How We Should Write Claims of Biological Sequences to Get Favors from Examiners and Judges

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In China's patent practice, people have been contending about ways of writing a claim of a biological sequence that could balance between interests of the patentee and the public. Patentees argue that a claim of a biological sequence, if written in a closed form, or limited to a specific sequence, would cover a narrow scope of protection, thereby leading to easy evasion by others. Therefore, that writing form does not do any good to the protection of patent rights. Examiners think otherwise: a claim of a biological sequence, if written in an open form or limited by defining identity or homology, would lack support from the specification due to the low predictability in the biological field. Here are two recent judicial decisions concerning the claims of biological sequences, one of which comes from the Supreme People's Court and relates to patent validity, and another comes from the Guangdong Higher People's Court and relates to patent infringement, both issued at the end of 2016.

On December 30, 2016, the Supreme People's Court made the (2016) Supreme Court Administrative Retrial Case Decision No. 85 (hereinafter "Decision No. 85") and affirmed Invalidation Decision No. 17956 made by the Patent Reexamination Board of the State Intellectual Property Office (hereinafter "the Board"). Decision No. 85 concerns a lawsuit between Jiangsu Boli Biological Products Co., Ltd. as the plaintiff and the Board as the defendant. The two parties debated over validity of a patent entitled *Thermostable Glucoamylase* and owned by Novozymes, a Denmark company. Decision No. 85 makes clear that the biological sequence-related claims 10-14 are supported by the specification. Here are claims 10-14 of the patent in question (claim 6 is also listed below for the sake of convenient reference).

"6. An isolated enzyme with glucoamylase activity, wherein the enzyme has an amino acid sequence that is at least 99% identical with the glucoamylase of SEQ ID NO: 7 and has an isoelectric point below 3.5 determined by isoelectric focusing.

10. The isolated enzyme according to any one of claims 6-9, wherein the enzyme is derived from a Talaromyces strain of a filamentous fungus, the filamentous fungus being a *T. emersonii* strain.

11. The enzyme according to claim 10, wherein the filamentous fungus is *T. emersonii* CBS 793.97.

12. A cloned DNA sequence encoding an enzyme exhibiting glucoamylase activity, which DNA sequence comprises:

(a) the glucoamylase encoding part of the DNA sequence shown in SEQ ID NO: 33, or

(b) the DNA sequence shown in positions 649-2724 in SEQ ID NO: 33 or its complementary strand.

13. The DNA sequence according to claim 12, wherein the DNA sequence is derived from a Talaromyces strain of a filamentous fungus, the filamentous fungus being a *T. emersonii* strain.

14. The DNA sequence according to claim 13, wherein the filamentous fungus is *T. emersonii* CBS 793.97."

As Decision No. 85 holds, since claim 12, to which claims 13 and 14 refer, has the word "comprises", the DNA sequence of claim 13 or 14 is not limited to sequence (a) or sequence (b) per se, but rather it also includes DNA sequences formed by extending either or both of the ends of sequences (a) and (b). However, claims 13 and 14 contain the functional feature "encoding an enzyme exhibiting glucoamylase activity"—which is recited in claim 12, so DNA sequences among those sequences formed by extending either or both of the ends of sequences (a) and (b) that do not have such encoding function are actually excluded from the scope of protection of claim 13 or 14. Besides, claims 13 and 14 specify origins of the DNA sequences as a *T. emersonii* strain and *T. emersonii* CBS 793.97, respectively, so there are only definite, and limited number of DNA sequences that comprise sequence (a) or (b) and are derived from those specific strains. The Supreme Court therefore holds that the

technical solutions of claims 13 and 14 are supported by the specification.

However, Decision No. 85 holds that claim 6 is not supported by the description because it covers all enzymes that are at least 99% identical with SEQ ID NO: 7 but it is impossible for a skilled person to know whether all the enzymes have glucoamylase activity. Claims 10 and 11, however, specify the enzyme with glucoamylase activity as being derived from specific strains, so they cover only a few definite sequences and are even likely to be limited to SEQ ID NO: 7 per se. The Supreme Court therefore holds that claims 10 and 11, with features of identicalness and function, are supported by the specification.

As is evident from the Supreme Court's decision, a claim of a biological sequence is patentable if it is written in a closed form (e.g., in the form of "shown in") and has a functional feature about identity/homology. That is, when a claim of a biological sequence is written in a closed form, a feature about identity/homology (e.g., the feature "99% identical with") can be added to the claim, thus enabling the biological sequence to be variable. Then, there is a question arising here when it comes to the determination of patent infringement: Does a claim of a biological sequence written in a closed form protect merely products of the sequence per se? Or does a product of a sequence consisting of the claimed biological sequence and other sequences at either or both of the ends of the claimed biological sequence fall within the claim's scope of protection? We seem to be able to find an answer from the (2016) Yue Civil Final Case Decision No. 1094 (hereinafter "Decision No. 1094"), made by Guangdong Higher People's Court on December 2, 2016.

Decision No. 1094 concerns a lawsuit where Statens Serum Institut accused Beijing Wantai Biological Pharmaceutical Co., Ltd. (hereinafter "Wantai") of infringing on its patent (numbered ZL96197467.2)—which relates to a diagnostic kit for detecting tuberculosis. The kit comprises: a. polypeptide Tb38-1, and b. a detecting agent (as claim 2 recites). The patent's specification discloses the specific amino acid sequence of Tb38-1, which is derived from the DNA sequence shown in SEQ ID NO: 46. In Wantai' allegedly infringed product, the antigen is CFT10, which has, at its N terminal, five more amino acid residues MAEMK, as compared with Tb38-1.

Decision No. 1094 holds that although the sequence of CFP10 has five more amino acid residues at its N terminal than the patented Tb38-1, CFP10's antigenic determinant is not located in that segment. Tb38-1's antigenic determinant is the same as that of CFP10, and located, compared with that of CFP10, at their overlapping regions. Considering the function of the peptides, CFP10 and Tb38-1 both serve to detect in vitro whether a human body has been infected by mycobacterium tuberculosis. Whether the detection succeeds depends on the structure of their antigenic determinants. Hence, CFP10 is equivalent to TB38-1.

In other words, although CFP10 has five more amino acid residues at its N terminal than Tb38-1, Wantai's product is still determined as infringing on the patent under the doctrine of equivalents because the five amino acid residues have no influence on the product's function. As is evident from Decision No. 1094, even if a claim of a biological sequence is written in a closed form, the doctrine of equivalents may still apply to it in an infringement lawsuit.

Based on the above two latest precedents, we suggest writing a claim of a biological sequence in the same way that the Supreme Court permitted in the Novozymes case:

(1) a sequence with "a function", "comprising" (i.e., in an open form) a specific sequence and "derived from a specific thing (e.g., from a specific strain) " (see claims 13 and 14 involved in Decision No. 85); or

(2) a sequence "shown in SEQ ID NO: XX" (i.e., in a closed form) with "a function", which is "derived from a specific thing (e.g., from a specific strain)" and has a certain degree of "identity/homology" with a sequence (see claims 10 and 11 involved in Decision No. 85).

In addition, the SIPO's *Guidelines for Patent Examination* clearly stipulates ways of describing a sequence—such as "substitution, deletion or addition"—which applicants can also use in writing a claim thereof. What's more, when a claim of a sequence is written in a "generalization" way as above, it

would be better to describe the sequence from the perspective of a mechanism by, for example, pointing out the conserved regions or conserved sites, and provide more examples or experimental data to verify, instead of merely predicting through a bioinformatics method, the mechanism and the experimental results. By this way, examiners would be more likely to believe that the technical solution concerning "identity/homology" is supported by the specification.

However, applicants need to adequately consider risks that a claim of a sequence written in a "generalization" way may bring about. The *Guidelines for Determination of Patent Infringement* newly issued by the Beijing Higher People's Court, specifically Articles 61-63, explicitly stipulates the doctrine of estoppel: if the patent applicant or patentee renounces to his claim to something by way of narrowing the claim or stating his opinions in order to remove a defect of substance that disenables the obtainment of a patent—e.g., the lack of support from the specification, then in a patent infringement lawsuit, the patentee is prohibited from reincorporating the renounced into the scope of protection when the doctrine of equivalents is used to determine whether the claim is infringed. That is, if the examiner believes that a claim written in a "generalization" way is not supported by the specification and the applicant amends the claim by, for example, rewriting it in a closed form rather than an open form, then in a subsequent infringement determination, the patentee might not be allowed, due to the doctrine of estoppel, to turn to other technical solutions in order to benefit from the doctrine of equivalents, as opposed to the circumstance in Decision No. 1094.

In comparison with the SIPO, the USPTO and EPO are more tolerant in terms of determining whether a claim is supported by the specification. Hence, it would be better for applicants to take into account the scale difference between different countries or regions' similar laws and draft the claims with different scopes that can protect the invention on different levels and in different scopes. That may help applicants get the maximum protection in different countries or regions.

To sum up, it is still a major issue faced with every patent agency and every enterprise that how various factors such as the market, applying strategy and examining polices are comprehensively considered to get a more stable and broader scope of protection. With the development of biotechnology, standards for

determining “the predictability in the biological field” might change accordingly to keep up with the situation, whether in examining practice or in judicial practice. For every patent agency and every enterprise, following the change is likewise important.