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EXAMINER
ZHENG, LI

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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

Ex parte KENNETH E. NARVA, HUARONG LI, CHAOXIAN GENG, KANIKA ARORA, BALAJI VEERAMANI, PREMCHAND GANDRA, SARAH WORDEN, ANDREAS VILCINSKAS, EILEEN KNORR, ELANE FISHILEVICH, MURUGESAN RANGASAMY, and MEGHAN FREY

Appeal 2018-006168
Application 14/577,811
Technology Center 1600

Before JEFFREY N. FREDMAN, DEBORAH KATZ, and JOHN G. NEW, *Administrative Patent Judges*.

KATZ, *Administrative Patent Judge*.

DECISION ON APPEAL

Appellants[1] seek our review, under 35 U.S.C. § 134(a), of the Examiner's decision to reject claims 1, 2, 4, 7, 8, 12, 16–18, 21, and 31–38 (Appeal Brief filed October 10, 2017 ("App. Br.") 2.)

We have jurisdiction under 35 U.S.C. § 6(b). We reverse.

Appellants' Specification provides nucleic acid molecules for the control of coleopteran pests, including for example, *Diabrotica virgifera* LeConte (western com rootworm), *Meligethes aeneus* Fabricius, (pollen beetle), and hemipteran pests, including for example, *Euschistus heros* (Fabr.) (Neotropical brown stink bug). (Specification dated December 19, 2014 ("Spec.") ¶ 22.) The nucleic acid molecules may be used for post-transcriptional inhibition of a gene-encoding Ras-opposite protein ("ROP"). (Spec. ¶ 23.) ROP contains a conserved domain of the Sec1 family of proteins, which are known to be involved in synaptic transmission and general secretion. (Spec. ¶ 242.) The nucleic acid molecule may include a double stranded RNA (dsRNA) that inhibits target gene expression through RNA interference. (Spec. ¶¶ 15, 145.)

Appellants' claim 1 recites:

> A double-stranded ribonucleic acid (dsRNA) molecule comprising a first polyribonucleotide consisting of at least 23 contiguous nucleotides of the polyribonucleotide encoded by a polynucleotide selected from the group consisting of SEQ ID NO:1, SEQ ID NO:115, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO: 131, and SEQ ID NO: 133,
>
> wherein the first polyribonucleotide is hybridized in the dsRNA molecule to a second polyribonucleotide that is the

[1] Appellants report that the real party in interest is Dow AgroSciences.

> complement or reverse complement of the first polyribonucleotide, and
>
> wherein delivery of the dsRNA molecule inhibits the expression of a target gene in a coleopteran or hemipteran insect selected from the group consisting of *Diabrotica virgifera*, *Euschistus heros*, and *Meligethes aeneus*.

(App. Br. 6–9.)

The Examiner rejects the claims under the judicially approved improper Markush grouping doctrine. (Final Office Action mailed May 10, 2017) ("Final Act.") 2.)

Analysis

"A Markush claim contains an 'improper Markush grouping' if: (1) The species of the Markush group do not share a 'single structural similarity,' or (2) the species do not share a common use." *Supplementary Examination Guidelines for Determining Compliance With 35 U.S.C. 112, and for Treatment of Related Issued in Patent Applications,* 76 FR 7162, 7166 (2011) ("Guidelines").

The Examiner finds "the nucleotide sequences listed in claim 1 have distinct structure." (Examiner's Answer mailed March 22, 2018 ("Ans.") 3.) According to the Examiner, a substantial structural feature should be identified at a nucleotide sequence level, but no conserved region among the nucleotide sequences listed in the Markush group was presented. (*See* Ans. 5–6.)

Appellants argue that the Examiner erred in rejecting the claims because the polynucleotides recited share substantial structural features. (*See* App. Br. 5.) Appellants argue that the recited polynucleotides each

encode a polyribonucleotide consisting of at least 23 contiguous nucleotides which hybridizes in dsRNA to a second complementary polyribonucleotide. (*See* App. Br. 5.) Appellants also argue that the recited polynucleotides encode ROP proteins of specified plant pests. (*See id.*) According to Appellants, "a single structural similarity does not require nucleotide sequence level granularity" and "the 'art recognized class' may simply be that of polyribonuc[l]eotides." (Reply Brief filed May 22, 2018 ("Reply Br.") 3, citing MPEP 706.03(y).)

As to a common use, Appellants argue that the claimed polynucleotide sequences are functionally identical for inhibiting the expression of target genes encoding the ROP proteins of plant pests. (Reply Br. 5.) Appellants argue further that the claimed sequences share a common utility such that the sequences can "be substituted one for the other, with the expectation that the same intended result would be achieved." (*Id.*, citing MPEP 706.03(y).)

We agree with Appellants that the claimed Markush group is not improper, as the claimed species share a single structural similarity and a common use. (*See* Guidelines). The nucleic acid sequences recited in the rejected claims belong to the same recognized chemical class of polyribonucleotides that are hybridized in dsRNA molecules and encode ROP proteins. While the individual sequences differ because they are drawn to ROP sequences of different insects (e.g., SEQ ID NO:1 and 115) or different portions of the ROP sequence (e.g., SEQ ID NO:120, 131, and 133), all of the sequences share the common use of silencing ROP proteins.

Accordingly, we conclude that the Examiner erred in rejecting claims 1, 2, 4, 7, 8, 12, 16–18, 21, and 31–38.

Conclusion

Upon consideration of the record and the reasons given, the rejection of claims 1, 2, 4, 7, 8, 12, 16–18, 21, and 31–38 is not sustained.

Therefore, we reverse the decision of the Examiner.

REVERSED