and early spring before the seedpods explode and spread the weed further, this is also when Himalayan balsam is much more difficult to identify using morphological features alone.



Left: The characteristic flowers of Himalayan balsam. Right: Himalayan balsam is much more difficult to identify before flowering.

The Traditional Approach to Plant Identification

There are numerous plant identification books and keys available on the market, such as a dichotomous key which have a series of choices leading you to narrow down the species, as well as an increasing number of online tools which can aid identification.

Most existing identification keys offer limited choices and can be difficult to follow, for the untrained eye. Other problems arise where species are morphologically very similar, with small, discreet differences that would be difficult for anyone other than an expert botanist to identify based solely on morphology. An example of this is highlighted in the image of Japanese knotweed below, alongside a morphologically similar yet distinctly different species.



Can you identify which one of these images is Japanese knotweed?

The Requirement for Reliable Plant Identification

Invasive plants such as Japanese knotweed can cause problems for homeowners. Most mortgage providers will expect knotweed to be controlled by a professional which can cost thousands of pounds. Early identification could reduce the time and cost to eradicate this invasive weed. Other problems arise with different invasive species, for example water primrose. This weed, although currently only established in a few areas of England and Wales, has the potential, if allowed to spread, to block waterways, cause flooding and force out native species. Current programmes to eradicate this invasive species rely heavily on people reporting sightings of this weed, however it may be hard to identify for most of the public.

Protected, rare species hold extreme importance for biodiversity. Many plants and insects co-evolve and rely on each other for survival. The eradication of one can lead to the decline of the other and have negative knock-on effects for other species within its habitat. In the U.K, many plant species are listed as vulnerable or threatened and are protected under the wildlife and countryside act 1981. At SureScreen Scientifics, using molecular identification methods we have successfully identified the extremely rare lizard orchid from a section of the leaf, leaving the plant intact.



Lizard orchid.

The Molecular Approach to Plant Identification

The most common gene used for species identification of mammals, including our bat dropping identification service, is the mitochondrial Cytochrome Oxidase I gene (COI). This gene in plants, however, has a low evolutionary rate making it unsuitable for plant identification. Phylogenetic studies have shown that the internal transcribed spacer (ITS) region of the nuclear ribosomal cistron is successful in the identification of most flowering and non-flowering plants. Despite the difference in target genes, the process is similar to mammal identification using molecular methods.

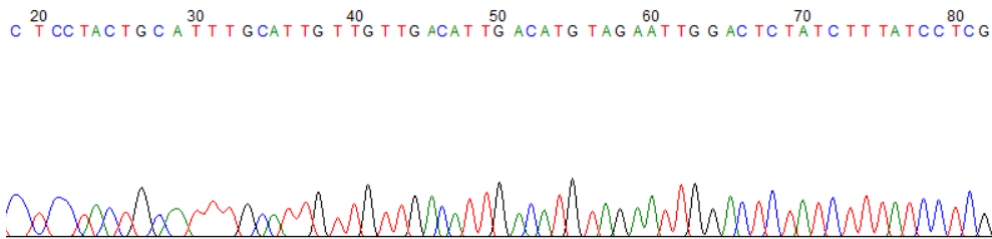


DNA Extraction, PCR and Sequencing

At SureScreen Scientifics, we have developed and refined a DNA based method for the identification of a wide range of plants using small amounts of fresh plant tissue.

To identify a plant using molecular methods, DNA needs to be extracted from the plant tissue (leaves, roots etc.). DNA extraction from plant tissue requires a number of steps, first the tissue must be broken down using bead beating technology, then a series of solutions are added, which help remove unnecessary parts of the plant and inhibitory molecules, resulting in pure DNA that is ready to analyse. Additional steps and alterations are used when extracting DNA from plants high in polyphenolic compounds such as pine needles and grape leaves and with plants which are protected by a tough external layer.

Polymerase chain reaction (PCR) is then performed by using molecular markers, known as primers, which specifically target the area of interest. A series of heating and cooling cycles amplifies the DNA of the majority of plant species. In some cases, this first step is not always successful due to high genetic variation in some species of plant – to combat this we have a range of alternative primers which can be used to enable successful amplification of plant DNA. Amplified DNA can then be genetically sequenced, resulting in a species-specific sequence of DNA bases. This sequence is compared with internal, national and international plant DNA reference databases and assigned a likelihood match to the species which is most genetically similar to the sequence of the sample.



DNA sequence from the leaf of a Himalayan cedar tree.

Sample collection

For successful and accurate identification, it is important that care is taken to ensure the best sample material is provided for analysis.

During the development of this service we tested our methodology on various parts of species of flowering and non-flowering plants. In all species DNA was successfully obtained from leaves with the flowers also yielding a sufficient quantity of DNA for a positive identification, however twigs and bark were for the most part less reliable due to their age and tough coating. Making it difficult to obtain DNA using conventional approaches. For our plant DNA identification service, we recommend the collection of fresh leaves, shoot tips, roots and flowers. It is important that samples are fresh due to the presence of fungal pathogens which may grow on dead plant material, so it is essential to send samples into the laboratory as soon as possible, or to freeze them immediately if you are intending to send samples in as a batch.

We would recommend therefore, young leaves in spring and summer for identification of flowering and non-flowering plants. Winter identification of invasive species such as Japanese knotweed can be carried out using parts of the root. Fresh samples should be placed in a small sealed bag or suitable container and sent to us as soon as possible to avoid degradation.

Case Studies

Below are a few examples of the species tested and the results we achieved during the development of our plant identification service.

Can you identify this tree?



The landowner had previously thought this tree was cedar of Lebanon, however as part of our plant identification research we discovered it was Himalayan cedar with a 98.8% sequence similarity. These results were from a leaf sample, we also attempted extraction from part of a twig with no results.

Identification of artificial or naturally hybridized plants is difficult. We had mixed results with Fuchsia and Buddleia, however we can provide the closest matches which may help with identification alongside other methods. Both leaves and flowers worked well with these plants.



Left: Buddleia. Right: Fuchsia.

Our process was highly successful in identifying Japanese knotweed both from leaves and part of the root. This may help with spring and winter identification of invasive species.



Left: Japanese Knotweed in spring. Right: Japanese Knotweed in winter.

eDNA@surescreen.com

(+44) 0 1332 292003

surescreenscientifics.com

