

## Examination of Patent Applications Containing Nucleotide Sequences

### I. Summary

The United States Patent and Trademark Office (Office) published an Official Gazette notice in November of 1996 providing a partial waiver of the requirements for restriction pursuant to 37 CFR 1.141 et seq. and for unity of invention determinations pursuant to 37 CFR 1.475 et seq. See Examination of Patent Applications Containing Nucleotide Sequences, 1192 Off. Gaz. Pat. Office 68 (Nov. 19, 1996) (1996 Notice). The 1996 Notice permitted examination of a reasonable number, normally up to ten, independent and distinct molecules described by their nucleotide sequence in a single patent application. The Office has reconsidered the policy set forth in the 1996 Notice in view of changes in the complexity of applications filed, the types of inventions claimed and the state of the prior art in this technology since that time. Because of these changes, the search and examination of up to ten molecules described by their nucleotide sequence often consumes a disproportionate amount of Office resources over that expended in 1996. Consequently, with this Notice the Office rescinds the partial waiver of 37 CFR 1.141 et seq. for restriction practice in national applications filed under 35 U.S.C. 111(a), and 37 CFR 1.475 et seq. for unity of invention determinations in both PCT international applications and the resulting national stage applications under 35 U.S.C. 371. This Notice is effective immediately and is applicable to all pending applications. Note, however, that supplemental restriction requirements will not be advanced in applications that have already received an action on their merits in the absence of extenuating circumstances.

### II. Background

In 1996, the Office held public hearings to address concerns relating to patent protection of nucleic acids described by their nucleotide sequences. The ease of using automated techniques for sequencing large numbers of nucleotides resulted in the filing of a growing number of patent applications, many of which recited thousands of individual nucleotide sequences. After the public hearings, the Office modified its restriction and unity of invention practice for the examination of patent applications that claim large numbers of polynucleotide molecules described by their nucleotide sequences in an effort to encourage and promote growth in this technology while taking into account the unprecedented search and examination challenges that such applications pose.

In the 1996 Notice, the Office partially waived the requirements of 37 CFR 1.141(a) and permitted applicant to claim and have examined in a single application a reasonable number, normally up to ten, independent and distinct inventions described by their nucleotide sequences. At that time, the Office determined that such a practice would not create an undue burden on the Office and would promote efficient, cost effective examination of these types of applications. The Office made a similar revision to practice for search and examination of applications filed under the PCT. Pursuant to the partial waiver of 37 CFR 1.475 et seq., up to ten nucleotide sequences would be searched

and/or examined in international applications or national stage applications filed under 35 U.S.C. 371; where applicants paid a fee for search and/or examination of at least one additional group (see 37 CFR 1.476(b)), up to four additional sequences would be searched and/or examined per group.

Patent applications that prompted the public hearings and the 1996 Notice often disclosed multiple partially characterized complementary DNA (cDNA) molecules, discovered by expressed sequence tag (EST) techniques, that were claimed and described by simple reference to a nucleotide sequence. At that time, and in many of those applications, little information was provided relating to function of the nucleic acid, nor was there significant description of the function or the information content (e.g., protein coding capacity) of the nucleic acid claimed. Consequently such claims were, in many instances, simple in format and narrow in scope. Often, the examination of narrowly drawn claims to EST-type nucleic acid molecules required little more than automated database searches. Further, the review and analysis of sequence search results could be accomplished within examination time constraints.

Since 1996, the technology has evolved and the types of nucleic acid sequence-based claims have become more diverse and complex. In 1996, polynucleotide molecules were often claimed by simple reference to a nucleotide sequence. Polynucleotide molecules are now often claimed in a single application in a variety of complex formats, some of which may embrace multiple inventions, such as by reference to: the amino acid sequence of the protein encoded; the ATCC number of a deposited plasmid containing the polynucleotide molecule; arbitrary laboratory designations; function of the nucleic acid alone or in combination with a partial linear nucleotide sequence; a genus described in terms of homology, percent identity, or hybridization; a genus (or subgenus) described by nucleic acid sequence with variable positions specified within the sequence listing; single nucleotide polymorphisms (SNPs); antisense; or interfering RNA. .

Advances over the past ten years in automated sequencing and polynucleotide characterization techniques have made such activities routine. The entire genome of several organisms, including humans, has been determined and deposited into nucleotide sequence databases. Consequently, patent applications claiming large numbers of lengthy polynucleotides, such as full-length open reading frames and entire genomes, have become more the norm rather than the exception. The advances in nucleic acid sequencing techniques have also lead to the exponential growth in the size of nucleic acid sequence databases and an increase in the number and complexity of such databases.

The GenBank<sup>®</sup> database in 1996 contained 651,972,984 nucleotides in 1,021,211 sequences. In 2000 the database contained 11,101,066,288 nucleotides in 10,106,023 sequences, about a seventeen-fold increase in the number of nucleotides and about a ten-fold increase in the number of sequences. In February 2006, the GenBank database contained 59,750,386,305 bases in 54,584,635 sequence records or about a ninety-one-fold increase in the number of nucleotides and about a fifty-four-fold increase in the number of sequences.

These factors are responsible for exacerbating the search and examination burden faced by the Office with respect to polynucleotide inventions claimed and described in currently filed applications. It now requires significantly more computational time to run individual nucleotide sequence searches for examination purposes than in 1996, and there is significantly more pertinent prior art to consider. In addition, it currently takes more Office resources to correlate the claimed polynucleotide with the polynucleotide as defined in the prior art because it is increasingly common for both patent applicants and prior art references to describe a polynucleotide molecule in different ways.

The foregoing illustrate that the evolution of the technology and current claim drafting practices are placing an ever-growing resource burden on the Office to search and examine patent applications disclosing and claiming nucleotide sequences. Rescission of the 1996 Notice is intended to enhance the Office's ability to provide a focused, thorough and quality examination of polynucleotide inventions, and to lead to consistency in the examination of polynucleotide molecules, regardless of the manner in which they are claimed, and equitable use of Office computational and examination resources. .

### **III. Examination Guidelines**

For National applications filed under 35 U.S.C. 111(a), polynucleotide inventions will be considered for restriction, rejoinder and examination practice in accordance with the standards set forth in MPEP Chapter 800 (except for MPEP 803.04 which is superceded by this Notice). Claims to polynucleotide molecules will be considered for independence, relatedness, distinction and burden as for claims to any other type of molecule.

For International applications and national stage filings of international applications under 35 U.S.C. 371, unity of invention determination will be made in view of PCT Rule 13.2, 37 CFR 1.475 and Chapter 10 of the ISPE Guidelines. Unity of invention will exist when the polynucleotide molecules, as claimed, share a general inventive concept, i.e., share a technical feature which makes a contribution over the prior art.

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