VI. Conclusion

Homology is a crucial concept in sequence-related biotechnological inventions. The homology language in a claim primarily seeks to defend against misappropriation by arbitrary modifications. However, this type of claim faces an insurmountable hurdle before the requirement of support, which currently requires an overwhelmingly high burden of experimental data.

The support requirement concerning homology is not standing alone in the patent law. Via the person skilled in the art, it can be aligned with the requirement of inventive step on the same coordinate axis of homology, when dealing with the same technical effect. Moreover, it should be distinguished from the requirement of sufficient disclosure due to the different knowledge those skilled persons have in these two requirements.

Novozymes implicates an unclaimable gap in biotechnology under the patent law, the formation of which comes from a very narrow allowance in the claimable scope of protection in contrast to a comparably large distance in establishing an inventive step. This gap significantly decoupled the skilled persons in the requirements of support and inventive step, with no relevant prior art or common and general knowledge to blame. Thus this gap may constitute a *de facto* discrimination towards biotechnology.

To restrict the unclaimable gap along homology, either reducing the bar for inventive step or relaxing the requirement for support can be opted for. But the former one is unfavourable and possibly leads to more problems. The latter one finds its grounds in that *Novozymes* implies a misapplication of sufficient disclosure standard onto the support test. The author opines that skilled persons in these two requirements have different knowledge relating to the sequence. The skilled person in the requirement of sufficient disclosure learns *ab initio* the first sequence-function correlation, which forms the most significant part of the patent's technical contributions. However, the skilled person in the support requirement has known the first sequence-function correlation, thus does not need to address the sufficiency *de novo*.

The skilled person in the requirement of support is thus to examine whether it is credible and without undue burden to reach a working variant within the claimed homology range. By pinpointing the claimed homology range as an indication of confidence, the author demonstrates that the

skilled person in the requirement of support can evaluate whether obtaining working variants is doubtful or needs undue burden. In line with the proposed approach to assessing the support requirement for homology, functional limitations must be duly acknowledged, not only to facilitate asserting the scope of protection but also to abalienate the rights on embraced sequences to the inventions bearing different inventive concepts.

The patent law safeguards the economic interests of inventors and promotes innovation and social development.¹⁵² Thus, the protection it confers to a patented invention should commensurate to the inventor's technical contribution. What a sequence-related invention contributes is the provision of a general sequence-function correlation. This technical contribution goes far beyond the identification of a particular sequence having a useful function. It also extends to the homologous sequences whose functions become expectable in light of the disclosed sequence-function correlation. Although it is not easy to quantify such contribution into a numerical homology value, the persons skilled in the art do have the ability to examine whether a given boundary is credible.

Lastly, the provision of protection should bear its genuine intention – to protect. When homology effects subsist, a patented invention exposes itself to numerous ways of misappropriation. No matter how forceful the patent is, homology could always be its *Achilles' heel*. If the patent law aims at building a strong shield to protect patentable inventions. Isn't homology the very place where the *Aegis* shall be?