

Constructive Approaches to Intellectual Property Complexity in Today's Agricultural Technology World

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Abstract Essential to progress in plant biotechnology for deliverable applications, patent and patent application data must be transparent in order to determine where there is whitespace for innovation. Furthermore, mechanisms to protect the capability to use and improve innovation are regarded as critical because uncertainty about intellectual property can be a barrier to investment that can bring innovations to delivery.

Informatics trends and international trade laws are making it increasingly possible and indeed urgent to make patent data from multiple countries side-by-side available for searching in order to determine freedom to operate (Connett-Porceddu *et al.* 2005). Although only a few databases such as the *Patent Lens* allow this to be done cost-free for multiple jurisdictions, it is useful to scientists to be able to do full-text searches of the patent literature, (Nature Biotech 2006). While some inventors also author journal articles on their inventions, many do not, and those that do often disclose information in patent applications different from what is submitted to journals. In particular this is because a requirement for patentability is that enabling description be provided, regardless of the number of pages in the publication. Furthermore, the patent literature is more likely to contain the subset of technologies considered to have commercial value, because the maintenance of a patent in force, which is a commercial right, requires payment of fees over time.

Although the technology to do sophisticated searches of biological sequences has been developed and improved over many years (a key reference, for example, is Altschul *et al.* 1990), ironically, some of the most difficult patent information to obtain has been on patenting of biological sequences. Many jurisdictions such as China (and the USA collect in electronic form sequences submitted for patent applications, but they had not been delineated as such in international searchable databases such as Genbank (Jensen and Murray, 2005). CAMBIA's Patent Lens team has created open source software tools to collate and search biological sequences in patent applications and patent documents, and has been using these to analyse the complexities in the intense patent landscape covering the rice (*Oryza sativa*) and *Arabidopsis* genomes (Connett-Porceddu *et al.* 2006). Large segments of each genome are covered in single patent applications with prospective claims covering the genomes of many related crop species.

Biotechnological inventions are often interdependent, so multiple patented technologies can be required to make a single product, and the need for cross-licensing or barriers to obtain even one commercial license can greatly delay or shut out new innovation. A creative and strategic lateral approach to accelerate progress over some of these barriers is being made through Biological Open Source. Within CAMBIA's BiOS initiative we have developed technology transfer arrangements suited for patented technology but similar to those that have secured wider freedom to operate for the highly prosperous software businesses of IBM, Apache, Sun, Google, and thousands of small and medium enterprises. Illustrations abound as to why this approach may be fruitful to address some concerns about IP in plant biotechnology (Louwaars 2006).

Keywords *Oryza sativa*, *Arabidopsis thaliana*, patents, licenses, materials transfer agreements, enabling technology.

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