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DOW AGROSCIENCES LLC
9330 ZIONSVILLE RD
INDIANAPOLIS, IN 46268

| EXAMINER |
|---|
| STANKOVIC, BRATISLAV |

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UNITED STATES PATENT AND TRADEMARK OFFICE

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BEFORE THE PATENT TRIAL AND APPEAL BOARD

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*Ex parte* RAMESH BUYYARAPU, RUIHUA REN, MUSTAFA MCPHERSON, SIVA P. KUMPATLA, CHANDRA CHANNABASAVARAHYA, JOE SPINKS, and KELLY PARLIAMENT

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Appeal 2018-006665
Application 14/212,469
Technology Center 1600

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Before ULRIKE W. JENKS, TIMOTHY G. MAJORS, and MICHAEL A. VALEK, *Administrative Patent Judges*.

VALEK, *Administrative Patent Judge.*

DECISION ON APPEAL

Appellants[1] submit this appeal under 35 U.S.C. § 134(a) involving claims to methods for producing a cotton plant comprising reniform nematode (RN) resistance. The Examiner rejected the claims on the basis

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[1] Appellants identify the real party in interest as Dow AgroSciences, LLC. App. Br. 2. Herein we refer to the Final Office Action mailed April 12, 2017 ("Final Act."), Response After Final Action filed June 12, 2107 ("Response After Final"), Appeal Brief filed November 14, 2017 ("App. Br."), Examiner's Answer mailed April 12, 2018 ("Ans."), and Reply Brief filed June 12, 2018 ("Reply Br.").

that they contain an improper Markush grouping. We have jurisdiction under 35 U.S.C. § 6(b).

We REVERSE.

STATEMENT OF THE CASE

Claims 12, 16–19, 23, 33, 34, 36 and 37 are on appeal and can be found in the Claims Appendix of the Appeal Brief. Claims 16–19, 23, 33, 34, 36 and 37 all depend from claim 12. Claim 12 contains the Markush group noted in italics below:

> 12. A method for producing a cotton plant comprising reniform nematode (RN) resistance, the method comprising:
>
> crossing a first parental cotton plant comprising the trait of RN resistance with a second parental cotton plant that is sensitive to RN infection as compared to the first parental cotton plant, to produce progeny cotton plants, wherein the first parental cotton plant comprises at least one marker that is linked to the RN resistance trait, the marker being *selected from the group consisting of SEQ ID NOs:58-62*, and wherein the second parental cotton plant does not comprise the marker that is linked to the RN resistance trait;
>
> isolating genomic DNA from the progeny cotton plants;
>
> screening the genomic DNA of the progeny cotton plants for the presence of the marker that is linked to the RN resistance trait; and
>
> selecting a progeny cotton plant having genomic DNA comprising the marker that is linked to the RN resistance trait, thereby producing a cotton plant comprising RN resistance.

App. Br. 16 (emphasis added).

The claimed Markush group consists of five distinct nucleotide sequences listed as SEQ ID NOs:58-62. These sequences range from about 300–600 nucleotides in length and are referred to in the Specification as DASCTP_28910_164, DC7_56523319, DCTE1_240981_97, DCTE1_317966_63 and DASCTP_1656_527. Ans. 6–7; App. Br. 3. Like

all nucleotide sequences, the markers corresponding to SEQ ID NOs:58-62 share a common sugar–phosphate backbone. But, as Appellants acknowledge, their primary structure, *i.e.*, the "series of nucleobases" joined by that common sugar-phosphate backbone, is "different." App. Br. 11.

Examiner determined that the Markush grouping in claim 12 is improper and finally–rejected Appellants' claims on that basis. There are no other rejections before us on appeal.[2]

Accordingly, the issue is: Does the evidence of record support Examiner's determination that claim 12, and claims 16–19, 23, 33, 34, 36 and 37 by dependency, contain an improper Markush grouping?

*Analysis*

According to the MPEP, "[a] Markush claim contains an 'improper Markush grouping' if either: (1) the members of the Markush group do not share a 'single structural similarity' or (2) the members do not share a common use." MPEP § 706.03(y)(II). Moreover, where the members do not belong to a recognized physical, chemical or art-recognized class, "the common use must flow from the substantial structural feature." MPEP § 706.03(y)(II)(B). Whether a Markush group is proper depends on the particular facts at issue and "must be decided on a case-by-case basis." MPEP § 706.03(y)(IV).

Examiner finds that the markers in the five member Markush group here "do not share a substantial [structural] feature and/or common use that flows from the substantial structural feature," because "they have no conserved structure throughout the genus other than a phosphodiester

[2] Claim 35 was rejected for indefiniteness, but has since been cancelled. Response after Final 5.

backbone." Final Act. 3–4. Examiner also determines that they share no common use because they "have different effects on trait expression, as evidenced by the different LOD numbers and different % explanation." Ans. 11 (referring to Spec. ¶ 253, Table 2).

Appellants argue that, in addition to their common sugar-phosphate backbone, the claimed markers share a structural feature because they are all located in "close physical proximity to the RN resistance locus on chromosome 21." App. Br. 12. According to Appellants, this feature is "directly responsible for their shared function of being linked to RN resistance, because their proximity results in the co-segregation of the markers with the RN resistance." *Id.* Moreover, according to Appellants, the fact that the markers have different nucleotide sequences is, in fact, integral to their common use because it allows them to be used collectively in "common assays" to "provide[] a better result than their independent use." *Id.* at 13. Thus, Appellants urge that Examiner erred by applying "a hard rule that different nucleotide sequences cannot be presented" in a Markush group, rather than considering the structure of the claimed markers as a whole in light of the particular facts of this case. Reply 6–8.

On the record before us, we determine that Appellants have the better position. The MPEP makes clear that the propriety of a particular Markush grouping is a fact-specific inquiry that "must" be decided on a case-by-case basis. MPEP § 706.03(y)(IV); *see also In re Harnisch*, 631 F.2d 716, 722 (CCPA 1980) ("[W]e decide this and like cases on their facts on a case-by-case basis."). To the extent Examiner applied a bright-line rule that focused solely on the sequence differences without consideration of other structural similarities, that approach is incorrect. *See Harnish*, 631 F.2d at 722 ("[I]n

determining the propriety of a Markush grouping the compounds must be considered as wholes and not broken down into elements or other components."); *see also* MPEP § 706.03 (y)(IV). Accordingly, we look to whole of the structure in the context of the particular facts of the claimed invention to determine whether the nucleotide sequences in SEQ ID NOs:58-62 are properly grouped together.

Here, the record supports, and Examiner does not dispute, that the claimed markers were selected out of a larger set of identified markers and grouped together because these five sequences are particularly tightly linked to the RN resistance trait locus in cotton. *See* Spec. ¶ 251 ("The major QTL[3] region was concentrated at the distal end of the chromosome, between 0 and 32.63 cM, with a maximum LOD score of 13.93 observed between DASCTP_28910_164 and DASCTP_1656_527. This major QTL explained 29.8% of the variation in the resistance phenotype."). The Specification further teaches that all five of these markers are physically located proximate to each other in a particular region, *i.e.*, the distal end between about 29–32 cM in chromosome 21. *Id.* at ¶¶ 251; 253, Table 2. Accordingly, in addition to sharing a sugar-phosphate backbone, each member of the claimed Markush group shares an additional structural feature, *i.e.*, their specific physical proximity to each other and overall location within cotton genome.

The record further demonstrates that each of the five group members shares a common use that directly flows from this shared structural similarity. The Specification teaches that "[i]n general, the closer one marker is to another marker or gene . . . the more tightly they are linked."

[3] According to the Specification, "QTL" stands for "quantitative trait locus." Spec. ¶ 44.

Spec. ¶ 89. Thus, the physical location of the claimed sequences is at least partially responsible for their utility as markers to screen for RN resistance in cross-bred cotton plants. In addition, the Specification reports that the five members of this Markush group have the highest LOD and % Explanation values out of a much larger set of markers identified though Appellants' experiments. *Id.* ¶ 154, Table 2. That data supports Appellants' argument that these sequences are particularly suited for use as markers to be used, alone or in combination, to screen for RN resistance in the cross-bred progeny plants of the claimed method. *See* Reply 7.

We disagree with Examiner's argument that there is no common use because the Specification reports slightly different LOD and % Explanation values for each of the five markers in the claimed group. *See* Ans. 11. At most, the data evidences that some members of the Markush group may be slightly more indicative of RN resistance than others. That is a difference in degree, not kind. There is no evidence, nor does Examiner find, that the members of the claimed Markush group are not alternatively useful as markers for RN resistance. For all of these reasons, we determine that Examiner's rejection is not supported by the evidence of record and therefore reverse.

## SUMMARY

We reverse the rejection of claims 12, 16–19, 23, 33, 34, 36 and 37 on the basis that they contain an improper Markush group.

## REVERSED